

This Page Is Inserted by IFW Operations
and is not a part of the Official Record

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

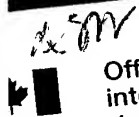
Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

IMAGES ARE BEST AVAILABLE COPY.

As rescanning documents *will not* correct images,
please do not report the images to the
Image Problem Mailbox.

THIS PAGE BLANK (USPTO)



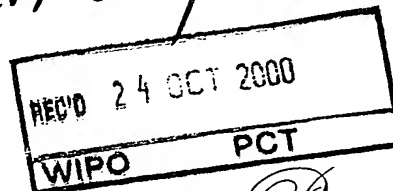
Office de la propriété
intellectuelle
du Canada

Un organisme
d'Industrie Canada

Canadian
Intellectual Property
Office

An Agency of
Industry Canada

CA 00 / 1150-



#2

CA 00 / 1150

⁴
*Bureau canadien
des brevets*
Certification

*Canadian Patent
Office*
Certification

La présente atteste que les documents
ci-joints, dont la liste figure ci-dessous,
sont des copies authentiques des docu-
ments déposés au Bureau des brevets.

This is to certify that the documents
attached hereto and identified below are
true copies of the documents on file in
the Patent Office.

Specification as originally filed, with Application for Patent Serial No: 2,307,010, on May
19, 2000, by **INFECTIO DIAGNOSTIC (I.D.I.) INC.**, assignee of Michel Bergeron,
Maurice Boissinot, Ann Huletsky, Christian Ménard, Marc Ouellette, François J. Picard and
Paul H. Roy, for "Highly Conserved Genes and Their Use to Generate Species-Specific,
Genus-Specific, Family-Specific, Group-Specific and Universal Nucleic Acid Probes and
Amplification Primers to Rapidly Detect and Identify Bacterial, Fungal and Parasitical
Pathogens From Clinical Specimens for Diagnosis".

PRIORITY DOCUMENT
SUBMITTED OR TRANSMITTED IN
COMPLIANCE WITH
RULE 17.1(a) OR (b)

S. H. H. H.
Agent certificateur/Certifying Officer

October 17, 2000

Date

OPIC



C

TITLE OF THE INVENTION

HIGHLY CONSERVED GENES AND THEIR USE TO GENERATE SPECIES-SPECIFIC, GENUS-SPECIFIC, FAMILY-SPECIFIC, GROUP-SPECIFIC AND UNIVERSAL NUCLEIC ACID PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY BACTERIAL, FUNGAL AND PARASITICAL PATHOGENS FROM CLINICAL SPECIMENS FOR DIAGNOSIS

BACKGROUND OF THE INVENTION

Classical methods for the identification of bacteria, fungi, and parasites.

Bacteria and fungi are classically identified by their ability to utilize different substrates as a source of carbon and nitrogen through the use of biochemical tests such as the API20E™ system (bioMérieux). For susceptibility testing, clinical microbiology laboratories use methods including disk diffusion, agar dilution and broth microdilution. Although identifications based on biochemical tests and antibacterial susceptibility tests are cost-effective, at least two days are required to obtain preliminary results due to the necessity of two successive overnight incubations to identify the bacteria from clinical specimens as well as to determine their susceptibility to antimicrobial agents. There are some commercially available automated systems (i.e. the MicroScan™ system from Dade Diagnostics Corp. and the Vitek™ system from bioMérieux) which use sophisticated and expensive apparatus for faster microbial identification and susceptibility testing (Stager and Davis, 1992, Clin. Microbiol. Rev. 5:302-327). These systems require shorter incubation periods, thereby allowing most bacterial identifications and susceptibility testing to be performed in less than 6 hours. Nevertheless, these faster systems always require the primary isolation of the bacteria or fungi as a pure culture, a process which takes at least 18 hours for a pure culture or 2 days for a mixed culture. So, the shortest time from sample reception to identification of the pathogen is around 24 hours. Moreover, fungi other than yeasts are often difficult or very slow to cultivate from clinical specimens. Identification must rely on labor-intensive techniques such as direct microscopic examination of the specimens and by direct and/or indirect immunological assays. Cultivation of most parasites is impractical in the clinical laboratory. Hence, microscopic examination of the specimen, a few immunological tests and clinical symptoms are often the only methods used for an identification that frequently remains presumptive.

The fastest bacterial identification system, the autoSCAN-Walk-Away™ system

(Dade Diagnostics Corp.) identifies both gram-negative and gram-positive bacterial species from standardized inoculum in as little as 2 hours and gives susceptibility patterns to most antibiotics in 5.5 hours. However, this system has a particularly high percentage (i.e. 3.3 to 40.5%) of non-conclusive identifications with bacterial species other than *Enterobacteriaceae* (Croizé J., 1995, Lett. Infectiol. 10:109-113; York *et al.*, 1992, J. Clin. Microbiol. 30:2903-2910). For *Enterobacteriaceae*, the percentage of non-conclusive identifications was 2.7 to 11.4%.

A wide variety of bacteria and fungi are routinely isolated and identified from clinical specimens in microbiology laboratories. Tables 1 and 2 give the incidence for the most commonly isolated bacterial and fungal pathogens from various types of clinical specimens. These pathogens are the main organisms associated with nosocomial and community-acquired human infections and are therefore considered the most clinically important.

15 *Clinical specimens tested in clinical microbiology laboratories*

Most clinical specimens received in clinical microbiology laboratories are urine and blood samples. At the microbiology laboratory of the Centre Hospitalier de l'Université Laval (CHUL), urine and blood account for approximately 55% and 30% of the specimens received, respectively (Table 3). The remaining 15% of clinical specimens comprise various biological fluids including sputum, pus, cerebrospinal fluid, synovial fluid, and others (Table 3). Infections of the urinary tract, the respiratory tract and the bloodstream are usually of bacterial etiology and require antimicrobial therapy. In fact, all clinical samples received in the clinical microbiology laboratory are tested routinely for the identification of bacteria and susceptibility testing.

Conventional pathogen identification from clinical specimens

30 *Urine specimens*

The search for pathogens in urine specimens is so preponderant in the routine microbiology laboratory that a myriad of tests have been developed. However, the gold standard remains the classical semi-quantitative plate culture method in which 1 μ L of urine is streaked on plates and incubated for 18-24 hours. Colonies are then counted to determine the total number of colony forming units (CFU) per liter of urine. A bacterial urinary tract infection (UTI) is normally associated with a bacterial count of 10^7 CFU/L or more in urine. However, infections with less than 10^7 CFU/L in urine are possible, particularly in patients with a high incidence of diseases or those catheterized (Stark and Maki, 1984, N. Engl. J. Med. 311:560-564).

Importantly, approximately 80% of urine specimens tested in clinical microbiology laboratories are considered negative (i.e. bacterial count of less than 10^7 CFU/L; Table 3). Urine specimens found positive by culture are further characterized using standard biochemical tests to identify the bacterial pathogen and are also tested for susceptibility to antibiotics. The biochemical and susceptibility testing normally require 18-24 hours of incubation.

Accurate and rapid urine screening methods for bacterial pathogens would allow a faster identification of negative specimens and a more efficient treatment and care management of patients. Several rapid identification methods (Uriscreen™, UTIscreen™, Flash Track™ DNA probes and others) have been compared to slower standard biochemical methods, which are based on culture of the bacterial pathogens. Although much faster, these rapid tests showed low sensitivities and poor specificities as well as a high number of false negative and false positive results (Koenig *et al.*, 1992, J. Clin. Microbiol. 30:342-345; Pezzlo *et al.*, 1992, J. Clin. Microbiol. 30:640-684).

Blood specimens

The blood specimens received in the microbiology laboratory are always submitted for culture. Blood culture systems may be manual, semi-automated or completely automated. The BACTEC™ system (from Becton Dickinson) and the BacTAlert™ system (from Organon Teknika Corporation) are the two most widely used automated blood culture systems. These systems incubate blood culture bottles under optimal conditions for bacterial growth. Bacterial growth is monitored continuously to detect early positives by using highly sensitive bacterial growth detectors. Once growth is detected, a Gram stain is performed directly from the blood culture and then used to inoculate nutrient agar plates. Subsequently, bacterial identification and susceptibility testing are carried out from isolated bacterial colonies with automated systems as described previously. The bottles are normally reported as negative if no growth is detected after an incubation of 6 to 7 days. Normally, the vast majority of blood cultures are reported negative. For example, the percentage of negative blood cultures at the microbiology laboratory of the CHUL for the period February 1994-January 1995 was 93.1% (Table 3).

Other clinical samples

Upon receipt by the clinical microbiology laboratory, all body fluids other than blood and urine that are from normally sterile sites (i.e. cerebrospinal, synovial, pleural, pericardial and others) are processed for direct microscopic examination and subsequent culture. Again, most clinical samples are negative for culture (Table 3). In these normally sterile sites, a test for the universal detection of bacteria, fungi and

parasites would be very useful.

Regarding clinical specimens which are not from sterile sites such as sputum or stool specimens, the laboratory diagnosis by culture is more problematic because of the contamination by the normal flora. The bacterial or fungal pathogens potentially associated with the infection are grown and separated from the colonizing microbes using selective methods and then identified as described previously. Of course, the universal detection of bacteria would not be useful for the diagnosis of bacterial infections at these non-sterile sites. On the other hand, DNA-based assays for species or genus or family or group detection and identification as well as for the detection of antibiotic resistance genes from these specimens would be very useful and would offer several advantages over classical identification and susceptibility testing methods.

DNA-based assays with any specimen

There is an obvious need for rapid and accurate diagnostic tests for the detection and identification of bacteria, fungi and parasites directly from clinical specimens. DNA-based technologies are rapid and accurate and offer a great potential to improve the diagnosis of infectious diseases (Persing *et al.*, 1993, Diagnostic Molecular Microbiology: Principles and Applications, American Society for Microbiology, Washington, D.C.; Bergeron and Ouellette, 1995, Infection 23:69-72; Bergeron and Ouellette, 1998, J Clin Microbiol. 36:2169-72). The DNA probes and amplification primers which are objects of the present invention are applicable for the detection and identification of bacteria, fungi, and parasites directly from any clinical specimen such as blood cultures, blood, urine, sputum, cerebrospinal fluid, pus, genital and gastro-intestinal tracts, skin or any other type of specimens (Table 3). The DNA-based tests proposed in this invention are superior in terms of both rapidity and accuracy to standard biochemical methods currently used for routine diagnosis from any clinical specimens in microbiology laboratories. Since these tests can be performed in one hour or less, they provide the clinician with new diagnostic tools which should contribute to a better management of patients with infectious diseases. Specimens from sources other than humans (e.g. other primates, birds, plants, mammals, farm animals, livestock, food products, environment such as water or soil, and others) may also be tested with these assays.

A high percentage of culture negative specimens

Among all the clinical specimens received for routine diagnosis, approximately 80% of urine specimens and even more (around 95%) for other types of normally sterile clinical specimens are negative for the presence of bacterial pathogens (Table 3). It would also be desirable, in addition to identify bacteria at the species or genus or family or group level in a given specimen, to screen out the high proportion of

negative clinical specimens with a test detecting the presence of any bacterium (i.e. universal bacterial detection). Such a screening test may be based on DNA amplification by PCR of a highly conserved genetic target found in all bacteria. Specimens negative for bacteria would not be amplified by this assay. On the other hand, those that are positive for any bacterium would give a positive amplification signal with this assay. Similarly, highly conserved genes of fungi and parasites could serve not only to identify particular species or genus or family or group but also to detect the presence of any fungi or parasite in the specimen.

10 *Towards the development of rapid DNA-based diagnostic tests*

A rapid diagnostic test should have a significant impact on the management of infections. DNA probe and DNA amplification technologies offer several advantages over conventional methods for the identification of pathogens and antibiotic resistance genes from clinical samples (Persing *et al.*, 1993, Diagnostic Molecular Microbiology: Principles and Applications, American Society for Microbiology, Washington, D.C.; Ehrlich and Greenberg, 1994, PCR-based Diagnostics in Infectious Disease, Blackwell Scientific Publications, Boston, MA). There is no need for culture of the pathogens, hence the organisms can be detected directly from clinical samples, thereby reducing the time associated with the isolation and identification of pathogens. Furthermore, DNA-based assays are more accurate for microbial identification than currently used phenotypic identification systems which are based on biochemical tests and/or microscopic examination. Commercially available DNA-based technologies are currently used in clinical microbiology laboratories, mainly for the detection and identification of fastidious bacterial pathogens such as *Mycobacterium tuberculosis*, *Chlamydia trachomatis*, *Neisseria gonorrhoeae* as well as for the detection of a variety of viruses (Podzorski and Persing, Molecular detection and identification of microorganisms, In: P. Murray *et al.*, 1995, Manual of Clinical Microbiology, ASM press, Washington D.C.). There are also other commercially available DNA-based assays which are used for culture confirmation assays.

Others have developed DNA-based tests for the detection and identification of bacterial pathogens which are objects of the present invention for example: *Staphylococcus* sp. (US patent serial no. 5,437,978), *Neisseria* sp. (US patent serial no. 5,162,199 and European patent serial no. 0,337,896,131) and *Listeria monocytogenes* (US patent serial nos. 5,389,513 and 5,089,386). However, the diagnostic tests described in these patents are based either on rRNA genes or on genetic targets different from those described in the present invention. To our knowledge there are only three patents published by others mentioning the use of any of the three targets described in the present invention for diagnostic purposes (PCT

international publication number WO92/03455, European patent publication number 0 133 671 B1, and European patent publication number 0 133 288 A2). WO92/03455 is focused on the inhibition of *Candida* species for therapeutic purposes. It describes antisense oligonucleotide probes hybridizing to *Candida* messenger RNA. Two of the numerous mRNA proposed as target are coding for translation elongation factor 1 (tef1) and the beta subunit of ATPase. DNA amplification or hybridization are not under the scope of their invention and although diagnostic use is briefly mentioned in the body of the application, no specific claim is made regarding diagnostics. In the main body of the text, EP 0 133 671 B1 describes the use of bacterial *tuf* sequence for diagnostics based on hybridization with bacterial RNA. To hybridize RNA, an oligonucleotide probe must be antisense. DNA amplification techniques require the use of both sense and antisense primers. Hence, claim number one from EP 0 133 671 B1 precludes PCR or other DNA-based amplification techniques. Furthermore, EP 0 133 671 B1 makes no specific claim on the use of *tuf* sequences for diagnostics; only ribosomal RNA sequences are claimed. Patent EP 0 133 288 A2 describes and claims the use of bacterial *tuf* sequence for diagnostics based on hybridization of a *tuf* probe with bacterial DNA. DNA amplification is not in the scope of EP 0 133 288 A2. Nowhere it is mentioned that multiple *tuf* probes could be used simultaneously. The sensitivity of the *tuf* hybridizations reported are, at 1×10^6 bacteria or 1-100 ng of DNA, much lower than those achievable by nucleic acid amplification technologies.

Although there are phenotypic identification methods which have been used for more than 125 years in clinical microbiology laboratories, these methods do not provide information fast enough to be useful in the initial management of patients. There is a need to increase the speed of the diagnosis of commonly encountered bacterial, fungal and parasitical infections. Besides being much faster, DNA-based diagnostic tests are more accurate than standard biochemical tests presently used for diagnosis because the microbial genotype (e.g. DNA level) is more stable than the phenotype (e.g. physiologic level).

Knowledge of the genomic sequences of bacterial, fungal and parasitical species continuously increases as testified by the number of sequences available from public databases such as GenBank. From the sequences readily available from those public databases, there is no indication therefrom as to their potential for diagnostic purposes. For determining good candidates for diagnostic purposes, one could select sequences for DNA-based assays for (i) the species-specific detection and identification of commonly encountered bacterial, fungal and parasitical pathogens, (ii) the genus-specific detection and identification of commonly encountered bacterial, fungal or parasitical pathogens, (iii) the family-specific detection and identification of commonly encountered bacterial, fungal or parasitical pathogens, (iv) the group-specific detection and identification of commonly encountered bacterial, fungal or parasitical pathogens, (v) the universal detection of bacterial,

5 fungal or parasitical pathogens, and/or (vi) the specific detection and identification of antibiotic resistance genes, and/or (vii) the specific detection and identification of bacterial toxin genes. All of the above types of DNA-based assays may be performed directly from any type of clinical specimens or from a microbial culture.

10 In our co-pending U.S. patent 6,001,564 and WO98/20157 patent application, we described DNA sequences suitable for (i) the species-specific detection and identification of clinically important bacterial pathogens, (ii) the universal detection of bacteria, and (iii) the detection of antibiotic resistance genes.

15 The latter co-pending application described proprietary *tuf* DNA sequences as well as *tuf* sequences selected from public databases (in both cases, fragments of at least 100 base pairs), as well as oligonucleotide probes and amplification primers derived from these sequences. All the nucleic acid sequences described in that patent application can enter in the composition of diagnostic kits or product and methods capable of a) detecting the presence of bacteria, fungi and parasites b) detecting specifically at the species, genus, family or group levels, the presence of bacteria, 20 fungi and parasites and antibiotic resistance genes associated with these pathogens. However, these methods and kits need to be improved, since the ideal kit and method should be capable of diagnosing close to 100% of microbial pathogens and associated antibiotic resistance genes and toxins genes. For example, infections caused by *Enterococcus faecium* have become a clinical problem because of its resistance to many antibiotics. Both the detection of these bacteria and the evaluation of their resistance profiles are desirable. Besides that, novel DNA sequences (probes and primers) capable of recognizing the same and other microbial pathogens or the same and additional antibiotic resistance genes are also desirable to aim at detecting more 25 target genes and complement our earlier patent applications.

30 The present invention improves the co-pending application by disclosing new proprietary *tuf* sequences as well as describing new ways to obtain *tuf* sequences. In addition we disclose new proprietary *atpD* and *recA* sequences. In addition, new uses of *tuf*, *atpD* and *recA* DNA sequences selected from public databases (Table 11) are disclosed.

Highly conserved genes for identification and diagnostics

35 Highly conserved genes are useful for identification of microorganisms. For bacteria, the most studied genes for identification of microorganisms are the universally conserved ribosomal RNA genes (rRNA). Among those, the principal targets used for identification purposes are the small subunit (SSU) ribosomal 16S rRNA genes (in prokaryotes) and 18S rRNA genes (in eukaryotes) (Relman and Persing, Genotyping Methods for Microbial Identification, *In*: D.H. Persing, 1996, PCR Protocols for Emerging Infectious Diseases, ASM Press, Washington D.C.). The 40 rRNA genes are also the most commonly used targets for universal identification of bacteria (Chen *et al.*, 1988, FEMS Microbiol. Lett. 57:19-24; McCabe *et al.*, 1999, Mol. Genet. Metabol. 66:205-211) and fungi (Van Burik *et al.*, 1998, J. Clin. Microbiol. 36:1169-1175).

However, it may be difficult to discriminate between closely related species when using primers derived from the 16S rRNA. In some instances, 16S rRNA sequence identity may not be sufficient to guarantee species identity (Fox *et al.*, 1992, Int. J. Syst. Bacteriol. 42:166-170) and it has been shown that inter-operon sequence variation as well as strain to strain variation could undermine the application of 16S rRNA for identification purposes (Clayton *et al.*, 1995, Int. J. Syst. Bacteriol. 45:595-599).

STATEMENT OF THE INVENTION

It is an object of the present invention to provide a specific, ubiquitous and sensitive method using probes and/or amplification primers for determining the presence and/or amount of nucleic acids:

- from any bacterial, fungal or parasitical species in any sample suspected of containing said nucleic acids, and optionally,
- from specific microbial species or genera selected from the group consisting of the species or genera listed in Table 4
- from an antibiotic resistance gene selected from the group consisting of the genes listed in Table 5, and optionally,
- from a toxin gene selected from the group consisting of the genes listed in Table 6,

wherein each of said nucleic acids or a variant or part thereof comprises a selected target region hybridizable with said probe or primers;

said method comprising the steps of contacting said sample with said probes or primers and detecting the presence and/or amount of hybridized probes or amplified products as an indication of the presence and/or amount of said any microbial species, specific microbial species or genus or family or group and antibiotic resistance gene and/or toxin gene.

In a specific embodiment, a similar method directed to each specific microbial species or genus or family or group detection and identification, antibiotic resistance genes detection, toxin genes detection, and universal bacterial detection, separately, is provided.

In a more specific embodiment, the method makes use of DNA fragments from conserved genes (proprietary sequences and sequences obtained from public databases), selected for their capacity to sensitively, specifically and ubiquitously detect the targeted bacterial, fungal or parasitical nucleic acids.

In a particularly preferred embodiment, oligonucleotides of at least 12

nucleotides in length have been derived from the longer DNA fragments, and are used in the present method as probes or amplification primers.

In another particularly preferred embodiment, oligonucleotides primers and probes of at least 12 nucleotides in length are designed for their specificity and ubiquity based upon analysis of our databases of *tuf*, *atpD* and *recA* sequences. These databases are generated using both proprietary and public sequence information. Altogether, these databases form a sequence repertory useful for the design of primers and probes for the detection and identification of bacterial, fungal and parasitical microorganisms. The repertory can also be subdivided into subrepertories for analysis leading to the design of primers and probes.

The *tuf*, *atpD* and *recA* sequences databases as a product to assist the design of oligonucleotides primers and probes for the detection and identification of bacterial, fungal and parasitical microorganisms are also an object of this invention.

The proprietary oligonucleotides (probes and primers) are also another object of the invention.

Diagnostic kits comprising probes or amplification primers for the detection of a microbial species or genus or family or group selected from the following list consisting of *Bordetella* sp., *Candida albicans*, *Candida dubliniensis*, *Candida* sp., *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium* sp., *Corynebacterium* sp., *Cryptosporidium parvum*, *Entamoeba* sp., *Enterobacteriaceae* group, *Enterococcus casseliflavus-flavescens-gallinarum* group, *Enterococcus faecalis*, *Enterococcus faecium*, *Enterococcus gallinarum*, *Enterococcus* sp., *Escherichia coli*, *Giardia* sp., *Haemophilus influenzae*, *Trypanosomatidae* family, *Leishmania* sp., *Mycobacteriaceae* family, *Neisseria gonorrhoeae*, platelets contaminants group (see Table 14), *Pseudomonads* group, *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Staphylococcus hominis*, *Staphylococcus saprophyticus*, *Staphylococcus* sp., *Streptococcus agalactiae*, *Streptococcus* sp., *Trypanosoma brucei*, *Trypanosoma cruzi*, *Trypanosoma* sp., are also objects of the present invention.

Diagnostic kits further comprising probes or amplification primers for the detection of an antibiotic resistance gene selected from the group listed in Table 5 are also objects of this invention.

Diagnostic kits further comprising probes or amplification primers for the detection of a toxin gene selected from the group listed in Table 6 are also objects of this invention.

Diagnostic kits further comprising probes or amplification primers for the detection of any bacterial, fungal or parasitical species, comprising or not comprising those for the detection of the specific microbial species or genus or family or group listed above, and further comprising or not comprising probes and primers for the antibiotic resistance genes listed above, and further comprising or not comprising

probes and primers for the toxin genes listed above are also objects of this invention.

In a preferred embodiment, such a kit allows for the separate or the simultaneous detection and identification of the above-listed microbial species or genus or family or group, antibiotic resistance genes, toxin genes and for the
5 detection of any microorganism (bacteria, fungi or parasite).

In the above methods and kits, amplification reactions may include but are not restricted to: a) polymerase chain reaction (PCR), b) ligase chain reaction (LCR), c) nucleic acid sequence-based amplification (NASBA), d) self-sustained sequence replication (3SR), e) strand displacement amplification (SDA), f) branched DNA
10 signal amplification (bDNA), g) transcription-mediated amplification (TMA), h) cycling probe technology (CPT), i) nested PCR, j) multiplex PCR, k) solid phase amplification (SPA), l) nuclease dependent signal amplification (NDSA), m) rolling circle amplification technology (RCAT).

In the above methods and kits, detection of the nucleic acids of target genes
15 may include real-time or post-amplification technologies. These detection technologies can include, but are not limited to, fluorescence resonance energy transfer (FRET)-based methods such as adjacent hybridization to FRET probes (including probe-probe and probe-primer methods), Taqman, molecular beacons and Scorpions. Other detection methods include target genes nucleic acids detection via
20 immunological methods, solid phase hybridization methods on filters, chips or any other solid support, whether the hybridization is monitored by fluorescence, chemiluminescence, potentiometry, mass spectrometry, plasmon resonance, polarimetry, or colorimetry. Sequencing, including sequencing by dideoxy termination or sequencing by hybridization, is another possible method to detect and
25 identify the nucleic acids of target genes.

In a preferred embodiment, a PCR protocol is used for nucleic acid amplification.

In a particularly preferred embodiment, a PCR protocol is provided, comprising, an initial denaturation step of 1-3 minutes at 95 °C, followed by an
30 amplification cycle including a denaturation step of one second at 95 °C and an annealing step of 30 seconds at 45-65 °C, without any time allowed specifically for the elongation step. This PCR protocol has been standardized to be suitable for PCR reactions with most selected primer pairs, which greatly facilitates the testing because each clinical sample can be tested with universal, species-specific, genus-specific,
35 antibiotic resistance gene and toxin gene PCR primers under uniform cycling conditions. Furthermore, various combinations of primer pairs may be used in multiplex PCR assays.

It is also an object of the present invention that *tuf* sequences, *atpD* sequences and *recA* sequences could serve as drug targets and these sequences and means to
40 obtain them revealed in the present invention can assist the screening, design and modeling of these drugs.

It is also an object of the present invention that *tuf* sequences, *atpD* sequences and *recA* sequences could serve for vaccine purposes and these sequences and means to obtain them revealed in the present invention can assist the screening, design and modeling of these vaccines.

5

We aim at developing a rapid test or kit (universal) to discard rapidly all the samples which are negative for bacterial, fungal or parasitical cells. This test could be used alone or combined with more specific identification to detect and identify the above bacterial and/or fungal and/or parasitical species and genera and to determine rapidly the bacterial resistance to antibiotics and/or presence of bacterial toxins. Although the sequences from the selected antibiotic resistance genes are available from public databases and have been used to develop DNA-based tests for their detection, our approach is unique because it represents a major improvement over current diagnostic methods based on bacterial cultures. Using an amplification method for the simultaneous bacterial detection and identification and antibiotic resistance genes detection, there is no need for culturing the clinical sample prior to testing. Moreover, a modified PCR protocol has been developed to detect all target DNA sequences in approximately one hour under uniform amplification conditions. This procedure will save lives by optimizing treatment, will diminish antibiotic resistance because less antibiotics will be prescribed, will reduce the use of broad spectrum antibiotics which are expensive, decrease overall health care costs by preventing or shortening hospitalizations, and decrease the time and costs associated with clinical laboratory testing.

The diagnostic kits, primers and probes mentioned above can be used to identify bacteria, fungi, parasites, antibiotic resistance genes and toxin genes on any type of sample, whether said diagnostic kits, primers and probes are used for *in vitro* or *in situ* applications. The said samples may include but are not limited to: any clinical sample, any environment sample, any microbial culture, any microbial colony, any tissue, and any cell line.

It is also an object of the present invention that said diagnostic kits, primers and probes can be used alone or in conjunction with any other assay suitable to identify microorganisms, including but not limited to: any immunoassay, any enzymatic assay, any biochemical assay, any lysotypic assay, any serological assay, any differential culture medium, any enrichment culture medium, any selective culture medium, any specific assay medium, any identification culture medium, any enumeration culture medium, any cellular stain, any culture on specific cell lines, and any infectivity assay on animals.

In the methods and kits described herein below, the oligonucleotide probes and amplification primers have been derived from larger sequences (i.e. DNA fragments of at least 100 base pairs). All DNA fragments have been obtained either from

proprietary fragments or from public databases. DNA fragments selected from public databases are newly used in a method of detection according to the present invention, since they have been selected for their diagnostic potential.

In another embodiment, the amino acid sequences translated from the repertoire of *tuf*, *atpD* and *recA* sequences are also an object of the present invention.

It is clear to the individual skilled in the art that other oligonucleotide sequences appropriate for (i) the universal bacterial detection, (ii) the detection and identification of the above microbial species or genus or family or group, and (iii) the detection of antibiotic resistance genes, and (iv) the detection of toxin genes other than those listed in Annexes I to III and XXI may also be derived from the proprietary fragments or selected public databases sequences. For example, the oligonucleotide primers or probes may be shorter or longer than the ones we have chosen; they may also be selected anywhere else in the proprietary DNA fragments or in the sequences selected from public databases; they may be also variants of the same oligonucleotide. If the target DNA or a variant thereof hybridizes to a given oligonucleotide, or if the target DNA or a variant thereof can be amplified by a given oligonucleotide PCR primer pair, the converse is also true; a given target DNA may hybridize to a variant oligonucleotide probe or be amplified by a variant oligonucleotide PCR primer. Alternatively, the oligonucleotides may be designed from any DNA fragment sequences for use in amplification methods other than PCR. Consequently, the core of this invention is the identification of universal, species-specific, genus-specific, resistance gene-specific, toxin gene-specific genomic or non-genomic DNA fragments which are used as a source of specific and ubiquitous oligonucleotide probes and/or amplification primers. Although the selection and evaluation of oligonucleotides suitable for diagnostic purposes requires much effort, it is quite possible for the individual skilled in the art to derive, from the selected DNA fragments, oligonucleotides other than the ones listed in Annexes I to III and XXI which are suitable for diagnostic purposes. When a proprietary fragment or a public databases sequence is selected for its specificity and ubiquity, it increases the probability that subsets thereof will also be specific and ubiquitous.

Since a high percentage of clinical specimens are negative for bacteria (Table 3), DNA fragments having a high potential for the selection of universal oligonucleotide probes or primers were selected from proprietary and public databases sequences. The amplification primers were selected from genes highly conserved in bacteria, fungi and parasites, and are used to detect the presence of any bacterial or fungal or parasitical pathogen in clinical specimens in order to determine rapidly (less than one hour) whether it is positive or negative for bacteria, fungi or parasites. The selected genes, designated *tuf*, *atpD* and *recA*, encode respectively 2 proteins (elongation factors Tu and G) involved in the translational process during protein synthesis, a protein (beta subunit) responsible for the catalytic activity of

proton pump ATPase and a protein responsible for the homologous recombination of genetic material. The alignments of *tuf*, *atpD* and *recA* sequences used to derive the universal primers include both proprietary and public databases sequences. The universal primer strategy allows the rapid screening of the numerous negative clinical specimens (around 80% of the specimens received, see Table 3) submitted for bacteriological testing.

Table 4 provides a list of the bacterial, fungal and parasitical species for which *tuf* and/or *atpD* and/or *recA* sequences are revealed in the present invention. Tables 5 and 6 provide a list of antibiotics resistance genes and toxin genes selected for diagnostic purposes. Table 7 provides the origin of *tuf*, *atpD* and *recA* sequences listed in the sequence listing. Tables 8-10 provide lists or species used to test specificity and ubiquity of some assays described in examples.

DETAILED DESCRIPTION OF THE INVENTION

HIGHLY CONSERVED GENES AND THEIR USE TO GENERATE SPECIES-SPECIFIC, GENUS-SPECIFIC, FAMILY-SPECIFIC, GROUP-SPECIFIC AND UNIVERSAL NUCLEIC ACID PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY BACTERIAL, FUNGAL AND PARASITICAL PATHOGENS FROM CLINICAL SPECIMENS FOR DIAGNOSIS

The present inventors compared the published *Haemophilus influenzae* and *Mycoplasma genitalium* genomes and searched for the most conserved genes, which would then serve, as paradigm to develop primers and probes. This sequence comparison is highly informative as these two bacteria are distantly related and most genes present in the minimal genome of *M. genitalium* are likely to be present in every bacterium. Therefore genes conserved between these two bacteria are likely to be conserved in all other bacteria.

Following the genomic comparison, it was found that several protein-coding genes were conserved in evolution. Highly conserved proteins included the translation elongation factor Tu (EF-Tu) and the β subunit of F₀F₁ type ATP-synthase, and to a lesser extent, the RecA recombinase.

Translation elongation factor Tu is a member of a family of GTP-binding proteins which intervene in the interactions of tRNA molecules with the ribosome machinery during essential steps of protein synthesis. The role of elongation factor Tu is to facilitate the binding of aminoacylated tRNA molecules to the A site of the ribosome. The eukaryotic and archaeobacterial homolog of EF-Tu is called elongation factor 1 alpha (EF-1 α). All protein synthesis factors originated from a common ancestor via gene duplications and fusions (Cousineau *et al.*, 1997, J. Mol. Evol. 45:661-670). In particular, elongation factor G (EF-G), although having a functional role in promoting the translocation of aminoacyl-tRNA molecules from the A site to the P site of the ribosome, shares sequence homologies with EF-Tu and is thought to have arisen from the duplication and fusion of an ancestor of the EF-Tu gene.

In addition, EF-Tu is known to be the target for antibiotics belonging to the elfamycin's group as well as to other structural classes (Anborgh and Parmeggiani, 1991, EMBO J. 10:779-784; Luiten *et al.*, 1992, European patent application serial No. EP 0 466 251 A1). EF-G for its part, is the target of the antibiotic fusidic acid. In addition to its crucial activities in translation, EF-Tu has chaperone-like functions in protein folding, protection against heat denaturation of proteins and interactions with unfolded proteins (Caldas *et al.*, 1998, J. Biol. Chem. 273:11478-11482). Interestingly, a form of the EF-Tu protein has been identified as a dominant component of the periplasm of *Neisseria gonorrhoeae* (Porcella *et al.*, 1996, Microbiology 142:2481-2489), hence suggesting that at least in some bacterial species, EF-Tu might be an antigen with vaccine potential.

F₀F₁ type ATP-synthase belongs to a superfamily of proton-translocating ATPases divided in three major families: P, V and F (Nelson and Taiz,

1989, TIBS 14:113-116). P-ATPases (or E₁-E₂ type) operate via a phosphorylated intermediate and are not evolutionarily related to the other two families. V-ATPases (or V₀V₁ type) are present on the vacuolar and other endomembranes of eukaryotes, on the plasma membrane of archaeobacteria and also on the plasma membrane of some eubacteria especially species belonging to the order *Spirochaetales* as well as to the *Chlamydiaceae* and *Deinococcaceae* families. F-ATPases (or F₀F₁ type) are found on the plasma membrane of most eubacteria, on the inner membrane of mitochondria and on the thylakoid membrane of chloroplasts. They function mainly in ATP synthesis. They are large multimeric enzymes sharing numerous structural and functional features with the V-ATPases. F and V-type ATPases have diverged from a common ancestor in an event preceding the appearance of eukaryotes. The β subunit of the F-ATPases is the catalytic subunit and it possesses low but significant sequence homologies with the catalytic A subunit of V-ATPases.

The translation elongation factors EF-Tu, EF-G and EF-1 α , and the catalytic subunit of F or V-types ATP-synthase, are highly conserved proteins sometimes used for phylogenetic analysis and their genes are also known to be highly conserved (Iwabe *et al.*, 1989, Proc. Natl. Acad. Sci. USA 86:9355-9359, Gogarten *et al.*, 1989, Proc. Natl. Acad. Sci. USA 86:6661-6665, Ludwig *et al.*, 1993, Antonie van Leeuwenhoek 64:285-305). A recent BLAST (Altschul *et al.*, 1997, J. Mol. Biol. 215:403-410) search performed by the present inventors on the GenBank, EMBL, DDBJ and specific genome project databases indicated that throughout bacteria, the EF-Tu and the β subunit of F₀F₁ type ATP-synthase genes may be more conserved than other genes that are well-conserved between *H. influenzae* and *M. genitalium*.

The RecA recombinase is a multifunctional protein encoded by the *recA* gene. It plays a central role in homologous recombination, it is critical for the repair of DNA damage and it is involved in the regulation of the SOS system by promoting the proteolytic digestion of the LexA repressor. It is highly conserved in bacteria and could serve as a useful genetic marker to reconstruct bacterial phylogeny (Miller and Kokjohn, 1990, Annu. Rev. Microbiol. 44:365-394). Although *recA* possesses some highly conserved sequence segments that we used to design universal primers aimed at sequencing the *recA* fragments, it is clearly not as well conserved as *tuf* and *atpD*. Hence, *recA* may not be optimal for universal detection of bacteria with high sensitivity but it was chosen because preliminary data indicated that *tuf* and *atpD* may sometimes be too closely related to find specific primer pairs that could discriminate between certain very closely related species and genera. While RecA, like *tuf* and *atpD*, possesses highly conserved regions suitable for the design of universal sequencing primers, the less conserved region between primers should be divergent enough to allow species-specific and genus-specific primers in those cases.

Thus, as targets to design primers and probes for the genetic detection of microorganisms, the present inventors have focused on the genes encoding these three proteins: *tuf*, the gene for elongation factor Tu; *atpD*, the gene for β subunit of F₀F₁ type ATP-synthase; and *recA*, the gene encoding the RecA recombinase. In several bacterial genomes *tuf* is often found in two highly similar duplicated copies named *tufA* and *tufB* (Filer and Furano, 1981, J. Bacteriol. 148:1006-1011, Sela *et al.*,

1989, J. Bacteriol. 171:581-584). In some particular cases, more divergent copies of the *tuf* genes can exist in some bacterial species such as some Actinomycetes (Luiten *et al.* European patent application publication No. EP 0 446 251 A1; Vijgenboom *et al.*, 1994, Microbiology 140:983-998) and, as revealed as part of this invention, in several enterococcal species. In several bacterial species, *tuf* is organized in an operon with its homolog gene for the elongation factor G (EF-G) encoded by the *fusA* gene. This operon is often named the *str* operon. The *tuf*, *atpD* and *recA* genes were chosen as they are well conserved in evolution and have highly conserved stretches as well as more variable segments. Moreover, these three genes have eukaryotic orthologs which are described in the present invention as targets to identify fungi and parasites. The eukaryotic homolog of elongation factor Tu is called elongation factor 1-alpha (EF-1 α) (gene name: *tef*, *tef1*, *ef1*, *ef-1* or *EF-1*). In fungi, the gene for EF-1 α occurs sometimes in two or more highly similar duplicated copies (often named *tef1*, *tef2*, *tef3*...). In addition, eukaryotes have a copy of elongation factor Tu which is originating from their organelle genome ancestry (gene name: *tuf1*, *tufM* or *tufA*). For the purpose of the current invention, the genes for these four functionally and evolutionarily linked elongation factors (bacterial EF-Tu and EF-G, eukaryotic EF-1 α , and organellar EF-Tu) will hereafter be designated as «*tuf* sequences». The eukaryotic (mitochondrial) F₀F₁ type ATP-synthase beta subunit gene is named *atp2* in yeast. For the purpose of the current invention, the genes of catalytic subunit of either F or V-type ATP-synthase will hereafter be designated as «*atpD* sequences». The eukaryotic homologs of RecA are distributed in two families, typified by the Rad51 and Dmc1 proteins. For the purpose of the current invention, the genes corresponding to the latter proteins will hereafter be designated as «*recA* sequences».

Analysis of multiple sequence alignments of *tuf* and *atpD* sequences permitted the design of oligonucleotide primers (and probes) capable of amplifying (or hybridizing to) segments of *tuf* and *atpD* genes from a wide variety of bacterial species (see Examples 1 to 4 and Table 7). Sequencing primer pairs for *tuf* sequences are listed in Annex I and hybridization probes are listed in Annex III. Sequencing primer pairs for *atpD* sequences are listed in Annex II. Analysis of the main subdivisions of *tuf* and *atpD* sequences (see Figures 1 and 2) permitted to design sequencing primers amplifying specifically each of these subdivisions. It should be noted that these sequencing primers could also be used as universal primers. However, since some of these sequencing primers include several variable sequence (degenerated) positions, their sensitivity could be lower than that of universal primers developed for diagnostic purposes. Further subdivisions could be done on the basis of the various phyla where these genes are encountered.

Similarly, analysis of multiple sequence alignments of *recA* sequences present in the public databases permitted the design of oligonucleotide primers capable of amplifying segments of *recA* genes from a wide variety of bacterial species. Sequencing primer pairs for *recA* sequences are listed in Annex XXI. The main subdivisions of *recA* sequences comprise *recA*, *rad51* and *dmc1*. Further subdivisions could be done on the basis of the various phyla where these genes are encountered.

The present inventor's strategy is to get as much sequence data information from the three conserved genes (*tuf*, *atpD* and *recA*). This ensemble of sequence data forming a repertory (with subrepertories corresponding to each target gene and their main sequence subdivisions) and then using the sequence information of the sequence repertory (or subrepertories) to design primer pairs that could permit either universal detection of bacteria or fungi or parasites, detection of a family or group of microorganism (e.g. *Enterobacteriaceae*), detection of a genus (e.g. *Streptococcus*) or finally a specific species (e.g. *Staphylococcus aureus*). It should be noted that for the purpose of the present invention a group of microorganisms is defined depending on the needs of the particular diagnostic test. It does not need to respect a particular taxonomical grouping or phylum. See example 12 where primers were designed to amplify a group of bacteria consisting of the 17 major bacterial species encountered as contaminants of platelet concentrates. Also remark that in that example, the primers' specificity is not perfect since the objective of that particular test is to be able to sensitively and rapidly detect at least the 17 important bacterial species, but the primers could also detect other species as well, as shown in Table 14. In these circumstances the primers shown in example 12 are considered universal for platelet-contaminating bacteria. To develop an assay specific for the latter, one or more primers or probes specific to each species could be designed. Another example of primers and/or probes for group detection is given by the *Pseudomonas* group primers. These primers were designed based upon alignment of *tuf* sequences from real *Pseudomonas* species as well as from former *Pseudomonas* species such as *Stenotrophomonas maltophilia*. The resulting primers are able to amplify all *Pseudomonas* species tested as well as several species belonging to different genera, hence as being specific for a group including *Pseudomonas* and other species, we defined that group as Pseudomonads as several members were former *Pseudomonas*.

For certain applications, it may be possible to develop a universal, group, family or genus-specific reaction and to proceed to species identification using sequence information within the amplicon to design species-specific internal probes or primers, or alternatively, to proceed directly by sequencing the amplicon. The various strategies will be discussed further below.

The ensembles formed by public and proprietary *tuf*, *atpD* and *recA* sequences are used in a novel fashion so they constitute three databases containing useful information for the identification of microorganisms.

Oligonucleotide primers and probes design and synthesis

The *tuf*, *atpD* and *recA* DNA fragments sequenced by us or selected from public databases (GenBank and EMBL) were used to design oligonucleotides primers and probes for diagnostic purposes. We also relied on the corresponding peptide sequence of *tuf*, *atpD* and *recA* sequences to facilitate the identification of regions suitable for primers and probes design. As part of the design rules, all oligonucleotides (probes for hybridization and primers for DNA amplification) were evaluated for their

suitability for hybridization or DNA amplification by polymerase chain reaction (PCR) by computer analysis using standard programs (i.e. the Genetics Computer Group (GCG) programs and the primer analysis software Oligo™ 5.0). The potential suitability of the PCR primer pairs was also evaluated prior to the synthesis by verifying the absence of unwanted features such as long stretches of one nucleotide and a high proportion of G or C residues at the 3' end (Persing *et al.*, 1993, Diagnostic Molecular Microbiology: Principles and Applications, American Society for Microbiology, Washington, D.C.). Oligonucleotide probes and amplification primers were synthesized using an automated DNA synthesizer (Perkin-Elmer Corp., Applied Biosystems Division).

The oligonucleotide primers or probes may be derived from either strand of the duplex DNA. The primers or probes may consist of the bases A, G, C, or T or analogs and they may be degenerated at one or more chosen nucleotide position(s). The primers or probes may be of any suitable length and may be selected anywhere within the DNA sequences from proprietary fragments or from selected database sequences which are suitable for (i) the universal detection of bacteria or fungi or parasites, (ii) the species-specific detection and identification of any microorganism, including but not limited to: *Candida albicans*, *Candida dubliniensis*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Cryptosporidium parvum*, *Enterococcus faecalis*, *Enterococcus faecium*, *Enterococcus gallinarum*, *Escherichia coli*, *Haemophilus influenzae*, *Neisseria gonorrhoeae*, *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Staphylococcus hominis*, *Staphylococcus saprophyticus*, *Streptococcus agalactiae*, *Trypanosoma brucei*, *Trypanosoma cruzi*, (iii) the genus-specific detection of *Bordetella* species, *Candida* species, *Clostridium* species, *Corynebacterium* species, *Entamoeba* species, *Enterococcus* species, *Giardia* species, *Leishmania* species, *Staphylococcus* species, *Streptococcus* species, *Trypanosoma* species, (iv) the family-specific detection of *Enterobacteriaceae* family members, *Mycobacteriaceae* family members, (v) the detection of *Enterococcus casseliflavus-flavescens-gallinarum* group, *Trypanosomatidae* family, Pseudomonads extended group, Platelet-contaminating bacteria group, or (vi) the detection of clinically important antibiotic resistance genes listed in Table 5, or (vii) the detection of clinically important toxin genes listed in Table 6.

Variants for a given target bacterial gene are naturally occurring and are attributable to sequence variation within that gene during evolution (Watson *et al.*, 1987, Molecular Biology of the Gene, 4th ed., The Benjamin/Cummings Publishing Company, Menlo Park, CA; Lewin, 1989, Genes IV, John Wiley & Sons, New York, NY). For example, different strains of the same bacterial species may have a single or more nucleotide variation(s) at the oligonucleotide hybridization site. The person skilled in the art is well aware of the existence of variant bacterial or fungal DNA sequences for a specific gene and that the frequency of sequence variations depends

on the selective pressure during evolution on a given gene product. The detection of a variant sequence for a region between two PCR primers may be demonstrated by sequencing the amplification product. In order to show the presence of sequence variants at the primer hybridization site, one has to amplify a larger DNA target with PCR primers outside that hybridization site. Sequencing of this larger fragment will allow the detection of sequence variation at this site. A similar strategy may be applied to show variants at the hybridization site of a probe. Insofar as the divergence of the target sequences or a part thereof does not affect the specificity and ubiquity of the amplification primers or probes, variant bacterial DNA is under the scope of this invention. Variants of the selected primers or probes may also be used to amplify or hybridize to a variant DNA.

Sequencing of *tuf* sequences from a variety of bacterial, fungal and parasitical species

The nucleotide sequence of a portion of *tuf* sequences was determined for a variety of bacterial, fungal and parasitical species. The amplification primers (SEQ ID NOs. 107 and 108 in previous patent application WO98/20157), which amplify a *tuf* gene portion of approximately 890 bp, were used along with newly designed sequencing primer pairs (See Annex I for the sequencing primers for *tuf* sequences). Most primer pairs can amplify different copies of *tuf* genes (*tufA* and *tufB*). This is not surprising since it is known that for several bacterial species these two genes are nearly identical. For example, the entire *tufA* and *tufB* genes from *E. coli* differ at only 13 nucleotide positions (Neidhardt *et al.*, 1996, *Escherichia coli* and *Salmonella*: Cellular and Molecular Biology, 2nd ed., American Society for Microbiology Press, Washington, D.C.). Similarly, some fungi are known to have two nearly identical copies of *tuf* sequences (EF-1 α). These amplification primers are degenerated at several nucleotide positions and contain inosines in order to allow the amplification of a wide range of *tuf* sequences. The strategy used to select these amplification primers is similar to that illustrated in Annex I for the selection of universal primers. The *tuf* sequencing primers even sometimes amplified highly divergent copies of *tuf* genes (*tufC*) as illustrated in the case of some enterococcal species (SEQ ID NOs.: 73, 75, 76, 614 to 618, 621 and 987 to 989). To prove this we first had to clone PCR products before being able to sequence them. Using the cloned sequence data we designed a new pair of sequencing primers specific to the divergent (*tufC*) copy of enterococci (SEQ ID NOs.: 658-659 and 661) and then sequenced directly the *tufC* amplicons. The amplification primers (SEQ ID NOs.: 543, 556, 557, 660, 664, 694, 696 and 697) could be used to amplify the *tuf* sequences from any bacterial species. The amplification primers (SEQ ID NOs.: 558, 559, 560, 653, 654, 655, 813 and 815) could be used to amplify the *tuf* (EF-1 α) genes from any fungal and parasitical

species. The amplification primers SEQ ID NOs. 1221-1228 could be used to amplify bacterial *tuf* sequences of the EF-G subdivision (*fusA*) (Figure 3). The amplification primer SEQ ID NOs 1224, and 1227-1229 could be used to amplify bacterial *tuf* sequences comprising the end of EF-G (*fusA*) and the beginning of EF-Tu (*tuf*), as shown in Figure 3.

The *tuf* fragments to be sequenced were amplified using the following amplification protocol: One μ l of cell suspension (or of purified genomic DNA 0.1-0.5 ng/ μ l) was transferred directly to 19 μ l of a PCR reaction mixture. Each PCR reaction contained 50 mM KCl, 10 mM Tris-HCl (pH 9.0), 0.1% Triton X-100, 2.5 mM $MgCl_2$, 1 μ M of each of the 2 primers, 200 μ M of each of the four dNTPs, 0.5 unit of *Taq* DNA polymerase (Promega Corp., Madison, WI). PCR reactions were subjected to cycling using a PTC-200 thermal cycler (MJ Research Inc., Watertown, Mass.) as follows: 3 min at 96 °C followed by 30-45 cycles of 1 min at 95 °C for the denaturation step, 1 min at 50-55 °C for the annealing step and 1 min at 72 °C for the extension step. Subsequently, twenty microliters of the PCR-amplified mixture were resolved by electrophoresis in a 1.5% agarose gel. The amplicon was then visualized by staining with methylene blue (Flores *et al.*, 1992, Biotechniques, 13:203-205). The size of the amplification products was estimated by comparison with a 100-bp molecular weight ladder. The band corresponding to the specific amplification product was excised from the agarose gel and purified using the QIAquick™ gel extraction kit (QIAGEN Inc., Chatsworth, CA). The gel-purified DNA fragment was then used directly in the sequencing protocol. Both strands of the *tuf* genes amplification product were sequenced by the dideoxynucleotide chain termination sequencing method by using an Applied Biosystems automated DNA sequencer (model 377) with their Big Dye™ Terminator Cycle Sequencing Ready Reaction Kit (Perkin-Elmer Corp., Applied Biosystems Division, Foster City, CA). The sequencing reactions were performed by using the same amplification primers and 10 ng/100 bp of the gel-purified amplicon per reaction. For the sequencing of long amplicons such as those of eukaryotic *tuf* (EF-1 α) sequences, we designed internal sequencing primers (SEQ ID NOs.: 654, 655 and 813) to be able to obtain sequence data on both strands for most of the fragment length. In order to ensure that the determined sequence did not contain errors attributable to the sequencing of PCR artefacts, we have sequenced two preparations of the gel-purified *tuf* amplification product originating from two independent PCR amplifications. For most target microbial species, the sequences determined for both amplicon preparations were identical. In case of discrepancies, a third independant PCR amplification was sequenced. Furthermore, the sequences of both strands were 100% complementary thereby confirming the high accuracy of the determined sequence. The *tuf* sequences determined using the above strategy are described in the Sequence Listing. Table 7 gives the originating microbial species and the source for each *tuf* sequence in the

Sequence Listing.

The alignment of the *tuf* sequences determined by us or selected from databases reveals clearly that the length of the sequenced portion of the *tuf* genes is variable. There may be insertions or deletions of several amino acids. In addition, in several fungi introns were observed. Intron sequences are part of *tuf* sequences and could be useful in the design of species-specific primers and probes. This explains why the size of the sequenced *tuf* amplification products was variable from one species to another. Consequently, the nucleotide positions indicated on top of each of Annexes IV to XXI, XXIII to XXXI, XXXVIII and XLII do not correspond for sequences having insertions or deletions.

It should also be noted that the various *tuf* sequences determined by us occasionally contain degenerescences. These degenerated nucleotides correspond to sequence variations between *tufA* and *tufB* genes (or copies of the EF-G subdivision of *tuf* sequences, or copies of EF-1 α subdivision of *tuf* sequences for fungi and parasites) because the amplification primers amplify both *tuf* genes. These nucleotide variations were not attributable to nucleotide misincorporations by the *Taq* DNA polymerase because the sequence of both strands was identical and also because the sequences determined with both preparations of the gel-purified *tuf* amplicons were identical.

The selection of amplification primers from *tuf* sequences

The *tuf* sequences determined by us or selected from public databases were used to select PCR primers for (i) the universal detection of bacteria, (ii) the genus-specific detection and identification of *Enterococcus* sp. and *Staphylococcus* sp. and (iii) the species-specific detection and identification of *Candida albicans*. The strategy used to select these PCR primers was based on the analysis of multiple sequence alignments of various *tuf* sequences. For more details about the selection of PCR primers from *tuf* sequences please refer to Examples and Annexes.

Sequencing of *atpD* and *recA* sequences from a variety of bacterial, fungal and parasitical species

The method use to obtain *atpD* and *recA* sequences is similar to that described above for *tuf* sequences.

The selection of amplification primers from *atpD* or *recA*

The comparison of the nucleotide sequence for the *atpD* or *recA* genes from

various bacterial fungal and parasitical species allowed the selection of PCR primers (refer to Examples 1, 2 and 6 and Annexes IV, V, X, XX, XXI).

DNA amplification

For DNA amplification by the widely used PCR (polymerase chain reaction) method, primer pairs were derived from proprietary DNA fragments or from database sequences. Prior to synthesis, the potential primer pairs were analyzed by using the Oligo™ 5.0 software to verify that they were good candidates for PCR amplification.

During DNA amplification by PCR, two oligonucleotide primers binding respectively to each strand of the heat-denatured target DNA from the bacterial genome are used to amplify exponentially *in vitro* the target DNA by successive thermal cycles allowing denaturation of the DNA, annealing of the primers and synthesis of new targets at each cycle (Persing *et al.*, 1993, Diagnostic Molecular Microbiology: Principles and Applications, American Society for Microbiology, Washington, D.C.).

Briefly, the PCR protocols were as follows: Treated clinical specimens or standardized bacterial or fungal or parasitical suspensions (see below) or purified genomic DNA from bacteria, fungi or parasites were amplified in a 20 µl PCR reaction mixture. Each PCR reaction contained 50 mM KCl, 10 mM Tris-HCl (pH 9.0), 2.5 mM MgCl₂, 0.4 µM of each primer, 200 µM of each of the four dNTPs and 0.5 unit of *Taq* DNA polymerase (Promega) combined with the TaqStart™ antibody (Clontech Laboratories Inc., Palo Alto, CA). The TaqStart™ antibody, which is a neutralizing monoclonal antibody to *Taq* DNA polymerase, was added to all PCR reactions to enhance the specificity and the sensitivity of the amplifications (Kellogg *et al.*, 1994, Biotechniques 16:1134-1137). The treatment of the clinical specimens varies with the type of specimen tested, since the composition and the sensitivity level required are different for each specimen type. It consists in a rapid protocol to lyse the bacterial cells and eliminate the PCR inhibitory effects. For amplification from bacterial or fungal cultures or from purified genomic DNA, the samples were added directly to the PCR amplification mixture without any pre-treatment step. An internal control was derived from sequences not found in the target microorganisms or in the human genome. The internal control was integrated into all amplification reactions to verify the efficiency of the PCR assays and to ensure that significant PCR inhibition was absent. Alternatively, an internal control derived from rRNA was also useful to monitor the efficiency of microbial lysis protocols.

PCR reactions were then subjected to thermal cycling (3 min at 95 °C followed by 30 cycles of 1 second at 95 °C for the denaturation step and 30 seconds at 50-65 °C for the annealing-extension step) using a PTC-200 thermal cycler (MJ Research Inc.). The number of cycles performed for the PCR assays varies according to the

sensitivity level required. For example, the sensitivity level required for microbial detection directly from clinical specimens is higher for blood specimens than for urine specimens because the concentration of microorganisms associated with a septicemia can be much lower than that associated with a urinary tract infection.

Consequently, more sensitive PCR assays having more thermal cycles are required for direct detection from blood specimens. Similarly, PCR assays performed directly from bacterial or fungal or parasitical cultures may be less sensitive than PCR assays performed directly from clinical specimens because the number of target organisms is normally much lower in clinical specimens than in microbial cultures.

The person skilled in the art of DNA amplification knows the existence of other rapid amplification procedures such as ligase chain reaction (LCR), transcription-mediated amplification (TMA), self-sustained sequence replication (3SR), nucleic acid sequence-based amplification (NASBA), strand displacement amplification (SDA), branched DNA (bDNA), cycling probe technology (CPT), solid phase amplification (SPA), rolling circle amplification technology (RCAT), and nuclease dependent signal amplification (NDSA) (Lee *et al.*, 1997, Nucleic Acid Amplification Technologies: Application to Disease Diagnosis, Eaton Publishing, Boston, MA; Persing *et al.*, 1993, Diagnostic Molecular Microbiology: Principles and Applications, American Society for Microbiology, Washington, D.C.). The scope of this invention is not limited to the use of amplification by PCR, but rather includes the use of any rapid nucleic acid amplification method or any other procedure which may be used to increase rapidity and sensitivity of the nucleic acid-based tests. The scope of the present invention also covers the use of any nucleic acids amplification and detection technology including real-time or post-amplification detection technologies, any amplification technology combined with detection, any hybridization nucleic acid chips or arrays technologies, any amplification chips or combination of amplification and hybridization chips technologies. Detection and identification by any sequencing method is also under the scope of the present invention.

Any oligonucleotide suitable for the amplification of nucleic acids by approaches other than PCR or for DNA hybridization and derived from the species-specific, genus-specific and universal DNA fragments as well as from selected antibiotic resistance or toxin gene sequences included in this document are also under the scope of this invention.

Detection of amplification products

Classically, detection of amplification is performed by standard ethidium bromide-stained agarose gel electrophoresis. It is clear that other methods for the detection of specific amplification products, which may be faster and more practical for routine diagnosis, may be used. Such methods may be based on the detection of fluorescence after or during amplification. One simple method for monitoring

amplified DNA is to measure its rate of formation by measuring the increase in fluorescence of intercalating agents such as ethidium bromide or SYBR® Green I. If more specific detection is required, fluorescence-based technologies can monitor the appearance of a specific product during the reaction. The use of dual-labeled fluorogenic probes such as in the TaqMan™ system which utilizes the 5'-3' exonuclease activity of the *Taq* polymerase is a good example (Livak K.J. *et al.* 1995, PCR Methods Appl. 4:357-362). TaqMan™ can be performed during amplification and this "real-time" detection can be done in a single closed tube hence eliminating post-PCR sample handling and consequently preventing the risk of amplicon carryover (TaqMan™ system from Perkin Elmer or Amplisensor™ from Biotronics). Several other fluorescence-based detection methods can be performed in real-time. Fluorescence resonance energy transfer (FRET) is the principle behind the use of adjacent hybridization probes and molecular beacons. Adjacent hybridization probes are designed to be internal to the amplification primers. The 3' end of one probe is labelled with a donor fluorophore while the 5' end of an adjacent probe is labelled with an acceptor fluorophore. When the two probes are specifically hybridized in closed proximity (spaced by 1 to 5 nucleotides) the donor fluorophore which has been excited by an external light source emits light that is absorbed by a second acceptor that emit more fluorescence and yields a FRET signal. Molecular beacons possess a stem-and-loop structure where the loop is the probe and at the bottom of the stem a fluorescent moiety is at one end while a quenching moiety is at the other end. The beacons undergo a fluorogenic conformational change when they hybridize to their targets hence separating the fluorochrome from its quencher. The FRET principle is also used in an air thermal cycler with a built-in fluorometer (Wittwer, C.T. *et al.* 1997. BioTechniques 22:130-138). The amplification and detection are extremely rapid as reactions are performed in capillaries : it takes 18 min to complete 45 cycles. Those techniques are suitable especially in the case where few pathogens are searched for. Boehringer-Roche Inc. sells the LightCycler™, an apparatus capable of rapid cycle PCR combined with fluorescent SYBR® Green I or FRET detection. We recently demonstrated in our laboratory, real-time detection of 10 CFU in less than 40 minutes using adjacent hybridization probes on the LightCycler™. Methods based on the detection of fluorescence are particularly promising for utilization in routine diagnosis as they are very rapid, quantitative and can be automated.

Microbial pathogens detection and identification may also be performed by solid support or liquid hybridization using species-specific internal DNA probes hybridizing to an amplification product. Such probes may be generated from any sequences from our repertory and designed to specifically hybridize to DNA amplification products which are objects of the present invention. Alternatively, the internal probes for species or genus or family or group detection and identification may be derived from the amplicons produced by a universal, family, group or genus

amplification assay. The oligonucleotide probes may be labeled with biotin or with digoxigenin or with any other reporter molecule (for more details see below the section on hybrid capture). Hybridization on a solid support is amenable to miniaturization.

At present the oligonucleotide nucleic acid microarray technology is appealing. Currently, available low to medium density arrays (Heller *et al.*, An integrated microelectronics hybridization system for genomic research and diagnostic applications. *In*: Harrison, D.J., and van den Berg, A., 1998, Micro total analysis systems '98, Kluwer Academic Publisher, Dordrecht.) could specifically capture fluorescent-labelled amplicons. Detection methods for hybridization are not limited to fluorescence; potentiometry, colorimetry and plasmon resonance are some examples of alternative detection methods. In addition to detection by hybridization, nucleic acid microarrays could be used to perform rapid sequencing by hybridization. Mass spectrometry could also be applicable for rapid identification of the amplicon or even for sequencing of the amplification products (Chiu and Cantor, 1999, Clinical Chemistry **45**:1578; Berkenkamp *et al.*, 1998, Science **281**:260).

We also keep in mind the major challenge of molecular diagnostics tools, *i.e.* : integration of the major steps including sample preparation, genetic amplification, detection, data analysis and presentation (Anderson *et al.*, Advances in integrated genetic analysis. *In*: Harrison, D.J., and van den Berg, A., 1998, Micro total analysis systems '98, Kluwer Academic Publisher, Dordrecht.).

To ensure PCR efficiency, glycerol, dimethyl sulfoxide (DMSO) or other related solvents can be used to increase the sensitivity of the PCR and to overcome problems associated with the amplification of a target DNA having a high GC content or forming strong secondary structures (Dieffenbach and Dveksler, 1995, PCR Primer: A Laboratory Manual, Cold Spring Harbor Laboratory Press, Plainview, New York). The concentration ranges for glycerol and DMSO are 5-15% (v/v) and 3-10% (v/v), respectively. For the PCR reaction mixture, the concentration ranges for the amplification primers and MgCl₂ are 0.1-1.5 μ M and 1.0-10.0 mM, respectively. Modifications of the standard PCR protocol using external and nested primers (*i.e.* nested PCR) or using more than one primer pair (*i.e.* multiplex PCR) may also be used (Persing *et al.*, 1993, Diagnostic Molecular Microbiology: Principles and Applications, American Society for Microbiology, Washington, D.C.). For more details about the PCR protocols and amplicon detection methods, see Examples.

Hybrid capture and chemiluminescence detection of amplification products

Hybridization and detection of amplicons by chemiluminescence were adapted from Nikiforov *et al.* (1994, PCR Methods and Applications **3**:285-291 and 1995, Anal. Biochem. **227**:201-209) and from the DIGTM system protocol of Boehringer Mannheim. Briefly, 50 μ l of a 25 picomoles solution of capture probe diluted in EDC {1-ethyl-3-(3-dimethylaminopropyl) carbodiimide hydrochloride} are immobilized in

each well of 96-wells plates (Microlite™ 2, Dynex) by incubation overnight at room temperature. The next day, the plates are incubated with a solution of 1% BSA diluted into TNTw (10 mM Tris-HCl, pH 7.5; 150 mM NaCl; 0.05% Tween™ 20) for 1 hour at 37 °C. The plates are then washed on a Wellwash Ascent™
 5 (Labystems) with TNTw followed by Washing Buffer (100 mM maleic acid pH7.5; 150 mM NaCl; 0.3% Tween™ 20).

The amplicons were labelled with DIG-11-dUTP during PCR using the PCR DIG Labelling Mix from Boehringer Mannheim according to the manufacturer's instructions. Hybridization of the amplicons to the capture probes is performed in
 10 triplicate at stringent temperature (generally, probes are designed to allow hybridization at 55 °C, the stringent temperature) for 30 minutes in 1.5 M NaCl; 10 mM EDTA. It is followed by two washes in 2 X SSC; 0.1% SDS, then by four washes in 0.1X SSC; 0.1% SDS at the stringent temperature (55 °C). Detection with 1,2 dioxetane chemiluminescent alkaline phosphatase substrates like CSPD® (Tropix inc.) is
 15 performed according to the manufacturer's instructions but with shorter incubations times and a different antibody concentration. The plates are agitated at each step, the blocking incubation is performed for only 5 minutes, the anti-DIG-AP1 is used at a 1:1000 dilution, the incubation with antibody lasts 15 minutes, the plates are washed twice for only 5 minutes. Finally, after a 2 minutes incubation into the detection
 20 buffer, the plates are incubated 5 minutes with CSPD® at room temperature followed by a 10 minutes incubation at 37 °C without agitation. Luminous signal detection is performed on a Dynex Microtiter Plate Luminometer using RLU (Relative Light Units).

25 ***Specificity and ubiquity tests for oligonucleotide primers and probes***

The specificity of oligonucleotide primers and probes was tested by amplification of DNA or by hybridization with bacterial or fungal or parasitological species selected from a panel comprising closely related species and species sharing
 30 the same anatomo-pathological site (see Annexes and Examples). All of the bacterial, fungal and parasitological species tested were likely to be pathogens associated with infections or potential contaminants which can be isolated from clinical specimens. Each target DNA could be released from bacterial cells using standard chemical and/or physical treatments to lyse the cells (Sambrook *et al.*, 1989, Molecular
 35 Cloning: A Laboratory Manual, 2nd ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY) or alternatively, genomic DNA purified with the GNOME™ DNA kit (Bio101, Vista, CA) was used. Subsequently, the DNA was subjected to amplification with the primer pairs.

Oligonucleotides primers found to amplify specifically the target species, genus,
 40 family or group were subsequently tested for their ubiquity by amplification (i.e.

ubiquitous primers amplified most or all isolates of the target species or genus or family or group). The specificity and ubiquity of the PCR assays using the selected amplification primer pairs were tested either directly from cultures of microbial species or from purified microbial genomic DNA.

Probes were tested in hybrid capture assays as described above. An oligonucleotide probe was considered specific only when it hybridized solely to DNA from the species or genus or family or group from which it was selected. Oligonucleotide probes found to be specific were subsequently tested for their ubiquity (i.e. ubiquitous probes recognized most or all isolates of the target species or genus or family or group) by hybridization to microbial DNAs from different clinical isolates of the species or genus or family or group of interest including ATCC reference strains. Similarly, oligonucleotide primers and probes could be derived from antibiotic resistance or toxin genes which are objects of the present invention.

Reference strains

The reference strains used to built proprietary *tuf*, *atpD* and *recA* sequence data subrepertories, as well as to test the amplification and hybridization assays were obtained from (i) the American Type Culture Collection (ATCC), (ii) the Laboratoire de santé publique du Québec (LSPQ), (iii) the Centers for Disease Control and Prevention (CDC), (iv) the National Culture Type Collection (NCTC) and (v) several other reference laboratories throughout the world. The identity of our reference strains was confirmed by phenotypic testing and reconfirmed by analysis of *tuf*, *atpD* and *recA* sequences (see example 13).

Antibiotic resistance genes

Antimicrobial resistance complicates treatment and often leads to therapeutic failures. Furthermore, overuse of antibiotics inevitably leads to the emergence of bacterial resistance. Our goal is to provide clinicians, in approximately one hour, the needed information to prescribe optimal treatments. Besides the rapid identification of negative clinical specimens with DNA-based tests for universal bacterial detection and the identification of the presence of a specific pathogen in the positive specimens with species- and/or genus- and/or family- and/or group-specific DNA-based tests, clinicians also need timely information about the ability of the bacterial pathogen to resist antibiotic treatments. We feel that the most efficient strategy to evaluate rapidly bacterial resistance to antimicrobials is to detect directly from the clinical specimens the most common and clinically important antibiotic resistance genes (i.e. DNA-based tests for the detection of antibiotic resistance genes). Since the sequence from the most important and common bacterial antibiotic resistance genes are available

from public databases, our strategy is to use the sequence from a portion or from the entire resistance gene to design specific oligonucleotide primers or probes which will be used as a basis for the development of rapid DNA-based tests. The list of each of the bacterial antibiotic resistance genes selected on the basis of their clinical relevance (i.e. high incidence and importance) is given in Table 5. Our approach is unique because the antibiotic resistance genes detection and the bacterial detection and identification can be performed simultaneously in multiplex assays under uniform PCR amplification conditions. These amplifications can also be done separately.

Toxin genes

Toxin identification is often very important to prescribe optimal treatments. Besides the rapid identification of negative clinical specimens with DNA-based tests for universal bacterial detection and the identification of the presence of a specific pathogen in the positive specimens with species- and/or genus- and/or family- and/or group-specific DNA-based tests, clinicians sometimes need timely information about the ability of certain bacterial pathogens to produce toxins. Since the sequence from the most important and common bacterial toxin genes are available from public databases, our strategy is to use the sequence from a portion or from the entire toxin gene to design specific oligonucleotide primers or probes which will be used as a basis for the development of rapid DNA-based tests. The list of each of the bacterial toxin genes selected on the basis of their clinical relevance (i.e. high incidence and importance) is given in Table 6. Our approach is unique because the toxin genes detection and the bacterial detection and identification can be performed simultaneously in multiplex assays under uniform PCR amplification conditions.

Universal bacterial detection

In the routine microbiology laboratory, a high percentage of clinical specimens sent for bacterial identification are negative by culture. Testing clinical samples with universal amplification primers or universal probes to detect the presence of bacteria prior to specific identification and screening out the numerous negative specimens is thus useful as it reduces costs and may rapidly orient the clinical management of the patients. Several amplification primers and probes were therefore synthesized from highly conserved portions of bacterial sequences from the *tuf* and *atpD* sequences. The universal primers selection was based on a multiple sequence alignment constructed with sequences from our repertoire.

All computer analysis of amino acid and nucleotide sequences were performed by using the GCG programs. Subsequently, optimal PCR primers for the universal

amplification of bacteria were selected with the help of the Oligo™ program. The selected primers are degenerated at several nucleotide positions and contain several inosines in order to allow the amplification of all clinically relevant bacterial species (Annex I). Inosine is a nucleotide analog able to specifically bind to any of the four nucleotides A, C, G or T. Degenerated oligonucleotides consist of an oligonucleotide mix having two or more of the four nucleotides A, C, G or T at the site of mismatches. The inclusion of inosine and/or of degenerescences in the amplification primers allow mismatch tolerance thereby permitting the amplification of a wider array of target nucleotide sequences (Dieffenbach and Dveksler, 1995 PCR Primer: A Laboratory Manual, Cold Spring Harbor Laboratory Press, Plainview, NY).

The amplification conditions with the universal primers are very similar to those used for the species- and genus-specific amplification assays except that the annealing temperature is slightly lower. The original universal PCR assay described in our co-pending WO98/20157 (SEQ ID NOs. 23-24 of the latter application) was specific and nearly ubiquitous for the detection of bacteria. The specificity for bacteria was verified by amplifying genomic DNA isolated from the 12 fungal species as well as genomic DNA from *Leishmania donovani*, *Saccharomyces cerevisiae* and human lymphocytes. None of the above eukaryotic DNA preparations could be amplified by the universal assay, thereby suggesting that this test is specific for bacteria. The ubiquity of the universal assay was verified by amplifying genomic DNAs from 116 reference strains which represent 95 of the most clinically relevant bacterial species. These species have been selected from the bacterial species listed in Table 4. We found that at least 104 of these species could be amplified. However, the assay could be improved since bacterial species which could not be amplified with the original *tuf* sequences-based assay included species belonging to the following genera: *Corynebacterium* (11 species) and *Stenotrophomonas* (1 species). Sequencing of the *tuf* genes from these bacterial species and others has been performed in the scope of the present invention in order to improve the universal assay. This sequencing data has been used to select new universal primers which may be more ubiquitous. Also, we improved our primer and probes design strategy by taking into consideration the phylogeny observed in analysing our repertoire of *tuf*, *atpD* and *recA* sequences. Data from each of the 3 main subrepertoires (*tuf*, *atpD* and *recA*) was subjected to a basic phylogenetic analysis using the Pileup command from version 10 of the GCG package (Genetics Computer Group, inc.). This analysis indicated the main branches or phyla reflecting the relationships between sequences. Instead of trying to design primers or probes able to hybridize to all phyla, we designed primers or probes able to hybridize to the main phyla while trying to use the largest phylum possible. This strategy should allow less degenerated primers hence improving sensitivity and by combining primers in a multiplex assay, improve ubiquity. Universal primers SEQ ID NOs. 643-645 based on *tuf* sequences have been designed

to amplify most pathogenic bacteria except *Actinomycetaceae*, *Clostridiaceae* and the *Cytophaga*, *Flexibacter* and *Bacteroides* phylum (pathogenic bacteria of this phylum include mostly *Bacteroides*, *Porphyromonas* and *Prevotella* species). Primers to fill these gaps have been designed for *Actinomycetaceae* (SEQ ID NOs. 646-648),
 5 *Clostridiaceae* (SEQ ID NOs. 796-797, 808-811), and the *Cytophaga*, *Flexibacter* and *Bacteroides* phylum (SEQ ID NOs. 649-651). These primers sets could be used alone or in conjunction to render the universal assay more ubiquitous. These primers are in the process of being tested.

Universal primers derived from *atpD* sequences include SEQ ID NOs. 562-565.
 10 Combination of these primers does not amplify human DNA but should amplify almost all pathogenic bacterial species except proteobacteria belonging to the epsilon subdivision (*Campylobacter* and *Helicobacter*), the bacteria from the *Cytophaga*, *Flexibacter* and *Bacteroides* group and some actinomycetes and corynebacteria. By analysing *atpD* sequences from the latter species, primers and probes to specifically
 15 fill these gaps could be designed and used in conjunction with primers SEQ ID NOs. 562-565. These primers are in the process of being tested.

In addition, universality of the assay could be expanded by mixing *atpD* sequences-derived primers with *tuf* sequences-derived primers. Ultimately, even *recA* sequences-derived primers could be added to fill some gaps in the universal assay.

20 It is important to note that the 95 bacterial species selected to test the ubiquity of the universal assay include all of the most clinically relevant bacterial species associated with a variety of human infections acquired in the community or in hospitals (nosocomial infections). The most clinically important bacterial and fungal pathogens are listed in Tables 1 and 2.

25 Amino acid sequences derived from *tuf*, *atpD* and *recA* sequences

The amino acid sequences translated from the repertory of *atpD*, *tuf* and *recA* sequences are also an object of the present invention. The amino acid sequence data
 30 will be particularly useful for homology modeling of three-dimensional (3D) structure of the elongation factor Tu, elongation factor G, elongation factor 1 α , ATPase subunit beta and RecA recombinase. For all these proteins, at least one structure model has been published using X-ray diffraction data from crystals. Based on those structural informations it is possible to use computer software to build 3D
 35 model structures for any other protein having peptide sequence homologies with the known structure (Greer, 1991, Methods in Enzymology, 202:239-252, Taylor, 1994, Sali, 1995, Curr. Opin. Biotechnol. 6:437-451, Sanchez and Sali, 1997, Curr. Opin. Struct. Biol. 7:206-214, Fischer and Eisenberg, 1999, Curr. Opin. Struct. Biol. 9:208-211, Guex *et al.*, 1999, Trends Biochem. Sci. 24: 364-367). Model structures of target
 40 proteins are used for the design or to predict the behavior of ligands and inhibitors

such as antibiotics. Since EF-Tu and EF-G are already known as antibiotic targets (see above) and since the beta subunit of ATPase and RecA recombinase are essential to the survival of the microbial cells in natural conditions of infection, all four proteins could be considered antibiotic targets. Sequence data, especially the new
5 data generated by us could be very useful to assist the creation of new antibiotic molecules with desired spectrum of activity. In addition, model structures could be used to improve protein function for commercial purposes such as improving antibiotic production by microbial strains or increasing biomass.

BRIEF SUMMARY OF THE INVENTION

5 Three highly conserved genes, encoding translation elongation factor Tu, the catalytic subunit of proton-translocating ATPase and the RecA recombinase, are used to generate species-specific, genus-specific, group-specific and universal nucleic acid probes and amplification primers to rapidly detect and identify bacterial, fungal and parasitical pathogens from clinical specimens for diagnosis. The concomittant detection of associated antibiotic resistance and toxin genes are also under the scope
10 of the present invention.

DESCRIPTION OF THE DRAWINGS

15 Figures 1 and 2 illustrate the principal subdivisions of the *tuf* and *atpD* sequences repertoires, respectively. For the design of primers and probes, depending on the needs, one may want to use the complete data set illustrated on the top of the pyramid or use only a subset illustrated by the different branching points. Smaller
20 subdivisions, representing groups, families, genus and species, could even be made to extend to the bottom of the pyramid. Because the *tuf* and *atpD* sequences are highly conserved and evolved with each species, the design of primers and probes does not need to include all the sequences within the database or its subdivisions. As illustrated, in Annexes IV to XX, depending on the use, sequences from a limited
25 number of species can be carefully selected to represent: i) only the main phylogenetic branches from which the intended probes and primers need to be differentiating, and ii) only the species for which they need to be matching. However, for ubiquity purposes, and especially for primers and probes identifying large groups of species (genus, family, group or universal, or sequencing primers), the more data is
30 included into the sequence analysis, the better the probes and primers will be suitable for each particular intended use. Similarly, for specificity purposes, a larger data set (or repertoire) ensures optimal primers and probes design by reducing the chance of employing nonspecific oligonucleotides.

35 Figure 3 illustrates the approach used to design specific amplification primers from *fusA* as well as from the region between the end of *fusA* and the beginning of *tuf* in the streptomycin (*str*) operon.

EXAMPLES AND ANNEXES

40

The following examples and annexes are intended to be illustrative of the various methods and compounds of the invention, rather than limiting the scope thereof.

The various annexes show the strategies used for the selection of DNA amplification primers, nucleic acid hybridization probes or molecular beacon internal probes from *tuf*, *atpD*, *recA*, *speA*, *stx*, *van*, *pbp*, *mecA*, *hexA*, *pcp*, *ddl*, *mtl* or unknown gene sequences:

- (i) Annex I shows the amplification primers used for *tuf* sequences.
- (ii) Annex II shows the amplification primers used for *atpD* sequences.
- (iii) Annex III shows the internal probes for nucleic acid hybridization and specific detection of *tuf* sequences.
- 10 (iv) Annex IV illustrates the strategy used for the selection of the amplification primers specific for *atpD* sequences of the F-type.
- (v) Annex V illustrates the strategy used for the selection of the amplification primers specific for *atpD* sequences of the V-type.
- 15 (vi) Annex VI illustrates the strategy used for the selection of the amplification primers specific for the *tuf* sequences of organelle lineage (M, the letter M is used to indicate that in most cases, the organelle is the mitochondria).
- (vii) Annex VII illustrates the strategy used for the selection of the amplification primers specific for the *tuf* sequences of eukaryotes (EF-1).
- 20 (viii) Annex VIII illustrates the strategy for the selection of *Streptococcus agalactiae*-specific amplification primers from *tuf* sequences.
- (ix) Annex IX illustrates the strategy for the selection of *Streptococcus agalactiae*-specific hybridization probes from *tuf* sequences.
- (x) Annex X illustrates the strategy for the selection of *Streptococcus agalactiae*-specific amplification primers from *atpD* sequences.
- 25 (xi) Annex XI illustrates the strategy for the selection from *tuf* sequences of *Candida albicans/dubliniensis*-specific amplification primers, *Candida albicans*-specific hybridization probe and *Candida dubliniensis*-specific hybridization probe.
- 30 (xii) Annex XII illustrates the strategy for the selection of *Staphylococcus*-specific amplification primers from *tuf* sequences.
- (xiii) Annex XIII illustrates the strategy for the selection of the *Staphylococcus* genus-specific hybridization probe from *tuf* sequences.
- (xiv) Annex XIV illustrates the strategy for the selection of *Staphylococcus saprophyticus*-specific and *Staphylococcus haemolyticus*-specific hybridization probes from *tuf* sequences.
- 35 (xv) Annex XV illustrates the strategy for the selection of *Staphylococcus aureus*-specific and *Staphylococcus epidermidis*-specific hybridization probes from *tuf* sequences.
- 40 (xvi) Annex XVI illustrates the strategy for the selection of the *Staphylococcus hominis*-specific hybridization probe from *tuf* sequences.

- (xvii) Annex XVII illustrates the strategy for the selection of the *Enterococcus* genus-specific amplification primers from *tuf* sequences.
- (xviii) Annex XVIII illustrates the strategy for the selection of the *Enterococcus faecalis*-specific hybridization probe, of the *Enterococcus faecium*-specific hybridization probe and of the *Enterococcus casseliflavus-flavescens-gallinarum* group-specific hybridization probe from *tuf* sequences.
- (xix) Annex XIX illustrates the strategy for the selection of primers from *tuf* sequences for the identification of platelets contaminants.
- (xx) Annex XX illustrates the strategy for the selection of the universal amplification primers from *atpD* sequences.
- (xxi) Annex XXI illustrates the amplification primers used for nucleic acid amplification from *recA* sequences.
- (xxii) Annex XXII shows the specific and ubiquitous primers for nucleic acid amplification from *speA* sequences.
- (xxiii) Annex XXIII illustrates the first strategy for the selection of *Streptococcus pyogenes*-specific amplification primers from *speA* sequences.
- (xxiv) Annex XXIV illustrates the second strategy for the selection of *Streptococcus pyogenes*-specific amplification primers from *speA* sequences.
- (xxv) Annex XXV illustrates the strategy for the selection of *Streptococcus pyogenes*-specific amplification primers from *tuf* sequences.
- (xxvi) Annex XXVI illustrates the strategy for the selection of Shiga-toxin-producing, *Escherichia coli*-specific amplification primers and hybridization probe from *stx₁* sequences.
- (xxvii) Annex XXVII illustrates the strategy for the selection of Shiga toxin-producing, *Escherichia coli*-specific amplification primers and hybridization probe from *stx₂* sequences.
- (xxviii) Annex XXVIII illustrates the strategy for the selection of *vanA*-specific amplification primers from *van* sequences.
- (xxix) Annex XXIX illustrates the strategy for the selection of *vanB*-specific amplification primers from *van* sequences.
- (xxx) Annex XXX illustrates the strategy for the selection of *vanC*-specific amplification primers from *vanC* sequences.
- (xxxi) Annex XXXI illustrates the strategy for the selection of *Streptococcus pneumoniae*-specific amplification primers and hybridization probes from *pbp1a* sequences.
- (xxxii) Annex XXXII shows the specific and ubiquitous primers for nucleic acid amplification from *stx* sequences.
- (xxxiii) Annex XXXIII shows the molecular beacon internal probes for hybridization and specific detection of toxin sequences.
- (xxxiv) Annex XXXIV shows the specific and ubiquitous primers for nucleic acid

amplification from *van* sequences.

(xxxv) Annex XXXV shows the internal probes for nucleic acid hybridization and specific detection of *van* sequences.

(xxxvi) Annex XXXVI shows the specific and ubiquitous primers for nucleic acid amplification from *pbp* sequences.

(xxxvii) Annex XXXVII shows the internal probes for nucleic acid hybridization and specific detection of *pbp* sequences.

(xxxviii) Annex XXXVIII illustrates the strategy for the selection of *vanAB*-specific amplification primers and specific hybridization probes *vanA* and *vanB* from *van* sequences.

(xxxix) Annex XXXIX shows the internal probe for nucleic acid hybridization and specific detection of *mecA*.

(xl) Annex XL shows the specific and ubiquitous primers for nucleic acid amplification from *hexA* sequences.

(xli) Annex XLI shows the internal probe for nucleic acid hybridization and specific detection of *hexA*.

(xlii) Annex XLII illustrates the strategy for the selection of *Streptococcus pneumoniae* species-specific amplification primers and hybridization probe from *hexA* sequences.

(xliii) Annex XLIII shows the specific and ubiquitous primers for nucleic acid amplification from *pcp* sequences.

(xliv) Annex XLIV shows the specific and ubiquitous primers for nucleic acid amplification from unknown *S. saprophyticus* gene sequences.

(xlv) Annex XLV shows the molecular beacon internal probes for hybridization and specific detection of antibiotic resistance gene sequences.

(xlvi) Annex XLVI shows the molecular beacon internal probe for hybridization and specific detection of an unknown *S. aureus* gene sequence.

(xlvii) Annex XLVII shows the molecular beacon internal probe for hybridization and specific detection of *tuf* sequences.

(xlviii) Annex XLVIII shows the molecular beacon internal probes for hybridization and specific detection of *ddl* and *mtl* gene sequences.

(xlix) Annex XLIX shows the internal probe for nucleic acid hybridization and specific detection of the unknown *S. aureus* gene.

As shown in these annexes, the selected amplification primers may contain inosines and/or degenerescences. Inosine is a nucleotide analog able to specifically bind to any of the four nucleotides A, C, G or T. Alternatively, degenerated oligonucleotides which consist of an oligonucleotide mix having two or more of the four nucleotides A, C, G or T at the site of mismatches were used. The inclusion of inosine and/or of degenerescences in the amplification primers allows mismatch

tolerance thereby permitting the amplification of a wider array of target nucleotide sequences (Dieffenbach and Dveksler, 1995 PCR Primer: A Laboratory Manual, Cold Spring Harbor Laboratory Press, Plainview, New York).

5

EXAMPLES

EXAMPLE 1:

10

Sequencing of bacterial *atpD* (F-type and V-type) gene fragments. As shown in Annex IV, the comparison of publicly available *atpD* (F-type) sequences from a variety of bacterial species revealed conserved regions allowing the design of PCR primers able to amplify *atpD* sequences (F-type) from a wide range of bacterial species. Using primers pairs SEQ ID NOs. 566 and 567, 566 and 814, 568 and 567, 15 570 and 567, 572 and 567, 569 and 567, 571 and 567, and 700 and 567, it was possible to amplify and sequence *atpD* sequences SEQ ID NOs. 242-270, 272-398, 673-674, 737-767, 866-867 and 942-955.

20 Similarly, Annex V shows how were designed the PCR primers able to amplify *atpD* sequences of the V-type from a wide range of bacterial species. Using primers SEQ ID NOs. 681-683, it was possible to amplify and sequence *atpD* sequences SEQ ID Nos. 827-832, 929-931, 958 and 966. As the gene was difficult to amplify for several species, additional amplification primers were designed inside the original amplicon 25 (SEQ ID NOs.1203-1207).

EXAMPLE 2:

30 Sequencing of eukaryotic *atpD* (F-type and V-type) gene fragments. The comparison of publicly available *atpD* (F-type) sequences from a variety of fungal and parasitical species revealed conserved regions allowing the design of PCR primers able to amplify *atpD* sequences from a wide range of fungal and parasitical species. Using primers pairs SEQ ID NOs. 568 and 573, 574 and 573, 574 and 708, and 566 and 567, it was possible to amplify and sequence *atpD* sequences SEQ ID NOs. 458-497, 35 530-538, 663, 667, 676, 678-680, 768-778, 856-862, 889-896 and 941.

In the same manner, the primers described in Annex V (SEQ ID NOs. 681-683) could amplify the *atpD* (V-type) gene from fungal and parasitical species. We were thus able to sequence SEQ ID Nos. 834-839, 956-957, and 959-965.

40

EXAMPLE 3:

Sequencing of eukaryotic *tuf* (EF-1) gene fragments. As shown in Annex VII, the comparison of publicly available *tuf* (EF-1) sequences from a variety of fungal and

parasitica species revealed conserved regions allowing the design of PCR primers able to amplify *tuf* sequences from a wide range of fungal and parasitica species. Using primers pairs SEQ ID NOs. 558 and 559, 813 and 559, 558 and 815, 560 and 559, 653 and 559, 558 and 655, and 654 and 559, it was possible to amplify and sequence *tuf* sequences SEQ ID NOs. 399-457, 509-529, 622-624, 677, 779-790, 840-842, 865, and 897-903.

EXAMPLE 4:

10 Sequencing of eukaryotic *tuf* (organelle origin, M) gene fragments. As shown in Annex VI, the comparison of publicly available *tuf* (organelle origin, M) sequences from a variety of fungal and parasitica organelles revealed conserved regions allowing the design of PCR primers able to amplify *tuf* sequences of several organelles belonging to a wide range fungal and parasitica species. Using primers
15 pairs SEQ ID NOs. 664 and 652, 664 and 561, 911 and 914, 912 and 914, 913 and 915, 916 and 561, and 664 and 917, it was possible to amplify and sequence *tuf* sequences SEQ ID NOs. 498-508, 791-792, 843-855, and 904-910.

EXAMPLE 5:

20 Specific identification of *Streptococcus agalactiae* using *tuf* sequences. As shown in Annex VIII, the comparison of *tuf* sequences from a variety of bacterial species allowed the selection of PCR primers specific for *S. agalactiae*. The strategy used to design the PCR primers was based on the analysis of a multiple sequence alignment
25 of various *tuf* sequences. The multiple sequence alignment includes the *tuf* sequences of four bacterial strains from the target species as well as *tuf* sequences from other species and bacterial genera, especially representatives of closely related species. A careful analysis of this alignment allowed the selection of oligonucleotide sequences which are conserved within the target species but which discriminate sequences from
30 other species and genera, especially from the closely related species, thereby permitting the species-specific and ubiquitous detection and identification of the target bacterial species.

The chosen primer pair, oligos SEQ ID NO. 549 and SEQ ID NO. 550, gives an
35 amplification product of 252 bp. Standard PCR was carried out using 0.4 μ M of each primer, 2.5 mM $MgCl_2$, BSA 0.05 mM, 1X Taq Buffer (Promega), dNTP 0.2 mM (Pharmacia), 1 μ l Taq DNA polymerase (Promega) 0.025 U/ μ l combined with TaqStart 5 ng/ μ l (Clontech Laboratories Inc., Palo Alto), 1 μ l of genomic DNA sample in a final volume of 20 μ l using a PTC-200 thermocycler (MJ Research Inc.).
40 The optimal cycling conditions for maximum sensitivity and specificity were 3 minutes at 95 °C for initial denaturation, then forty cycles of two steps consisting of 1 second at 95 °C and 30 seconds at 62 °C, followed by terminal extension at 72 °C for

2 minutes. Amplification was monitored on agarose gel electrophoresis by staining the DNA with ethidium bromide.

Specificity of the assay was tested by adding into the PCR reactions, 0.1 ng of genomic DNA from each of the bacterial species listed in Table 8. Strong amplification was observed only for the 5 *S. agalactiae* strains listed. Of the other bacterial species, including 32 species representative of the vaginal flora and 27 other streptococcal species, only *S. acidominimus* yielded amplification. The signal for 0.1 ng of *S. acidominimus* genomic DNA was weak and the detection limit for this species was 10 pg (corresponding to more than 4000 genome copies) while the detection limit for *S. agalactiae* was 2.5 fg (corresponding to one genome copy) of genomic DNA.

To increase the specificity of the assay, internal probes were designed for FRET (Fluorescence Resonance Energy Transfer) detection using the LightCycler (Idaho Technology). As illustrated in Annex IX, a multiple sequence alignment of streptococcal *tuf* sequence fragments corresponding to the 252 bp region amplified by primers SEQ ID NO. 549 and SEQ ID NO. 550, was used for the design of internal probes TSagHF436 (SEQ ID NO. 582) and TSagHF465 (SEQ ID NO. 583). The region of the amplicon selected for internal probes contained sequences unique and specific to *S. agalactiae*. SEQ ID NO. 583, the more specific probe, is labelled with fluorescein in 3', while SEQ ID NO. 582, the less discriminant probe, is labelled with CY5 in 5' and blocked in 3' with a phosphate group. However, since the FRET signal is only emitted if both probes are adjacently hybridized on the same target amplicon, detection is highly specific.

Real-time detection of PCR products using the LightCycler™ was carried out using 0.4 µM of each primer (SEQ ID NO. 549-550), 0.2 µM of each probe (SEQ ID NO. 582-583), 2.5 mM MgCl₂, BSA 450 µg/ml, 1X PC2 Buffer (AB Peptides, St-Louis, MO), dNTP 0.2 mM (Pharmacia), KlenTaq1™ DNA polymerase 0.5 U (AB Peptides) 0.025 U/µl combined with TaqStart (Clontech Laboratories Inc., Palo Alto), 0.7 µl of genomic DNA sample in a final volume of 7 µl using a LightCycler thermocycler (Idaho Technology). The optimal cycling conditions for maximum sensitivity and specificity were 3 minutes at 94 °C for initial denaturation, then forty cycles of three steps consisting of 0 second (this setting meaning the LightCycler will reach the target temperature and stay at it for its minimal amount of time) at 94 °C, 10 seconds at 64 °C, 20 seconds at 72 °C. Amplification was monitored during each annealing steps using the fluorescence ratio. The streptococcal species having close sequence homologies with the *tuf* sequence of *S. agalactiae* (*S. acidominimus*, *S. anginosus*, *S. bovis*, *S. dysgalactiae*, *S. equi*, *S. ferus*, *S. gordonii*, *S. intermedius*, *S.*

parasanguis, *S. parauberis*, *S. salivarius*, *S. sanguis*, *S. suis*, and of course *S. agalactiae*) were tested in the LightCycler with 0.07 ng of genomic DNA per reaction. This time, only *S. agalactiae* yielded an amplification signal, hence demonstrating that the assay is species-specific. With the LightCycler assay using the internal FRET probes, the detection limit for *S. agalactiae* was 12.5 fg (corresponding to five genome copies) of genomic DNA.

EXAMPLE 6:

Specific identification of *Streptococcus agalactiae* using *atpD* sequences. As shown in Annex XIV, the comparison of *atpD* sequences from a variety of bacterial species allowed the selection of PCR primers specific for *S. agalactiae*. The primer design strategy is similar to the strategy described in the preceding example except that *atpD* sequences were used in the alignment (see Annex X).

Four primers were selected, ASag42 (SEQ ID NO. 627), ASag52 (SEQ ID NO. 628), ASag206 (SEQ ID NO. 625) and ASag371 (SEQ ID NO. 626). The following combinations of these four primers give four amplicons; SEQ ID NO. 627 + SEQ ID NO. 625 = 190 bp, SEQ ID NO. 628 + SEQ ID NO. 625 = 180 bp, SEQ ID NO. 627 + SEQ ID NO. 626 = 355 bp, and SEQ ID NO. 628 + SEQ ID NO. 626 = 345 bp.

Standard PCR was carried out on PTC-200 thermocyclers (MJ Research Inc) using 0.4 μ M of each primers pair, 2.5 mM $MgCl_2$, BSA 0.05 mM, 1X *taq* Buffer (Promega), dNTP 0.2 mM (Pharmacia), 1 μ l *taq* DNA polymerase (Promega) 0.025 U/ μ l combined with TaqStart 5 ng/ μ l (Clontech Laboratories Inc., Palo Alto), 1 μ l of genomic DNA sample in a final volume of 20 μ l using a PTC-200 thermocycler (MJ Research Inc.). The optimal cycling conditions for maximum sensitivity and specificity were adjusted for each primer pair. Three minutes at 95 °C for initial denaturation, then forty cycles of two steps consisting of 1 second at 95 °C and 30 seconds at the optimal temperature specified below were followed by terminal extension at 72 °C for 2 minutes. Amplification was monitored on agarose gel electrophoresis by staining the DNA with ethidium bromide. Since *atpD* sequences are relatively more specific than *tuf* sequences, only the more closely related species namely, the streptococcal species listed in table 9, were tested.

All four primer pairs only amplified the six *S. agalactiae* strains. With an annealing temperature of 63 °C, the primer pair SEQ ID NO. 627 + SEQ ID NO. 625 had a sensitivity of 1-5 fg (equivalent to 1-2 genome copies). At 55 °C, the primer pair SEQ ID NO. 628 + SEQ ID NO. 625 had a sensitivity of 2.5 fg (equivalent to 1 genome copy). At 60 °C, the primer pair SEQ ID NO. 627 + SEQ ID NO. 626 had a

sensitivity of 10 fg (equivalent to 4 genome copies). At 58 °C, the primer pair SEQ ID NO. 628 + SEQ ID NO. 626 had a sensitivity of 2.5-5 fg (equivalent to 1-2 genome copies). This proves that all four primer pairs can detect *S. agalactiae* with high specificity and sensitivity. Together with example 5, this example demonstrates that both *tuf* and *atpD* sequences are suitable targets for the identification of microorganisms at the species level.

EXAMPLE 7:

10 Development of a PCR assay for detection and identification of staphylococci at genus and species levels.

Materials and Methods

15 **Bacterial strains.** The specificity of the PCR assay was verified by using a panel of ATCC (America Type Culture Collection) and DSMZ (Deutsche Sammlung von Mikroorganismen und Zellkulturen GmbH ; German Collection of Microorganisms and Cell Cultures) reference strains consisting of 33 gram-negative and 47 gram-positive bacterial species (Table 12). In addition, 295 clinical isolates representing 11 different species of staphylococci from the microbiology laboratory of the Centre Hospitalier Universitaire de Québec, Pavillon Centre Hospitalier de l'Université Laval (CHUL) (Ste-Foy, Québec, Canada) were also tested to further validate the *Staphylococcus*-specific PCR assay. These strains were all identified by using (i) conventional methods or (ii) the automated MicroScan Autoscan-4 system equipped with the Positive BP Combo Panel Type 6 (Dade Diagnostics, Mississauga, Ontario, Canada). Bacterial strains from frozen stocks kept at -80 °C in brain heart infusion (BHI) broth containing 10% glycerol were cultured on sheep blood agar or in BHI broth (Quelab Laboratories Inc, Montréal, Québec, Canada).

30 **PCR primers and internal probes.** Based on multiple sequence alignments, regions of the *tuf* gene unique to staphylococci were identified. *Staphylococcus* genus-specific PCR primers TStaG422 (SEQ ID NO. 553) and TStaG765 (SEQ ID NO. 575) were derived from these regions (Annex XII). These PCR primers are displaced by two nucleotide positions compared to original *Staphylococcus* genus-specific PCR primers described in previous patent application WO98/20157 (SEQ ID NOs. 17 and 20 in the said patent application). These modifications were done to ensure specificity and ubiquity of the primer pair, in the light of new *tuf* sequence data revealed in the present patent application for several additional streptococcal species and strains.

40 Similarly, sequence alignments analysis were performed to design genus and species-

specific internal probes (see Annexes XIII to XVI). Two internal probes for *Staphylococcus*-genus (SEQ ID NOs. 605-606), five for *S. aureus* (SEQ ID NOs. 584-588), five for *S. epidermidis* (SEQ ID NO. 589-593), two for *S. haemolyticus* (SEQ ID NOs. 594-595), three for *S. hominis* (SEQ ID NOs. 596-598), four for *S. saprophyticus* (SEQ ID NOs. 599-601 and 695), and two for coagulase-negative *Staphylococcus* species *S. epidermidis*, *S. hominis*, *S. saprophyticus*, *S. auricularis*, *S. capitis*, *S. haemolyticus*, *S. lugdunensis*, *S. simulans*, *S. cohnii* and *S. warneri* (SEQ ID NOs. 1175-1176) were designed. The range of mismatches between the *Staphylococcus*-specific 371-bp amplicon and each of the 20-mer species-specific internal probes was from 1 to 5, in the middle of the probe when possible. No mismatches were present in the two *Staphylococcus*-genus probes for the 11 species analyzed: *S. aureus*, *S. auricularis*, *S. capitis*, *S. cohnii*, *S. epidermidis*, *S. haemolyticus*, *S. hominis*, *S. lugdunensis*, *S. saprophyticus*, *S. simulans* and *S. warneri*. In order to verify the intra-specific sequence conservation of the nucleotide sequence, sequences were obtained for the 371-bp amplicon from five unrelated ATCC and clinical strains for each of the species *S. aureus*, *S. epidermidis*, *S. haemolyticus*, *S. hominis* and *S. saprophyticus*. The Oligo™ (version 5.0) primer analysis software (National Biosciences, Plymouth, Minn.) was used to confirm the absence of self-complementary regions within and between the primers or probes. When required, the primers contained inosines or degenerated nucleotides at one or more variable positions. Oligonucleotide primers and probes were synthesized on a model 394 DNA synthesizer (Perkin-Elmer Corp., Applied Biosystems Division, Mississauga, Ontario, Canada). Detection of the hybridization was performed with the DIG-labeled dUTP incorporated during the amplification with the *Staphylococcus*-specific PCR assay, and the hybridization signal was detected with a luminometer (Dynex Technologies) as described above in the section on luminescent detection of amplification products. Annexes XIII to XVI illustrate the strategy for the selection of several internal probes.

PCR amplification. For all bacterial species, amplification was performed from purified genomic DNA or from a bacterial suspension whose turbidity was adjusted to that of a 0.5 McFarland standard, which corresponds to approximately 1.5×10^8 bacteria per ml. One nanogram of genomic DNA or 1 μ l of the standardized bacterial suspension was transferred directly to a 19 μ l PCR mixture. Each PCR reaction contained 50 mM KCl, 10 mM Tris-HCl (pH 9.0), 0.1% Triton X-100, 2.5 mM $MgCl_2$, 0.2 μ M (each) of the two *Staphylococcus* genus-specific primers (SEQ ID NOs. 553 and 575), 200 μ M (each) of the four deoxynucleoside triphosphates (Pharmacia Biotech), 3.3 μ g/ μ l bovine serum albumin (BSA) (Sigma-Aldrich Canada Ltd, Oakville, Ontario, Canada), and 0.5 U *Taq* polymerase (Promega) coupled with *TaqStart*™ Antibody (Clontech). The PCR amplification was performed as follows: 3 min. at 94

°C for initial denaturation, then forty cycles of two steps consisting of 1 second at 95 °C and 30 seconds at 55 °C, plus a terminal extension at 72 °C for 2 minutes. Amplification was monitored on agarose gel electrophoresis by staining the amplified DNA with ethidium bromide.

For determination of the sensitivities of the PCR assays, two-fold dilutions of purified genomic DNA were used to determine the minimal number of genome copies which can be detected.

Results

Amplifications with the *Staphylococcus* genus-specific PCR assay. The specificity of the assay was assessed by performing 30-cycle and 40-cycle PCR amplifications with the panel of gram-positive (47 species from 8 genera) and gram-negative (33 species from 22 genera) bacterial species listed in Table 12. The PCR assay was able to detect 27 of 27 staphylococcal species tested in both 30-cycle and 40-cycle regimens. For 30-cycle PCR, all bacterial species tested other than staphylococci were negative. For 40-cycle PCR, *Enterococcus faecalis*, *Lactobacillus acidophilus*, *Lactococcus lactis*, *Macrococcus caseolyticus*, *Streptococcus agalactiae* and *S. mutans* were slightly positive for the *Staphylococcus*-specific PCR assay. The other species tested remained negative. Ubiquity tests performed on a collection of 295 clinical isolates provided by the microbiology laboratory of the Centre Hospitalier Universitaire de Québec, Pavillon Centre Hospitalier de l'Université Laval (CHUL), including *Staphylococcus aureus* (n=34), *S. auricularis* (n=2), *S. capitis* (n=19), *S. cohnii* (n=5), *S. epidermidis* (n=18), *S. haemolyticus* (n=21), *S. hominis* (n=73), *S. lugdunensis* (n=17), *S. saprophyticus* (n=6), *S. simulans* (n=3), *S. warneri* (n=32) and *Staphylococcus* sp. (n=65), showed a uniform amplification signal with the 30-cycle PCR assays and a perfect relation between the genotype and classical identification schemes.

The sensitivity of the *Staphylococcus*-specific assay with 30-cycle and 40-cycle PCR protocols was determined by using purified genomic DNA from the 11 staphylococcal species previously mentioned. For PCR with 30 cycles, a detection limit of 50 copies of genomic DNA was consistently obtained. In order to enhance the sensitivity of the assay, the number of cycles was increased. For 40-cycle PCR assays, the detection limit was lowered to a range of 5-10 genome copies, depending on the staphylococcal species tested.

Hybridization between the *Staphylococcus*-specific 371-bp amplicon and species-specific or genus-specific internal probes. Inter-species polymorphism was sufficient to generate species-specific internal probes for each of the principal

species involved in human diseases (*S. aureus*, *S. epidermidis*, *S. haemolyticus*, *S. hominis* and *S. saprophyticus*). In order to verify the intra-species sequence conservation of the nucleotide sequence, sequences comparisons were performed on the 371-bp amplicon from five unrelated ATCC and clinical strains for each of 5 staphylococcal species: *S. aureus*, *S. epidermidis*, *S. haemolyticus*, *S. hominis* and *S. saprophyticus*. Results showed a high level of conservation of nucleotide sequence between different unrelated strains from the same species. This sequence information allowed the development of staphylococcal species identification assays using species-specific internal probes hybridizing to the 371-bp amplicon. These assays are specific and ubiquitous for those five staphylococcal species. In addition to the species-specific internal probes, the genus-specific internal probes were able to recognize most *Staphylococcus* species.

15 **EXAMPLE 8:**

Differentiating between the two closely related yeast species *Candida albicans* and *Candida dubliniensis*. It is often useful for the clinician to be able to differentiate between two very closely related species of microorganisms. *Candida albicans* is the most important cause of invasive human mycose. In the recent years, a very closely related species, *Candida dubliniensis*, was isolated in immunosuppressed patients. These two species are difficult to distinguish by classic biochemical methods. This example demonstrates the use of *tuf* sequences to differentiate *Candida albicans* and *Candida dubliniensis*. PCR primers TCal528 and TCal676 were selected for their ability to specifically amplify a *tuf* (elongation factor 1 alpha type) fragment from both species (see Annex XI for primer positions and previous patent application WO98/20157 for SEQ ID NOs. 11-12). Within this *tuf* fragment, a region differentiating *C. albicans* and *C. dubliniensis* by two nucleotides was selected and used to design two internal probes (see Annex XI for probe design, SEQ ID NOs. 577 and 578) specific for each species. Amplification of genomic DNA from *C. albicans* and *C. dubliniensis* was carried out using DIG-11-dUTP as described above in the section on chemiluminescent detection of amplification products. Internal probes SEQ ID NOs. 577 and 578 were immobilized on the bottom of individual microtiter plates and hybridization was carried out as described above in the above section on luminescent detection of amplification products. Luminometer data showed that the amplicon from *C. albicans* hybridized only to probe SEQ ID NO. 577 while the amplicon from *C. dubliniensis* hybridized only to probe SEQ ID NO. 578, thereby demonstrating that each probe was species-specific.

40 **EXAMPLE 9:**

Specific identification of *Entamoeba histolytica*. Upon analysis of *tuf* (elongation factor 1 alpha) sequence data, it was possible to find four regions where *Entamoeba histolytica* sequences remained conserved while other parasitological and eukaryotic species have diverged. Primers TEntG38 (SEQ ID NO. 703), TEntG442 (SEQ ID NO. 704), TEntG534 (SEQ ID NO. 705), and TEntG768 (SEQ ID NO. 706) were designed so that SEQ ID NO. 703 could be paired with the three other primers. On PTC-200 thermocyclers (MJ Research), the cycling conditions for initial sensitivity and specificity testing were 3 min. at 94 °C for initial denaturation, then forty cycles of two steps consisting of 1 second at 95 °C and 30 seconds at 55 °C, followed by terminal extension at 72 °C for 2 minutes. Amplification was monitored on agarose gel electrophoresis by staining the amplified DNA with ethidium bromide. The three primer pairs could detect the equivalent of less than 200 *E. histolytica* genome copies. Specificity was tested using 0.5 ng of purified genomic DNA from a panel of microorganisms including *Babesia bovis*, *Babesia microti*, *Candida albicans*, *Crithidia fasciculata*, *Leishmania major*, *Leishmania hertigi* and *Neospora caninum*. Only *E. histolytica* DNA could be amplified, thereby suggesting that the assay was species-specific.

20 **EXAMPLE 10:**

Sensitive identification of *Chlamydia trachomatis*. Upon analysis of *tuf* sequence data, it was possible to find two regions where *Chlamydia trachomatis* sequences remained conserved while other species have diverged. Primers Ctr82 (SEQ ID NO. 554) and Ctr249 (SEQ ID NO. 555) were designed. With the PTC-200 thermocyclers (MJ Research), the optimal cycling conditions for maximum sensitivity and specificity were determined to be 3 min. at 94 °C for initial denaturation, then forty cycles of two steps consisting of 1 second at 95 °C and 30 seconds at 60 °C, followed by terminal extension at 72 °C for 2 minutes. Amplification was monitored on agarose gel electrophoresis by staining the amplified DNA with ethidium bromide. The assay could detect the equivalent of 8 *C. trachomatis* genome copies. Specificity was tested on 0.1 ng of purified genomic DNA from a panel of microorganisms including 22 species commonly encountered in the vaginal flora (*Bacillus subtilis*, *Bacteroides fragilis*, *Candida albicans*, *Clostridium difficile*, *Corynebacterium cervicis*, *Corynebacterium urealyticum*, *Enterococcus faecalis*, *Enterococcus faecium*, *Escherichia coli*, *Fusobacterium nucleatum*, *Gardnerella vaginalis*, *Haemophilus influenzae*, *Klebsiella oxytoca*, *Lactobacillus acidophilus*, *Peptococcus niger*, *Peptostreptococcus prevotii*, *Porphyromonas asaccharolytica*, *Prevotella melaninogenica*, *Propionibacterium acnes*, *Staphylococcus aureus*, *Streptococcus acidominimus*, and *Streptococcus agalactiae*). Only *C. trachomatis* DNA could be

amplified, thereby suggesting that the assay was species-specific.

EXAMPLE 11:

5 Genus-specific identification of enterococci. Upon analysis of *tuf* sequence data and comparison with the repertory of *tuf* sequences, it was possible to find two regions where *Enterococcus* sequences remained conserved while other genera have diverged (Annex XVII). Primer pair Encg313dF and Encg599c (SEQ ID NOs. 1137 and 1136) was tested for its specificity by using purified genomic DNA from a panel of bacteria
10 listed in Table 10. Using the PTC-200 thermocycler (MJ Research), the optimal cycling conditions for maximum sensitivity and specificity were determined to be 3 min. at 94 °C for initial denaturation, then forty cycles of two steps consisting of 1 second at 95 °C and 30 seconds at 55 °C, followed by terminal extension at 72 °C for 2 minutes. Amplification was monitored on agarose gel electrophoresis by staining
15 the amplified DNA with ethidium bromide. The 18 enterococcal species listed in Table 10 were all amplified efficiently. The only other species amplified were *Abiotrophia adiacens*, *Gemella haemolysans* and *Gemella morbillorum*, three gram-positive species. Sensitivity tested with several strains of *E. casseliflavus*, *E. faecium*,
20 *E. faecalis*, *E. flavescens* and *E. gallinarum* and with one strain of each other *Enterococcus* species listed in Table 10 ranged from 1 to 10 genome copies. The sequence variation within the 308-bp amplicon was sufficient so that nested PCR or internal probes could be used to speciate the amplicon and differentiate enterococci from *Abiotrophia adiacens*, *Gemella haemolysans* and *Gemella morbillorum*, thereby
25 allowing to achieve excellent specificity. Species-specific internal probes were generated for each of the clinically important species, *E. faecalis* (SEQ ID NO. 1174), *E. faecium* (SEQ ID NO. 602), and the *E. casseliflavus*, *E. flavescens*, *E. gallinarum* group (SEQ ID NO. 1122) (Annex XVIII). The species-specific internal probes were able to differentiate their respective *Enterococcus* species from all other
30 *Enterococcus* species. These assays are sensitive, specific and ubiquitous for those five *Enterococcus* species.

EXAMPLE 12:

35 Identification of the major bacterial platelets contaminants using *tuf* sequences in a multiplex test. Blood platelets preparations need to be monitored for bacterial contaminations. The *tuf* sequences of 17 important bacterial contaminants of platelets were aligned. As shown in Annex XIX, analysis of these sequences allowed the design PCR primers. Since in the case of contamination of platelet concentrates, detecting all species (not just the more frequently encountered ones) is desirable,
40 perfect specificity of primers was not an issue in the design. However, sensitivity is

important. That is why, to avoid having to put too much degeneracy, only the most frequent contaminants were included in primer design, knowing that the selected primers would anyway be able to amplify more species than the 17 used in the design. Oligonucleotide sequences which are conserved in these 17 major bacterial contaminants of platelet concentrates were chosen (oligos Tplaq 769 and Tplaq 991, respectively SEQ ID NOs. 636 and 637) thereby permitting the detection of these bacterial species. However, sensitivity was slightly deficient with staphylococci. To ensure maximal sensitivity in the detection of all the more frequent bacterial contaminants, a multiplex assay also including oligonucleotide primers targetting the *Staphylococcus* genera (oligos Stag 422, SEQ ID NO. 553; and Stag 765, SEQ ID NO. 575) was developed. The bacterial species detected with the assay are listed in Table 14.

The primer pairs, oligos SEQ ID NO. 636 and SEQ ID NO. 637 that give an amplification product of 245 pb, and oligos SEQ ID NO. 553 and SEQ ID NO. 575 that give an amplification product of 368 pb, were used simultaneously in the multiplex PCR assay. Real-time detection of these PCR products was made on the LightCycler thermocycler (Idaho Technology) using SYBR® Green I (Molecular Probe Inc.). SYBR® Green I is a fluorescent dye that binds specifically to double-stranded DNA. It thus binds to DNA products as they are synthesized. The measure of SYBR® Green I fluorescence at the end of each elongation cycle indicates the amount of DNA duplex generated by specific DNA fragment amplification and primer-dimer formation.

Fluorogenic detection of PCR products with the LightCycler was carried out using 1.0 mM of both Tplaq primers (SEQ ID NOs. 636-637) and 0.4 mM of both TStaG primers (SEQ ID NOs. 553 and 575), 2.5 mM MgCl₂, BSA 500 mg/ml, dNTP 0.2 mM (Pharmacia), 10X PCR reaction buffer (Boehringer Mannheim) and *taq* DNA polymerase (Boehringer Mannheim) 0.025 U/ml combined with TaqStart 5 ng/ml (Clontech), and 0.7 ml of genomic DNA sample in a final volume of 7 ml. The optimal cycling conditions for maximum sensitivity were 1 minute at 94 °C for initial denaturation, then forty-five cycles of three steps consisting of 0 second at 95 °C, 5 seconds at 60 °C and 9 seconds at 72 °C. Amplification was monitored during each elongation cycle by measuring the level of SYBR® Green I. However, real analysis takes place after PCR. Melting curves are done for each sample and transformation of the melting peak allows determination of T_m. Thus primer-dimer and specific PCR product are discriminated. With this assay, all prominent bacterial contaminants of platelet concentrates listed in Annex XIX and Table 14 were detected. Sensitivity tests were performed on the 9 most frequent bacterial contaminants of platelets. The detection limit was less than 20 genome copies for *E. cloacae*, *B. cereus*, *S.*

choleraesuis and *S. marcescens*; less than 15 genome copies for *P. aeruginosa*; and 2 to 3 copies were detected for *S. aureus*, *S. epidermidis*, *E. coli* and *K. pneumoniae*. Further refinements of assay conditions should increase sensitivity levels.

5 EXAMPLE 13:

The resolving power of the *tuf* and *atpD* sequences databases is comparable to the biochemical methods for bacterial identification. The present gold standard for bacterial identification is mainly based on key morphological traits and batteries of biochemical tests. Here we demonstrate that the use of *tuf* and *atpD* sequences combined with simple phylogenetic analysis of databases formed by these sequences is comparable to the gold standard. In the process of acquiring data for the *tuf* sequences, we sequenced the *tuf* gene of a strain that was given to us labelled as *Staphylococcus hominis* ATCC 35982. That *tuf* sequence (SEQ ID NO. 192) was incorporated into the *tuf* sequences database and subjected to a basic phylogenetic analysis using the Pileup command from version 10 of the GCG package (Genetics Computer Group, inc.). This analysis indicated that SEQ ID NO. 192 is not associated with other *S. hominis* strains but rather with the *S. warneri* strains. The ATCC 35982 strain was sent to the reference laboratory of the Laboratoire de Santé publique du Québec (LSPQ). They used the classic identification scheme for staphylococci (Kloos and Schleifer, 1975., J. Clin. Microbiol. 1:82-88). Their results shown that although the colonial morphology could correspond to *S. hominis*, the more precise biochemical assays did not. These assays included discriminant mannitol, mannose and ribose acidification tests as well as rapid and dense growth in deep thioglycolate agar. The LSPQ report identified strain ATCC 35982 as *S. warneri* which confirms our database analysis. The same thing happened for *S. warneri* (SEQ ID NO. 187) which had initially been identified as *S. haemolyticus* by a routine clinical laboratory using a low resolving power automated system (MicroScan, AutoScan-4™). Again, the *tuf* and LSPQ analysis agreed on its identification as *S. warneri*. In numerous other instances, in the course of acquiring *tuf* and *atpD* sequence data from various species and genera, analysis of our *tuf* and/or *atpD* sequence databases permitted the exact identification of mislabelled or erroneously identified strains. These results clearly demonstrate the usefulness and the high resolving power of our sequence-based identification assays using the *tuf* and *atpD* sequences databases.

EXAMPLE 14:

Detection of group B streptococci in clinical specimens.

Introduction

Streptococcus agalactiae, the group B streptococcus (GBS), is responsible for a severe illness affecting neonate infants. The bacterium is passed from the healthy carrier mother to the baby during delivery. To prevent this infection, it is recommended to treat expectant mothers susceptible of carrying GBS in their anovaginal flora. Carrier status is often a transient condition and rigorous monitoring requires cultures and classic bacterial identification weeks before delivery. To improve the diagnostic and identification of GBS we developed a rapid, specific and sensitive PCR test fast enough to be performed right at delivery.

Materials and Methods

GBS Clinical Specimens. A total of 66 duplicate anovaginal swabs were collected from 41 consenting pregnant women admitted for delivery at the Centre Hospitalier Universitaire de Québec, Pavillon Saint-François d'Assise following the CDC recommendations. The samples were obtained either before or after rupture of membranes. The swab samples were tested at the Centre de Recherche en Infectiologie de l'Université Laval within 24 hours of collection. Upon receipt, one swab was cut and then the tip of the swab was added to GNS selective broth for identification of group B streptococci (GBS) by the standard culture methods recommended by the Center for Diseases Control. The other swab was processed following the instruction of the IDI DNA extraction kit (Infectio Diagnostics (IDI) Inc.) prior to PCR amplification.

Oligonucleotides. PCR primers, Tsag340 (SEQ ID NO. 549) and Tsag552 (SEQ ID NO. 550) complementary to the regions of the *tuf* gene unique for GBS were designed based upon a multiple sequence alignment using our repertory of *tuf* sequences. Oligo primer analysis software (version 5.0) (National Biosciences) was used to analyse primers annealing temperature, secondary structure potential as well as mispriming and dimerization potential. The primers were synthesized using a model 391 DNA synthesizer (Perkin-Elmer).

A pair of fluorescently labeled adjacent hybridization probes Sag465-F (SEQ ID NO. 583) and Sag436-C (SEQ ID NO. 582) were synthesized and purified by Operon Technologies. They were designed to meet the recommendations of the manufacturer (Idaho Technology) and based upon multiple sequence alignment analysis using our repertory of *tuf* sequences to be specific and ubiquitous for GBS. These adjacent probes, which are separated by one nucleotide, allow fluorescence resonance energy transfer (FRET), generating an increased fluorescence signal when both hybridized simultaneously to their target sequences. The probe SEQ ID NO. 583 was labeled with FITC in 3 prime while SEQ ID NO. 582 was labeled with Cy5 in 5 prime. The

Cy5-labeled probes contained a 3'-blocking phosphate group to prevent extension of the probes during the PCR reactions.

PCR Amplification. Conventional amplifications were performed either from 2 μ l of a purified genomic DNA preparation or cell lysates of anovaginal specimens. The 20 μ l PCR mixture contained 0.4 μ M of each GBS-specific primer (SEQ ID NOs. 549-550), 200 μ M of each deoxyribonucleotide (Pharmacia Biotech), 10 mM Tris-HCl (pH 9.0), 50 mM KCl, 0.1% Triton X-100, 2.5 mM MgCl₂, 3.3 mg/ml bovine serum albumin (BSA) (Sigma), and 0.5 U of *Taq* polymerase (Promega) combined with the TaqStart antibody (Clontech). The TaqStart antibody, which is a neutralizing monoclonal antibody of *Taq* DNA polymerase, was added to all PCR reactions to enhance the efficiency of the amplification. The PCR mixtures were subjected to thermal cycling (3 min at 95 °C and then 40 cycles of 1 s at 95 °C, and 30 s at 62 °C with a 2-min final extension at 72 °C) with a PTC-200 DNA Engine thermocycler (MJ research). The PCR-amplified reaction mixture was resolved by agarose gel electrophoresis.

The LightCyclerTM PCR amplifications were performed with 1 μ l of the same preparation as described above. The 10 μ l amplification mixture consisted of 0.4 μ M each GBS-specific primer (SEQ ID NOs. 549-550), 200 μ M each dNTP, 0.2 μ M each fluorescently labeled probe (SEQ ID NOs. 582-583), 300 μ g/ml BSA (Sigma), and 1 μ l of 10x PC2 buffer (containing 50 mM Tris-HCl (pH 9.1), 16 mM ammonium sulfate, 3.5 mM Mg²⁺, and 150 μ g/ml BSA) and 0.5 U KlenTaq1TM (AB Peptides) coupled with TaqStartTM antibody (Clontech). KlenTaq1TM is a highly active and more heat-stable DNA polymerase without 5'-exonuclease activity. This prevents hydrolysis of hybridized probes by the 5' to 3' exonuclease activity. A volume of 7 μ l of the PCR mixture was transferred into a composite capillary tube (Idaho Technology). The tubes were then centrifuged to move the reaction mixture to the tips of the capillaries and then cleaned with optical-grade methanol. Subsequently the capillaries were loaded into the carousel of a LC32 LightCyclerTM (Idaho Technology), an instrument that combines rapid-cycle PCR with fluorescence analysis for continuous monitoring during amplification. The PCR reaction mixtures were subjected to a denaturation step at 94 °C for 3 min followed by 45 cycles of 0 s at 94 °C, 20 s at 64 °C and 10 s at 72 °C with a temperature transition rate of 20 °C/s. Fluorescence signals were obtained at each cycle by sequentially positioning each capillary on the carousel at the focus of optical elements affiliated to the built-in fluorimeter for 100 milliseconds. Complete amplification and analysis required about 35 min.

Specificity And Sensitivity Tests. The specificity of the conventional and LightCyclerTM PCR assays was verified by using purified genomic DNA (0.1 ng/reaction) from a battery of ATCC reference strains representing 35 clinically relevant gram-positive species (*Abiotrophia defectiva* ATCC 49176, *Bifidobacterium*

breve ATCC 15700, *Clostridium difficile* ATCC 9689, *Corynebacterium urealyticum* ATCC 43042, *Enterococcus casseliflavus* ATCC 25788, *Enterococcus durans* ATCC 19432, *Enterococcus faecalis* ATCC 29212, *Enterococcus faecium* ATCC 19434, *Enterococcus gallinarum* ATCC 49573, *Enterococcus raffinosus* ATCC 49427, *Lactobacillus reuteri* ATCC 23273, *Lactococcus lactis* ATCC 19435, *Listeria monocytogenes* ATCC 15313, *Peptococcus niger* ATCC 27731, *Peptostreptococcus anaerobius* ATCC 27337, *Peptostreptococcus prevotii* ATCC 9321, *Staphylococcus aureus* ATCC 25923, *Staphylococcus epidermidis* ATCC 14990, *Staphylococcus haemolyticus* ATCC 29970, *Staphylococcus saprophyticus* ATCC 15305, *Streptococcus agalactiae* ATCC 27591, *Streptococcus anginosus* ATCC 33397, *Streptococcus bovis* ATCC 33317, *Streptococcus constellatus* ATCC 27823, *Streptococcus dysgalactiae* ATCC 43078, *Streptococcus gordonii* ATCC 10558, *Streptococcus mitis* ATCC 33399, *Streptococcus mutans* ATCC 25175, *Streptococcus oralis* ATCC 35037, *Streptococcus parauberis* ATCC 6631, *Streptococcus pneumoniae* ATCC 6303, *Streptococcus pyogenes* ATCC 19615, *Streptococcus salivarius* ATCC 7073, *Streptococcus sanguinis* ATCC 10556, *Streptococcus uberis* ATCC 19436). These microbial species included 15 species of streptococci and many members of the normal vaginal and anal floras. In addition, 40 GBS isolates of human origin, whose identification was confirmed by the Latex agglutination test (Streptex, Murex), were also used to evaluate the ubiquity of the assay.

For determination of the sensitivities (i.e., the minimal number of genome copies that could be detected) for conventional and LightCycler™ PCR assays, serial 10-fold or 2-fold dilutions of purified genomic DNA from 5 GBS ATCC strains were used.

Results

Evaluation of the GBS-specific conventional and LightCycler™ PCR assay.

The specificity of the two assays demonstrated that only DNAs from GBS strains could be amplified. Both PCR assays did not amplify DNAs from any other bacterial species tested including 14 streptococcal species other than GBS as well as phylogenetically related species belonging to the genera *Enterococcus*, *Peptostreptococcus* and *Lactococcus*. Important members of the vaginal or anal flora, including coagulase-negative staphylococci, *Lactobacillus* sp., and *Bacteriodes* sp. were also negative with the GBS-specific PCR assay. The LightCycler™ PCR assays detected only GBS DNA by producing an increased fluorescence signal which was interpreted as a positive PCR result. Both PCR methods were able to amplify all of 40 GBS clinical isolates, showing a perfect correlation with the phenotypic identification methods.

The sensitivity of the assay was determined by using purified genomic DNA

from the 5 ATCC strains of GBS. The detection limit for all of these 5 strains was one genome copy of GBS. The detection limit of the assay with the LightCycler™ was 3.5 fg of genomic DNA (corresponding to 1-2 genome copies of GBS). These results confirmed the high sensitivity of our GBS-specific PCR assay.

Direct Detection of GBS from anovaginal specimens. Among 66 anovaginal specimens tested, 12 were positive for GBS by culture. 11 of them were also identified by both PCR assays. The sensitivity of both PCR methods with vaginal/anal specimens for identifying colonization status in pregnant women at delivery was 91.7% when compared to culture results. The specificity and positive predictive values were both 100% and the negative predictive value was 97.8%. The time for obtaining results was approximately 45 min for LightCycler™ PCR, approximately 100 min for conventional PCR and 48 hours for culture.

Conclusion

We have developed for the detection of GBS two PCR assays (conventional and LightCycler™) which are specific (i.e., no amplification of DNA from a variety of bacterial species other than GBS) and sensitive (i.e., able to detect around 1 genome copy for several reference ATCC strains of GBS). Both PCR assays are able to detect GBS directly from anovaginal specimens in a very short turnaround time. Using the real-time PCR assay on LightCycler™, we can detect GBS carriage in pregnant women at delivery within 45 minutes.

EXAMPLE 15:

Simultaneous identification of *Streptococcus pyogenes* and its pyrogenic exotoxin A.
The rapid detection of *Streptococcus pyogenes* and of its pyrogenic exotoxin A is of clinical importance. We developed a multiplex assay which permits the detection of strains of *S. pyogenes* carrying the pyrogenic toxin A gene, which is associated with scarlet fever and other pathologies. In order to specifically detect *S. pyogenes*, nucleotide sequences of the pyrrolidone carboxyl peptidase gene (*pcp*) were aligned to design PCR primers Spy291 (SEQ ID NO. 1211) and Spy473 (SEQ ID NO. 1210). Next, we designed primers for the specific detection of the pyrogenic exotoxin A. Nucleotide sequences of the *speA* gene, carried on the bacteriophage T12, were aligned as shown in Annex XXIII to design PCR primers Spytx814 (SEQ ID NO. 994) and Spytx 927 (SEQ ID NO. 995).

The primer pairs : oligos SEQ ID NOs. 1210-1211, yielding an amplification product of 207 bp, and oligos SEQ ID NOs. 994-995, yielding an amplification product of 135 bp, were used in the PCR assay.

PCR amplification was carried out using 0.4 μ M of both pairs of primers, 2.5 mM MgCl_2 , BSA 0.05 μ M, dNTP 0.2 μ M (Pharmacia), 10X PCR reaction buffer (Promega), 0.025 U/ml *Taq* DNA polymerase (Promega) combined with TaqStart (Clontech Laboratories Inc.), and 1 μ l of genomic DNA sample in a final volume of 20 μ l. PCR amplification was performed using a PTC-200 thermal cycler (MJ Research). The optimal cycling conditions for maximum sensitivity were 3 minutes at 94 °C for initial denaturation, then forty cycles of two steps consisting of 1 second at 95 °C and 30 seconds at 63 °C, followed by a final step of 2 minutes at 72 °C. Detection of the PCR products was made by agarose gel (2%) electrophoresis containing 0.25 μ g/ml of ethidium bromide. Visualization of the PCR products was made under UV at 254 nm.

The detection limit was less than 5 genome copies for both *S. pyogenes* and its pyrogenic exotoxin A. The assay was specific for pyrogenic exotoxin A-producing *S. pyogenes*: strains of the 27 other species of *Streptococcus* tested were all negative, as well as 20 strains of various gram-positive and gram-negative bacterial species.

A similar approach was used to design an alternative set of *speA*-specific primers (SEQ ID NOs. 996 to 998, see Annex XXIV). In addition, another set of primers based on the *tuf* gene (SEQ ID NOs. 999 to 1001, see Annex XXV) could be used to specifically detect *Streptococcus pyogenes*.

EXAMPLE 16 :

Real-time identification of Shiga toxin-producing bacteria. Shiga toxin-producing *Escherichia coli* and *Shigella dysenteriae* cause bloody diarrhea. Currently, identification relies mainly on the phenotypic identification of *S. dysenteriae* and *E. coli* serotype O157:H7. However, other serotypes of *E. coli* are increasingly found to be producers of type 1 and/or type 2 Shiga toxins. Two pairs of PCR primers targeting highly conserved regions present in each of the Shiga toxin genes *stx*₁ and *stx*₂ were designed to amplify all variants of those genes (see Annexes XXVI and XXVII). The first primer pair, oligonucleotides 1SLT224 (SEQ ID NO. 1081) and 1SLT385 (SEQ ID NO. 1080), yields an amplification product of 186 bp from the *stx*₁ gene. For this amplicon, the 1SLTB1-Fam (SEQ ID NO. 1084) molecular beacon was designed for the specific detection of *stx*₁ using the fluorescent label 6-carboxy-fluorescein. A second pair of PCR primers, oligonucleotides 2SLT537 (SEQ ID NO. 1078) and 2SLT678b (SEQ ID NO. 1079), yields an amplification product of 160 bp from the *stx*₂ gene. Molecular beacon 2SLTB1-Tet (SEQ ID NO. 1085) was designed for the specific detection of *stx*₂ using the fluorescent label 5-tetrachloro-fluorescein.

Both primer pairs were combined in a multiplex PCR assay.

PCR amplification was carried out using 0.8 μ M of primers pair SEQ ID NOs. 1080-1081, 0.5 μ M of primer pair SEQ ID NOs. 1078-1079, 0.3 μ M of each molecular beacon, 8 mM MgCl₂, 12.25 μ g BSA, 0.2 mM dNTPs (Pharmacia), 50 mM Tris-HCl, 16 mM NH₄SO₄, 1X TaqMaster (Eppendorf), 2.5 U KlenTaq1 DNA polymerase (AB Peptides) combined with TaqStart (Clontech Laboratories Inc.), and 1 μ l of genomic DNA sample in a final volume of 25 μ l. PCR amplification was performed using a SmartCycler thermal cycler (Cepheid). The optimal cycling conditions for maximum sensitivity were 60 seconds at 95 °C for initial denaturation, then 45 cycles of three steps consisting of 10 seconds at 95 °C, 15 seconds at 56 °C and 5 seconds at 72 °C. Detection of the PCR products was made in real-time by measuring the fluorescent signal emitted by the molecular beacon when it hybridizes to its target at the end of the annealing step at 56 °C.

The detection limit was the equivalent of less than 5 genome copies. The assay was specific for the detection of both toxins, as demonstrated by the perfect correlation between PCR results and the phenotypic characterization performed using antibodies specific for each Shiga toxin type. The assay was successfully performed on several Shiga toxin-producing strains isolated from various geographic areas of the world, including 10 O157:H7 *E. coli*, 5 non-O157:H7 *E. coli* and 4 *S. dysenteriae*.

EXAMPLE 17:

Development of a PCR assay for the detection and identification of staphylococci at genus and species levels and its associated *mecA* gene. The *Staphylococcus* genus-specific PCR primers described in Example 7 (SEQ ID NOs. 553 and 575) were used in multiplex with the *mecA*-specific PCR primers described in previous US patent serial no. 5,994,066 (SEQ ID NOs. 261 and 262 in the said patent) as well as with the *S. aureus*-specific PCR primers SEQ ID NOs. 152 and 153 described in the said patent. Sequence alignment analysis of 10 publicly available *mecA* gene sequences were performed to design an internal probe for *mecA* (SEQ ID NO. 1177). An internal probe was also designed for the *S. aureus*-specific amplicon (SEQ ID NO 1234). PCR amplification and agarose gel analysis of the amplified products were performed as described in Example 7, with the exception that 0.4 μ M (each) of the two *Staphylococcus* genus-specific primers (SEQ ID NOs. 553 and 575) and 0.4 μ M (each) of the *mecA* gene primers and 0.4 μ M (each) of the *S. aureus*-specific primers were used in the PCR mixture. The specificity of the multiplex assay with 40-cycle PCR protocols was verified by using purified genomic DNA from five methicillin-resistant and fifteen methicillin-sensitive staphylococcal strains. The sensitivity of the

multiplex assay with 40-cycle PCR protocols was determined by using purified genomic DNA from five methicillin-resistant and seven methicillin-sensitive staphylococcal strains. A detection limit of 3-5 genome copies was obtained, depending on the staphylococcal species tested. Furthermore, the *mecA*-specific internal probe and the *S. aureus*-specific internal probe combined with (i) the species-specific internal probes, (ii) the genus-specific internal probes and (iii) the coagulase-negative staphylococci specific internal probes (described in Example 7) were able to recognize three methicillin-resistant staphylococcal strains with high sensitivity and specificity.

The format of the assay is not limited to the one described above. A person skilled in the art could adapt the assay for different formats such as PCR with real-time detection using molecular beacon probes. Molecular beacon probes designed to be used in this assay include, but are not limited to, SEQ ID NO. 1232 for detection of the *S. aureus*-specific amplicon, SEQ ID NO. 1233 for detection of coagulase-negative staphylococci and SEQ ID NO. 1231 for detection of *mecA*.

EXAMPLE 18:

Sequencing of *pbp1a*, *pbp2b* and *pbp2x* genes of *Streptococcus pneumoniae*. The comparison of publicly available *pbp1a*, *pbp2b* and *pbp2x* sequences from a variety of *S. pneumoniae* strains revealed conserved regions allowing the design of PCR primers able to amplify *pbp1a*, *pbp2b*, and *pbp2x* sequences of several strains of *S. pneumoniae* having various levels of resistance to penicillin and third-generation cephalosporins. Using primer pairs Spnpbp1a876 and Spnpbp1a2163 (SEQ ID NOs. 1125 and 1126), Spnpbp2b580 and Spnpbp2b2045 (SEQ ID NOs. 1142 and 1143), and Spnpbp2x469 and Spnpbp2x2212 (SEQ ID NOs. 1146 and 1147), it was possible to amplify and sequence *pbp1a* sequences SEQ ID NOs. 1004-1018, *pbp2b* sequences SEQ ID NOs. 1019-1033, and *pbp2x* sequences SEQ ID NOs. 1034-1048. Six other PCR primers (SEQ ID NOs. 1127-1128, 1144-1145, 1148-1149) were also designed and used to complete the sequencing of *pbp1a*, *pbp2b* and *pbp2x* amplification products.

EXAMPLE 19:

Sequencing of *hexA* genes of *Streptococcus* species. The *hexA* sequence of *S. pneumoniae* described in previous US patent serial no. 5,994,066 (SEQ ID NO. 31 in the said patent, SEQ ID NO. 1183 in the present application) allowed the design of a PCR primer (SEQ ID NO. 1182) which was used with primer Spn1401 described in previous US patent serial no. 5,994,066 (SEQ ID NO. 156 in the said patent, SEQ ID

NO. 1179 in the present application) to amplify the *hexA* gene of one strain of *S. oralis*, three strains of *S. mitis* and four strains of *S. pneumoniae* (Annex XLII). Using primers SEQ ID NO. 1179 and SEQ ID NO. 1182, it was possible to amplify and sequence *S. pneumoniae hexA* (SEQ ID NOs. 1184-1187), *S. mitis hexA* (SEQ ID NOs. 1189-1191) and *S. oralis hexA* (SEQ ID NO. 1188).

EXAMPLE 20:

10 Development of a multiplex PCR assay for the detection of *Streptococcus pneumoniae* and its penicillin resistance genes.

Material and Methods

15 **Bacterial strains.** The specificity of the multiplex PCR assay was verified by using a panel of ATCC (American Type Culture Collection) reference strains consisting of 33 gram-negative and 67 gram-positive bacterial species (Table 13). In addition, 55 clinical isolates of *Streptococcus pneumoniae* and 16 strains of *S. mitis* and 3 strains of *S. oralis* from the microbiology laboratory of the Centre Hospitalier
20 Universitaire de Québec, Pavillon Centre Hospitalier de l'Université Laval (CHUL) (Ste-Foy, Québec, Canada) and from the Laboratoire de santé publique du Québec (LSPQ) (Sainte-Anne de Bellevue, Québec, Canada) were also tested to further validate the *Streptococcus pneumoniae*-specific PCR assay. The penicillin MICs
25 (minimal inhibitory concentration) of 55 isolates were measured by the broth dilution method according to the recommended protocol of NCCLS.

PCR primers and internal probes. The comparison of *hexA* sequences from a variety of streptococcal species described in Example 19 (SEQ ID NOs. 1184-1191) allowed the selection of a PCR primer specific for *S. pneumoniae*, Spnhexa1613
30 (SEQ ID NO. 1181). This primer was used with the *S. pneumoniae* species-specific primer SEQ ID NO. 1179 to generate an amplification product of 213 bp (Annex XLII). The PCR primer SEQ ID NO. 1181 is located 87 nucleotides downstream on the *hexA* sequence compared to the original *S. pneumoniae* species-specific PCR
35 primer Spn1515 described in previous US patent serial no. 5,994,066 (SEQ ID NO. 157 in the said patent). These modifications were done to ensure the design of the *S. pneumoniae* species-specific internal probe according to the new *hexA* sequences of several close streptococcal species (SEQ ID NOs. 1184-1191). The comparison of
40 *pbpla* sequences from *S. pneumoniae* strains with various levels of penicillin resistance allowed the identification of amino acid substitutions Ile-459 to Met and

Ser-462 to Ala that occur in isolates with high-level penicillin resistance (MICs $\geq 1\mu\text{g/ml}$), and amino acid substitutions Ser-575 to Thr, Gln-576 to Gly and Phe-577 to Tyr that are common to all penicillin-resistant isolates with MICs $\geq 0.25\mu\text{g/ml}$. As shown in annex XXXI, PCR primer pair Spnpbp1a1365 and Spnpbp1a1747 (SEQ ID NOs. 1130 and 1131) were designed to detect high-level penicillin resistance (MICs $\geq 1\mu\text{g/ml}$), whereas PCR primer pair Spnpbp1a1591 (SEQ ID NO. 1129) and SEQ ID NO. 1131 were designed to detect intermediate-level penicillin resistance ($0.25 \leq \text{MICs} \leq 0.5\mu\text{g/ml}$).

The comparison of *hexA* sequences allowed the design of an internal probe specific for *S. pneumoniae* (SEQ ID NO. 1180) (Annex XLII). The range of mismatches between the *S. pneumoniae*-specific 213-bp amplicon was from 2 to 5, in the middle of the 19-bp probe. Five internal probes containing all possible mutations were designed to detect the high-level penicillin resistance 383-bp amplicon (SEQ ID NOs. 1197, 1217-1220) and five internal probes containing all possible mutations were designed to detect the 156-bp amplicon which includes both high-level and intermediate penicillin resistance (SEQ ID NOs. 1094, 1192, 1193, 1214 and 1216). Design and synthesis of primers and probes, and detection of the hybridization were performed as described in Example 7. Annex XXXI illustrates one of the internal probes for detection of the high-level penicillin resistance 383-bp amplicon (SEQ ID NO. 1197) and one of the internal probes for detection of the intermediate level penicillin resistance 156-bp amplicon (SEQ ID NO. 1193).

PCR amplification. For all bacterial species, amplification was performed from purified genomic DNA. One μl of 0.1 nanogram of genomic DNA was transferred directly to a 19 μl PCR mixture. Each PCR reaction contained 50 mM KCl; 10 mM Tris-HCl (pH 9.0); 0.1% Triton X-100; 2.5 mM MgCl_2 ; 0.1 μM (each) of the *S. pneumoniae* species-specific primers SEQ ID NO. 1179 and SEQ ID NO. 1181, 0.1 μM of the penicillin resistance primer SEQ ID NO. 1129, 0.7 μM of the other penicillin resistance primer SEQ ID NO. 1130, and 0.6 μM of the high-level penicillin resistance primer SEQ ID NO. 1131; 200 μM (each) of the four deoxynucleoside triphosphates; 3.3 $\mu\text{g}/\mu\text{l}$ bovine serum albumin (BSA); and 0.5 U *Taq* polymerase coupled with *TaqStart*TM Antibody.

For determination of the sensitivities of the PCR assays, two-fold dilutions of purified genomic DNA were used to determine the minimal number of genome copies which can be detected.

Results

Amplifications with the multiplex PCR assay. The specificity of the assay was

assessed by performing 40-cycle PCR amplifications with the panel of gram-positive (67 species from 12 genera) and gram-negative (33 species from 17 genera) bacterial species listed in Table 13. All bacterial species tested other than *S. pneumoniae* were negative except *S. mitis* and *S. oralis*. Ubiquity tests were performed using a collection of 55 clinical *S. pneumoniae* isolates provided by the microbiology laboratory of the CHUL and the LSPQ, including high-level penicillin resistance (n=37), intermediate resistance (n=11) and sensitive (n=7) strains. There was a perfect correlation between PCR and standard susceptibility testing for 37 isolates with high-level penicillin resistance and 7 penicillin-sensitive isolates. Among 11 isolates with intermediate penicillin resistance, 9 had intermediate resistance based on PCR but two isolates with MIC of 0.5 µg/ml showed a high-level penicillin resistance based on genotyping. This demonstrated that MIC of 0.5 µg/ml may represent intermediate or high-level penicillin resistance. In general, there was a good correlation between the genotype and classical identification schemes.

The sensitivity of the *S. pneumoniae*-specific assay with 40-cycle PCR protocols was determined by using purified genomic DNA from 9 isolates of *S. pneumoniae*. The detection limit was 2-10 genome copies, depending on the *pbp* amplification pattern.

Hybridization between multiplex PCR amplicons and internal probes. The *S. pneumoniae*-specific internal probe did not hybridize to the *S. mitis* and *S. oralis* non-specific PCR amplification products generated from the *S. pneumoniae*-specific PCR primers. More precisely, this specificity was tested by using genomic DNA purified from 16 strains of *S. mitis* and from 3 strains of *S. oralis*. The ubiquity of the assay was tested by using genomic DNA from 15 strains of *S. pneumoniae*. In summary, the combination of the PCR and hybridization assays results in a highly specific test for the detection of penicillin-resistant *Streptococcus pneumoniae*.

EXAMPLE 21:

Sequencing of the vancomycin resistance *vanA*, *vanC1*, *vanC2* and *vanC3* genes. The publicly available sequences of the *vanH-vanA-vanX-vanY* locus of transposon Tn1546 from *E. faecalis*, *vanC1* sequence from one strain of *E. gallinarum*, *vanC2* and *vanC3* sequences from a variety of *E. casseliflavus* and *Enterococcus flavescens* strains, respectively, allowed the design of PCR primers able to amplify the *vanA*, *vanC1*, *vanC2* and *vanC3* sequences of several *Enterococcus* species. Using primer pairs van6877 and van9106 (SEQ ID NOs. 1150 and 1155), vanC1-122 and vanC1-1315 (SEQ ID NOs. 1110 and 1109), and vanC2C3-1 and vanC2C3-1064 (SEQ ID NOs. 1108 and 1107), it was possible to amplify and sequence *vanA* sequences

SEQ ID NOs. 1049-1057, *vanC1* sequences SEQ ID NOs. 1058-1059, *vanC2* sequences SEQ ID NOs. 1060-1063 and *vanC3* sequences SEQ ID NOs. 1064-1066, respectively. Three other PCR primers (SEQ ID NOs. 1151-1154) were also designed and used to complete the sequencing of *vanA* amplification products.

5

EXAMPLE 22:

Development of a PCR assay for the detection and identification of enterococci at genus and species levels and its associated resistance genes *vanA* and *vanB*. The comparison of *vanA* and *vanB* sequences revealed conserved regions allowing the design of PCR primers specific for both *vanA* and *vanB* sequences (Annex XXXVIII). The PCR primer pair *vanAB459* and *vanAB830R* (SEQ ID NOs. 1112 and 1111) was used in multiplex with the *Enterococcus* genus-specific primers *Encg313dF* and *Encg599c* (SEQ ID NOs. 1137 and 1136) described in Example 11. Sequence alignment analysis of *vanA* and *vanB* sequences revealed regions suitable for the design of internal probes specific for *vanA* (SEQ ID NO. 1170) and *vanB* genes (SEQ ID NO. 1171). PCR amplification and agarose gel analysis of the amplified products were performed as described in Example 11. The specificity of the multiplex assay with 40-cycle PCR was verified by using 0.1 nanogram of purified genomic DNA from a panel of bacteria listed in Table 10. The sensitivity of the multiplex assay with 40-cycle PCR was verified with three strains of *E. casseliflavus*, eight strains of *E. gallinarum*, two strains of *E. flavescens*, two vancomycin-resistant strains of *E. faecalis* and one vancomycin-sensitive strain of *E. faecalis*, three vancomycin-resistant strains of *E. faecium* and one vancomycin-sensitive strain of *E. faecium*, and one strain of each of the other enterococcal species listed in Table 10. A detection limit of 1-10 genome copies was obtained, depending on the enterococcal species tested. In addition to the species-specific internal probes described in Example 11, the *vanA*- and *vanB*-specific internal probes were able to recognize vancomycin-resistant enterococcal species with high sensitivity, specificity and ubiquity and with a perfect correlation between the genotypic and phenotypic analysis.

The format of the assay is not limited to the one described above. A person skilled in the art could adapt the assay for different formats such as PCR with real-time detection using molecular beacon probes. Molecular beacon probes designed to be used in this assay include, but are not limited to, SEQ ID NO. 1236 for the detection of *E. faecalis*, SEQ ID NO. 1235 for the detection of *E. faecium*, SEQ ID NO. 1240 for the detection of *vanA*, and SEQ ID NO. 1241 for the detection of *vanB*.

40

EXAMPLE 23:

Development of a multiplex PCR assay for detection and identification of vancomycin-resistant *Enterococcus faecalis*, *Enterococcus faecium*, *Enterococcus gallinarum*, *Enterococcus casseliflavus*, and *Enterococcus flavescens*. The comparison of *vanA* and *vanB* sequences revealed conserved regions allowing design of a PCR primer pair (SEQ ID NOs. 1089 and 1090) specific for *vanA* sequences (Annex XXVIII) and a PCR primer pair (SEQ ID NOs. 1095 and 1096) specific for *vanB* sequences (Annex XXIX). The *vanA*-specific PCR primer pair (SEQ ID NOs. 1089 and 1090) was used in multiplex with the *vanB*-specific PCR primer pair (SEQ ID NOs. 1095 and 1096). The comparison of *vanC1*, *vanC2* and *vanC3* sequences revealed conserved regions allowing design of PCR primers (SEQ ID NOs. 1101 and 1102) able to generate a 158-bp amplicon specific for *E. gallinarum*, *E. casseliflavus* and *E. flavescens* (Annex XXX). The *vanC*-specific PCR primer pair (SEQ ID NOs. 1101 and 1102) was used in multiplex with the *E. faecalis* species-specific PCR primer pair described in previous US patent serial no. 5,994,066 (SEQ ID NOs. 40 and 41 in the said patent) and with the *E. faecium* species-specific PCR primer pair described in previous patent application WO98/20157 (SEQ ID NOs. 1 and 2 in the said application). For both multiplexes, the optimal cycling conditions for maximum sensitivity and specificity were found to be 3 min. at 94 °C, followed by forty cycles of two steps consisting of 1 second at 95 °C and 30 seconds at 58 °C, plus a terminal extension at 72 °C for 2 minutes. Amplification was monitored on agarose gel electrophoresis by staining the amplified DNA with ethidium bromide. The *vanA*-specific PCR primer pair (SEQ ID NOs. 1089 and 1090), the *vanB*-specific primers pair (SEQ ID NOs. 1095 and 1096) and the *vanC*-specific primer pair (SEQ ID NOs. 1101 and 1102) were tested for their specificity by using 0.1 nanogram of purified genomic DNA from a panel of 5 vancomycin-sensitive *Enterococcus* species, 3 vancomycin-resistant *Enterococcus* species, 13 other gram-positive bacteria and one gram-negative bacterium. Specificity tests using the *E. faecium* species-specific PCR primer pair described in previous patent application WO98/20157 (SEQ ID NOs. 1 and 2 in the said application) and the *E. faecalis* species-specific PCR primer pair described in previous US patent serial no. 5,994,066 (SEQ ID NOs. 40 and 41 in the said patent) were performed on a panel of 37 gram-positive bacterial species. All *Enterococcus* strains were amplified with high specificity and there was a perfect correlation between the genotypic and phenotypic analysis. Finally, the sensitivity of the assays was determined for several strains of *E. gallinarum*, *E. casseliflavus*, *E. flavescens* and vancomycin-resistant *E. faecalis* and *E. faecium*. Using each of the *E. faecalis* and *E. faecium* species-specific PCR primer pairs as well as *vanA*, *vanB* and *vanC*-specific PCR primers used alone or in multiplex as described above, the sensitivity ranged from 1 to 10 genome copies.

The format of the assay is not limited to the one described above. A person skilled in the art could adapt the assay for different formats such as PCR with real-time

detection using molecular beacon probes. Molecular beacon probes designed to be used in this assay include, but are not limited to, SEQ ID NO. 1238 for the detection of *E. faecalis*, SEQ ID NO. 1237 for the detection of *E. faecium*, SEQ ID NO. 1239 for the detection of *vanA*, and SEQ ID NO. 1241 for the detection of *vanB*.

5

EXAMPLE 24:

Universal amplification involving the EF-G (*fusA*) subdivision of *tuf* sequences. As shown in Figure 3, primers SEQ ID NOs. 1228 and 1229 were designed to amplify the region between the end of *fusA* and the beginning of *tuf* genes in the *str* operon. Genomic DNAs from a panel of 35 strains were tested for PCR amplification with those primers. The following strains showed a positive result: *Abiotrophia adiacens* ATCC 49175, *Abiotrophia defectiva* ATCC 49176, *Bacillus subtilis* ATCC 27370, *Clostridium difficile* ATCC 9689, *Enterococcus avium* ATCC 14025, *Enterococcus casseliflavus* ATCC 25788, *Enterococcus cecorum* ATCC 43198, *Enterococcus faecalis* ATCC 29212, *Enterococcus faecium* ATCC 19434, *Enterococcus flavescens* ATCC 49996, *Enterococcus gallinarum* ATCC 49573, *Enterococcus solitarius* ATCC 49428, *Escherichia coli* ATCC 11775, *Haemophilus influenzae* ATCC 9006, *Lactobacillus acidophilus* ATCC 4356, *Peptococcus niger* ATCC 27731, *Proteus mirabilis* ATCC 25933, *Staphylococcus aureus* ATCC 43300, *Staphylococcus auricularis* ATCC 33753, *Staphylococcus capitis* ATCC 27840, *Staphylococcus epidemidis* ATCC 14990, *Staphylococcus haemolyticus* ATCC 29970, *Staphylococcus hominis* ATCC 27844, *Staphylococcus lugdunensis* ATCC 43809, *Staphylococcus saprophyticus* ATCC 15305, *Staphylococcus simulans* ATCC 27848, and *Staphylococcus warneri* ATCC 27836. This primer pair could amplify additional bacterial species; however, there was no amplification for some species, suggesting that the PCR cycling conditions could be optimized or the primers modified. For example, SEQ ID NO. 1227 was designed to amplify a broader range of species. In addition to other possible primer combinations to amplify the region covering *fusA* and *tuf*, Figure 3 illustrates the positions of amplification primers SEQ ID NOs. 1221-1227 which could be used for universal amplification of *fusA* segments. All of the above mentioned primers (SEQ ID NOs. 1221-1229) could be useful for the universal and/or the specific detection of bacteria.

EXAMPLE 25:

DNA fragment isolation from *Staphylococcus saprophyticus* by arbitrarily primed PCR. DNA sequences of unknown coding potential for the species-specific detection and identification of *Staphylococcus saprophyticus* were obtained by the method of arbitrarily primed PCR (AP-PCR).

AP-PCR is a method which can be used to generate specific DNA probes for microorganisms (Fani *et al.*, 1993, Molecular Ecology 2:243-250). A description of the AP-PCR protocol used to isolate a species-specific genomic DNA fragment from *Staphylococcus saprophyticus* follows. Twenty different oligonucleotide primers of

10 nucleotides in length (all included in the AP-PCR kit OPAD (Operon Technologies, Inc., Alameda, CA)) were tested systematically with DNAs from 5 bacterial strains of *Staphylococcus saprophyticus* as well as with bacterial strains of 27 other staphylococcal (non-*S. saprophyticus*) species. For all bacterial species, amplification was performed directly from one μL (0.1 ng/ μL) of purified genomic DNA. The 25 μL PCR reaction mixture contained 50 mM KCl, 10 mM Tris-HCl (pH 9.0), 0.1% Triton X-100, 2.5 mM MgCl_2 , 1.2 μM of only one of the 20 different AP-PCR primers OPAD, 200 μM of each of the four dNTPs, 0.5 U of *Taq* DNA polymerase (Promega Corp., Madison, Wis.) combined with TaqStartTM antibody (Clontech Laboratories Inc., Palo Alto, CA). PCR reactions were subjected to cycling using a MJ Research PTC-200 thermal cycler as follows: 3 min at 96 °C followed by 42 cycles of 1 min at 94 °C for the denaturation step, 1 min at 31 °C for the annealing step and 2 min at 72 °C for the extension step. A final extension step of 7 min at 72 °C followed the 42 cycles to ensure complete extension of PCR products. Subsequently, twenty microliters of the PCR-amplified mixture were resolved by electrophoresis on a 1.5 % agarose gel containing 0.5 $\mu\text{g/mL}$ of ethidium bromide. The size of the amplification products was estimated by comparison with a 50-bp molecular weight ladder.

Amplification patterns specific for *Staphylococcus saprophyticus* were observed with the AP-PCR primer OPAD-16 (sequence: 5'-AACGGGCGTC-3'). Amplification with this primer consistently showed a band corresponding to a DNA fragment of approximately 380 bp for all *Staphylococcus saprophyticus* strains tested but not for any of the other staphylococcal species tested.

The band corresponding to the 380 bp amplicon, specific and ubiquitous for *S. saprophyticus* based on AP-PCR, was excised from the agarose gel and purified using the QIAquickTM gel extraction kit (QIAGEN Inc.). The gel-purified DNA fragment was cloned into the T/A cloning site of the pCR 2.1TM plasmid vector (Invitrogen Inc.) using T4 DNA ligase (New England BioLabs). Recombinant plasmids were transformed into *E. coli* DH5 α competent cells using standard procedures. All reactions were performed according to the manufacturer's instructions. Plasmid DNA isolation was done by the method of Birnboim and Doly (Nucleic Acid Res., 1979, 7:1513-1523) for small-scale preparations. All plasmid DNA preparations were digested with the EcoRI restriction endonuclease to ensure the presence of the approximately 380 bp AP-PCR insert into the plasmid. Subsequently, a large-scale and highly purified plasmid DNA preparation was performed from two selected clones shown to carry the AP-PCR insert by using the QIAGEN plasmid purification kit (midi format). These large-scale plasmid preparations were used for automated DNA sequencing.

The 380 bp nucleotide sequence was determined for three strains of *S. saprophyticus* (SEQ ID NOs. 74, 1093, and 1198). Both strands of the AP-PCR insert from the two selected clones were sequenced by the dideoxynucleotide chain termination sequencing method with SP6 and T7 sequencing primers by using the Applied Biosystems automated DNA sequencer (model 373A) with their PRISMTM Sequenase^{RTM} Terminator Double-stranded DNA Sequencing Kit (Perkin-Elmer Corp., Applied Biosystems Division, Foster City, CA).

Optimal species-specific amplification primers (SEQ ID NOs. 1208 and 1209) have been selected from the sequenced AP-PCR *Staphylococcus saprophyticus* DNA fragments with the help of the primer analysis software Oligo™ 4.0 (National BioSciences Inc.). The selected primers were tested in PCR assays to verify their specificity and ubiquity. Data obtained with DNA preparations from reference ATCC strains of 49 gram-positive and 31 gram-negative bacterial species, including 28 different staphylococcal species, indicate that the selected primer pairs are specific for *Staphylococcus saprophyticus* since no amplification signal has been observed with DNAs from the other staphylococcal or bacterial species tested.

This invention has been described herein above, and it is readily apparent that modifications can be made thereto without departing from the spirit of this invention. These modifications are under the scope of this invention, as defined in the appended claims.

Tabl 1. Distribution (%) of nosocomial pathogens for various human infections in USA (1990-1992)¹.

Pathogen	UTI ²	SSI ³	BSI ⁴	Pneumonia	CSF ⁵
<i>Escherichia coli</i>	27	9	5	4	2
<i>Staphylococcus aureus</i>	2	21	17	21	2
<i>Staphylococcus epidermidis</i>	2	6	20	0	1
<i>Enterococcus faecalis</i>	16	12	9	2	0
<i>Enterococcus faecium</i>	1	1	0	0	0
<i>Pseudomonas aeruginosa</i>	12	9	3	18	0
<i>Klebsiella pneumoniae</i>	7	3	4	9	0
<i>Proteus mirabilis</i>	5	3	1	2	0
<i>Streptococcus pneumoniae</i>	0	0	3	1	18
Group B <i>Streptococci</i>	1	1	2	1	6
Other streptococci	3	5	2	1	3
<i>Haemophilus influenzae</i>	0	0	0	6	45
<i>Neisseria meningitidis</i>	0	0	0	0	14
<i>Listeria monocytogenes</i>	0	0	0	0	3
Other enterococci	1	1	0	0	0
Other staphylococci	2	8	13	2	0
<i>Candida albicans</i>	9	3	5	5	0
Other <i>Candida</i>	2	1	3	1	0
<i>Enterobacter</i> sp.	5	7	4	12	2
<i>Acinetobacter</i> sp.	1	1	2	4	2
<i>Citrobacter</i> sp.	2	1	1	1	0
<i>Serratia marcescens</i>	1	1	1	3	1
Other <i>Klebsiella</i>	1	1	1	2	1
Others	0	6	4	5	0

¹ Data recorded by the National Nosocomial Infections Surveillance (NNIS) from 80 hospitals (Emori and Gaynes, 1993, *Clin. Microbiol. Rev.*, 6:428-442).

² Urinary tract infection.

³ Surgical site infection.

⁴ Bloodstream infection.

⁵ Cerebrospinal fluid.

Table 2. Distribution (%) of bloodstream infection pathogens in Quebec (1995), Canada (1992), UK (1969-1988) and USA (1990-1992).

5	Organism	Quebec ¹	Canada ²	UK ³		USA ⁴
				Community-acquired	Hospital-acquired	
	<i>E. coli</i>	15.6	53.8	24.8	20.3	5.0
10	<i>S. epidermidis</i> and other CoNS ⁵	25.8	-	0.5	7.2	31.0
	<i>S. aureus</i>	9.6	-	9.7	19.4	16.0
	<i>S. pneumoniae</i>	6.3	-	22.5	2.2	-
	<i>E. faecalis</i>	3.0	-	1.0	4.2	-
15	<i>E. faecium</i>	2.6	-	0.2	0.5	-
	<i>Enterococcus</i> sp.	-	-	-	-	9.0
	<i>H. influenzae</i>	1.5	-	3.4	0.4	-
	<i>P. aeruginosa</i>	1.5	8.2	1.0	8.2	3.0
	<i>K. pneumoniae</i>	3.0	11.2	3.0	9.2	4.0
20	<i>P. mirabilis</i>	-	3.9	2.8	5.3	1.0
	<i>S. pyogenes</i>	-	-	1.9	0.9	-
	<i>Enterobacter</i> sp.	4.1	5.5	0.5	2.3	4.0
	<i>Candida</i> sp.	8.5	-	-	1.0	8.0
	Others	18.5	17.4	28.7	18.9	19.0

25 ¹ Data obtained for 270 isolates collected at the Centre Hospitalier de l'Université Laval (CHUL) during a 5 month period (May to October 1995).

² Data from 10 hospitals throughout Canada representing 941 gram-negative isolates. (Chamberland *et al.*, 1992, *Clin. Infect. Dis.*, 15:615-628).

30 ³ Data from a 20-year study (1969-1988) for nearly 4000 isolates. (Eykyn *et al.*, 1990, *J. Antimicrob. Chemother.*, Suppl. C, 25:41-58).

⁴ Data recorded by the National Nosocomial Infections Surveillance (NNIS) from 80 hospitals (Emori and Gaynes, 1993, *Clin. Microbiol. Rev.*, 6:428-442).

⁵ Coagulase-negative staphylococci.

Table 3. Distribution of positive and negative clinical specimens tested at the microbiology laboratory of the CHUL (February 1994 – January 1995).

5	Clinical specimens and/or sites	No. of samples tested (%)	% of positive specimens	% of negative specimens
10	Urine	17,981 (54.5)	19.4	80.6
	Blood culture/marrow	10,010 (30.4)	6.9	93.1
	Sputum	1,266 (3.8)	68.4	31.6
	Superficial pus	1,136 (3.5)	72.3	27.7
	Cerebrospinal fluid	553 (1.7)	1.0	99.0
	Synovial fluid	523 (1.6)	2.7	97.3
	Respiratory tract	502 (1.5)	56.6	43.4
	Deep pus	473 (1.4)	56.8	43.2
	Ears	289 (0.9)	47.1	52.9
	Pleural and pericardial fluid	132 (0.4)	1.0	99.0
15	Peritoneal fluid	101 (0.3)	28.6	71.4
	Total:	32,966 (100.0)	20.0	80.0

Tabl 4. Non-limiting xample of microbial species for which *tuf* and/or *atpD* and/or *recA* sequences
ar us d in th present invention.

Bacterial species	
5	<i>Achromobacter xylosoxidans</i> subsp. <i>denitrificans</i>
	<i>Acetobacterium woodii</i>
	<i>Acetobacter aceti</i>
	<i>Acetobacter altoacetigenes</i>
10	<i>Acetobacter polyoxogenes</i>
	<i>Acholeplasma laidlawii</i>
	<i>Acidiphilum facilis</i>
	<i>Acinetobacter baumannii</i>
	<i>Acinetobacter calcoaceticus</i>
15	<i>Acinetobacter lwoffii</i>
	<i>Actinomyces meyeri</i>
	<i>Aerococcus viridans</i>
	<i>Aeromonas salmonicida</i>
	<i>Agrobacterium tumefaciens</i>
20	<i>Alcaligenes faecalis</i>
	<i>Allochromatium vinosum</i>
	<i>Anabaena variabilis</i>
	<i>Anacystis nidulans</i>
	<i>Anaerorhabdus furcosus</i>
25	<i>Aquifex aeolicus</i>
	<i>Aquifex pyrophilus</i>
	<i>Azotobacter vinelandii</i>
	<i>Bacillus anthracis</i>
	<i>Bacillus cereus</i>
30	<i>Bacillus firmus</i>
	<i>Bacillus halodurans</i>
	<i>Bacillus megaterium</i>
	<i>Bacillus stearothermophilus</i>
	<i>Bacillus subtilis</i>
35	<i>Bacteroides distasonis</i>
	<i>Bacteroides fragilis</i>
	<i>Bacteroides ovatus</i>
	<i>Bacteroides vulgatus</i>
	<i>Bartonella henselae</i>
40	<i>Bifidobacterium adolescentis</i>
	<i>Bifidobacterium breve</i>
	<i>Bifidobacterium dentium</i>
	<i>Bifidobacterium longum</i>
	<i>Blastochloris viridis</i>
45	<i>Borrelia burgdorferi</i>
	<i>Bordetella pertussis</i>
	<i>Bordetella bronchiseptica</i>
	<i>Branhamella catarrhalis</i>
	<i>Brucella abortus</i>
50	<i>Brevibacterium linens</i>
	<i>Brevibacterium flavum</i>
	<i>Buchnera aphidicola</i>
	<i>Burkholderia cepacia</i>
	<i>Burkholderia mallei</i>
55	<i>Burkholderia pseudomallei</i>
	<i>Campylobacter jejuni</i>
	<i>Cedecea davisae</i>
	<i>Cedecea lapagei</i>
	<i>Cedecea neteri</i>
60	<i>Chlamydia pneumoniae</i>
	<i>Chlamydia psittaci</i>
	<i>Chlamydia trachomatis</i>
	<i>Chlorobium vibrioforme</i>
	<i>Chloroflexus aurantiacus</i>
65	<i>Chryseobacterium meningosepticum</i>
	<i>Citrobacter amalonaticus</i>
	<i>Citrobacter braakii</i>
	<i>Citrobacter farmeri</i>
	<i>Citrobacter freundii</i>
70	<i>Citrobacter koseri</i>
	<i>Citrobacter sedlakii</i>
	<i>Citrobacter werkmanii</i>
	<i>Citrobacter youngae</i>
	<i>Clostridium acetobutylicum</i>
75	<i>Clostridium beijerinckii</i>
	<i>Clostridium bifementans</i>
	<i>Clostridium botulinum</i>
	<i>Clostridium difficile</i>
	<i>Clostridium innocuum</i>
80	<i>Clostridium histolyticum</i>
	<i>Clostridium novyi</i>
	<i>Clostridium septicum</i>
	<i>Clostridium perfringens</i>
	<i>Clostridium ramosum</i>
85	<i>Clostridium sordellii</i>
	<i>Clostridium tertium</i>
	<i>Clostridium tetani</i>
	<i>Comamonas acidovorans</i>
	<i>Corynebacterium bovis</i>
90	<i>Corynebacterium cervicis</i>
	<i>Corynebacterium diphtheriae</i>
	<i>Corynebacterium flavesens</i>
	<i>Corynebacterium glutamicum</i>
	<i>Corynebacterium kutscheri</i>
95	<i>Corynebacterium minutissimum</i>
	<i>Corynebacterium mycetoides</i>
	<i>Corynebacterium pseudodiphtheriticum</i>
	<i>Corynebacterium pseudogenitalium</i>
	<i>Corynebacterium pseudotuberculosis</i>
100	<i>Corynebacterium renale</i>
	<i>Corynebacterium ulcerans</i>
	<i>Corynebacterium urealyticum</i>
	<i>Corynebacterium xerosis</i>
	<i>Coxiella burnetii</i>
105	<i>Cytophaga lytica</i>
	<i>Deinococcus radiodurans</i>
	<i>Deinonema</i> sp.
	<i>Edwardsiella hoshinae</i>
	<i>Edwardsiella tarda</i>
110	<i>Ehrlichia canis</i>
	<i>Ehrlichia risticii</i>
	<i>Eikenella corrodens</i>
	<i>Enterobacter aerogenes</i>
	<i>Enterobacter agglomerans</i>
115	<i>Enterobacter amnigenus</i>
	<i>Enterobacter asburiae</i>
	<i>Enterobacter cancerogenus</i>

Table 4. N n-limitating example of microbial species for which *tuf* and/or *atpD* and/or *recA* sequences are used in the present invention (continued).

Bacterial species (continued)

5	<i>Enterobacter cloacae</i>		
	<i>Enterobacter gergoviae</i>		
	<i>Enterobacter hormaechei</i>		
	<i>Enterobacter sakazakii</i>		
10	<i>Enterococcus avium</i>		
	<i>Enterococcus casseliflavus</i>		
	<i>Enterococcus cecorum</i>		
	<i>Enterococcus columbae</i>		
	<i>Enterococcus dispar</i>		
15	<i>Enterococcus durans</i>		
	<i>Enterococcus faecalis</i>		
	<i>Enterococcus faecium</i>		
	<i>Enterococcus flavescens</i>		
	<i>Enterococcus gallinarum</i>		
20	<i>Enterococcus hirae</i>		
	<i>Enterococcus malodoratus</i>		
	<i>Enterococcus mundtii</i>		
	<i>Enterococcus pseudoavium</i>		
	<i>Enterococcus raffinosus</i>		
25	<i>Enterococcus saccharolyticus</i>		
	<i>Enterococcus solitarius</i>		
	<i>Enterococcus sulfureus</i>		
	<i>Erwinia carotovora</i>		
	<i>Escherichia coli</i>		
30	<i>Escherichia fergusonii</i>		
	<i>Escherichia hermannii</i>		
	<i>Escherichia vulneris</i>		
	<i>Eubacterium lentum</i>		
	<i>Eubacterium nodatum</i>		
35	<i>Ewingella americana</i>		
	<i>Francisella tularensis</i>		
	<i>Frankia alni</i>		
	<i>Fervidobacterium islandicum</i>		
	<i>Fibrobacter succinogenes</i>		
40	<i>Flavobacterium ferrugineum</i>		
	<i>Flexistipes sinusarabici</i>		
	<i>Fusobacterium gonidiaformans</i>		
	<i>Fusobacterium necrophorum</i> subsp. <i>necrophorum</i>		
	<i>Fusobacterium nucleatum</i> subsp. <i>polymorphum</i>		
45	<i>Gardnerella vaginalis</i>		
	<i>Gemella haemolysans</i>		
	<i>Gemella morbillorum</i>		
	<i>Gloeobacter violaceus</i>		
	<i>Gloeotheca</i> sp.		
50	<i>Gluconobacter oxydans</i>		
	<i>Haemophilus actinomycetemcomitans</i>		
	<i>Haemophilus aphrophilus</i>		
	<i>Haemophilus ducreyi</i>		
	<i>Haemophilus haemolyticus</i>		
55	<i>Haemophilus influenzae</i>		
	<i>Haemophilus parahaemolyticus</i>		
	<i>Haemophilus parainfluenzae</i>		
	<i>Haemophilus paraphrophilus</i>		
	<i>Haemophilus segnis</i>		
60	<i>Hafnia alvei</i>		
	<i>Haloarcula marismortui</i>		
	<i>Halobacterium salinarum</i>		
	<i>Haloferax volcanii</i>		
	<i>Helicobacter pylori</i>		
65	<i>Herpetosiphon aurantiacus</i>		
	<i>Kingella kingae</i>		
	<i>Klebsiella ornithinolytica</i>		
	<i>Klebsiella oxytoca</i>		
	<i>Klebsiella planticola</i>		
70	<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>		
	<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>		
	<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>		
	<i>Kluyvera ascorbata</i>		
75	<i>Kluyvera cryocrescens</i>		
	<i>Kluyvera georgiana</i>		
	<i>Lactobacillus acidophilus</i>		
	<i>Lactobacillus garvieae</i>		
	<i>Lactobacillus paracasei</i>		
80	<i>Lactobacillus casei</i> subsp. <i>casei</i>		
	<i>Lactococcus lactis</i> subsp. <i>lactis</i>		
	<i>Leclercia adecarboxylata</i>		
	<i>Legionella micdadei</i>		
	<i>Legionella pneumophila</i> subsp. <i>pneumophila</i>		
85	<i>Leminorella grimonii</i>		
	<i>Leminorella richardii</i>		
	<i>Leptospira biflexa</i>		
	<i>Leptospira interrogans</i>		
	<i>Listeria monocytogenes</i>		
90	<i>Macrococcus caseolyticus</i>		
	<i>Magnetospirillum magnetotacticum</i>		
	<i>Megamonas hypermegale</i>		
	<i>Methanobacterium thermoautotrophicum</i>		
	<i>Methanococcus jannaschii</i>		
95	<i>Methanococcus vanniellii</i>		
	<i>Methanosarcina barkeri</i>		
	<i>Methanosarcina jannaschii</i>		
	<i>Methylobacillus flagellatum</i>		
	<i>Methylomonas clara</i>		
100	<i>Micrococcus luteus</i>		
	<i>Micrococcus lylae</i>		
	<i>Mitsuokella multacida</i>		
	<i>Mobiluncus curtisii</i> subsp. <i>holmesii</i>		
	<i>Moellerella thermoacetica</i>		
105	<i>Moellerella wisconsensis</i>		
	<i>Moraxella osloensis</i>		
	<i>Morganella morganii</i> subsp. <i>morganii</i>		
	<i>Mycobacterium avium</i>		
	<i>Mycobacterium bovis</i>		
110	<i>Mycobacterium gordonae</i>		
	<i>Mycobacterium leprae</i>		
	<i>Mycobacterium tuberculosis</i>		
	<i>Mycoplasma capricolum</i>		
	<i>Mycoplasma gallisepticum</i>		
115	<i>Mycoplasma genitalium</i>		
	<i>Mycoplasma hominis</i>		
	<i>Mycoplasma pirum</i>		
	<i>Mycoplasma mycetoides</i>		
	<i>Mycoplasma pneumoniae</i>		
120	<i>Mycoplasma pulmonis</i>		

Table 4. Non-limitating example of microbial species for which *tuf* and/or *atpD* and/or *recA* sequences are used in the present invention (continued).

		Bact rial species (c ntinued)
5	<i>Mycoplasma salivarium</i>	<i>Rhodospirillum rubrum</i>
	<i>Myxococcus xanthus</i>	65 <i>Ruminococcus albus</i>
	<i>Neisseria animalis</i>	<i>Salmonella bongori</i>
	<i>Neisseria canis</i>	<i>Salmonella choleraesuis</i> subsp. <i>arizonae</i>
10	<i>Neisseria cinerea</i>	<i>Salmonella choleraesuis</i> subsp. <i>choleraesuis</i>
	<i>Neisseria cuniculi</i>	<i>Salmonella choleraesuis</i> subsp. <i>diarizonae</i>
	<i>Neisseria elongata</i> subsp. <i>elongata</i>	70 <i>Salmonella choleraesuis</i> subsp. <i>houtenae</i>
	<i>Neisseria elongata</i> subsp. <i>intermedia</i>	<i>Salmonella choleraesuis</i> subsp. <i>indica</i>
	<i>Neisseria flava</i>	<i>Salmonella choleraesuis</i> subsp. <i>salamae</i>
15	<i>Neisseria flavescens</i>	<i>Serpulina hyodysenteriae</i>
	<i>Neisseria gonorrhoeae</i>	<i>Serratia ficaria</i>
	<i>Neisseria lactamica</i>	75 <i>Serratia fonticola</i>
	<i>Neisseria meningitidis</i>	<i>Serratia grimesii</i>
	<i>Neisseria mucosa</i>	<i>Serratia liquefaciens</i>
20	<i>Neisseria perflava</i>	<i>Serratia marcescens</i>
	<i>Neisseria pharyngis</i>	<i>Serratia odorifera</i>
	<i>Neisseria polysaccharea</i>	80 <i>Serratia plymuthica</i>
	<i>Neisseria sicca</i>	<i>Serratia rubidaea</i>
	<i>Neisseria subflava</i>	<i>Shewanella putida</i>
25	<i>Neisseria weaveri</i>	<i>Shewanella putrefaciens</i>
	<i>Ochrobactrum anthropi</i>	<i>Shigella boydii</i>
	<i>Pantoea agglomerans</i>	85 <i>Shigella dysenteriae</i>
	<i>Pantoea dispersa</i>	<i>Shigella flexneri</i>
	<i>Paracoccus denitrificans</i>	<i>Shigella sonnei</i>
30	<i>Pasteurella multocida</i>	<i>Spirochaeta aurantia</i>
	<i>Pectinatus frisingensis</i>	<i>Staphylococcus aureus</i>
	<i>Peptococcus niger</i>	90 <i>Staphylococcus aureus</i> subsp. <i>aureus</i>
	<i>Peptostreptococcus anaerobius</i>	<i>Staphylococcus auricularis</i>
	<i>Peptostreptococcus asaccharolyticus</i>	<i>Staphylococcus capitis</i> subsp. <i>capitis</i>
35	<i>Peptostreptococcus prevotii</i>	<i>Staphylococcus cohnii</i>
	<i>Phormidium ectocarpi</i>	<i>Staphylococcus epidermidis</i>
	<i>Pirellula marina</i>	95 <i>Staphylococcus haemolyticus</i>
	<i>Planobispora rosea</i>	<i>Staphylococcus hominis</i>
	<i>Plectonema boryanum</i>	<i>Staphylococcus lugdunensis</i>
40	<i>Porphyromonas asaccharolytica</i>	<i>Staphylococcus saprophyticus</i>
	<i>Porphyromonas gingivalis</i>	<i>Staphylococcus sciuri</i> subsp. <i>sciuri</i>
	<i>Pragla fontium</i>	100 <i>Staphylococcus simulans</i>
	<i>Prevotella melaninogenica</i>	<i>Staphylococcus warneri</i>
	<i>Prevotella oralis</i>	<i>Stigmatella aurantiaca</i>
45	<i>Prevotella ruminicola</i>	<i>Stenotrophomonas maltophilia</i>
	<i>Prochlorothrix hollandica</i>	<i>Streptococcus acidominimus</i>
	<i>Propionibacterium acnes</i>	105 <i>Streptococcus agalactiae</i>
	<i>Propionigenium modestum</i>	<i>Streptococcus anginosus</i>
	<i>Proteus mirabilis</i>	<i>Streptococcus bovis</i>
50	<i>Proteus penneri</i>	<i>Streptococcus cricetus</i>
	<i>Proteus vulgaris</i>	<i>Streptococcus cristatus</i>
	<i>Providencia alcalifaciens</i>	110 <i>Streptococcus downei</i>
	<i>Providencia rettgeri</i>	<i>Streptococcus dysgalactiae</i>
	<i>Providencia rustigianii</i>	<i>Streptococcus equi</i> subsp. <i>equi</i>
55	<i>Providencia stuartii</i>	<i>Streptococcus ferus</i>
	<i>Pseudomonas aeruginosa</i>	<i>Streptococcus gordonii</i>
	<i>Pseudomonas fluorescens</i>	115 <i>Streptococcus macacae</i>
	<i>Pseudomonas stutzeri</i>	<i>Streptococcus mitis</i>
	<i>Psychrobacter phenylpyruvicus</i>	<i>Streptococcus mutans</i>
60	<i>Rahnella aquatilis</i>	<i>Streptococcus oralis</i>
	<i>Rickettsia prowazekii</i>	<i>Streptococcus parasanguinis</i>
	<i>Rhodobacter capsulatus</i>	120
	<i>Rhodobacter sphaeroides</i>	

Table 4. Non-limiting example of microbial species for which *tuf* and/or *atpD* and/or *recA* sequences are used in the present invention (continued).

Bacterial species (continued)

5	<i>Streptococcus pneumoniae</i>	<i>Aspergillus oryzae</i>
	<i>Streptococcus pyogenes</i>	<i>Aspergillus flavus</i>
	<i>Streptococcus rattus</i>	65 <i>Aspergillus fumigatus</i>
	<i>Streptococcus salivarius</i>	<i>Aspergillus niger</i>
10	<i>Streptococcus salivarius</i> subsp. <i>thermophilus</i>	<i>Aureobasidium pullulans</i>
	<i>Streptococcus sanguinis</i>	<i>Bipolaris hawaiiensis</i>
	<i>Streptococcus sobrinus</i>	<i>Blastoschizomyces capitatus</i>
	<i>Streptococcus suis</i>	70 <i>Candida albicans</i>
	<i>Streptococcus uberis</i>	<i>Candida catenulata</i>
15	<i>Streptococcus vestibularis</i>	<i>Candida dubliniensis</i>
	<i>Streptomyces anofaciens</i>	<i>Candida famata</i>
	<i>Streptomyces aureofaciens</i>	<i>Candida glabrata</i>
	<i>Streptomyces cinnamomeus</i>	75 <i>Candida guilliermondii</i>
	<i>Streptomyces coelicolor</i>	<i>Candida haemulonii</i>
20	<i>Streptomyces collinus</i>	<i>Candida inconspicua</i>
	<i>Streptomyces lividans</i>	<i>Candida kefyr</i>
	<i>Streptomyces ramocissimus</i>	<i>Candida krusei</i>
	<i>Streptomyces rimosus</i>	80 <i>Candida lambica</i>
	<i>Streptomyces venezuelae</i>	<i>Candida lusitanae</i>
25	<i>Synechococcus</i> sp.	<i>Candida norvegensis</i>
	<i>Synechocystis</i> sp.	<i>Candida parapsilosis</i>
	<i>Tatumella ptyseos</i>	<i>Candida rugosa</i>
	<i>Taxobacter occealus</i>	85 <i>Candida sphaerica</i>
	<i>Thermoplasma acidophilum</i>	<i>Candida tropicalis</i>
30	<i>Thermotoga maritima</i>	<i>Candida utilis</i>
	<i>Thermus aquaticus</i>	<i>Candida viswanathii</i>
	<i>Thermus thermophilus</i>	<i>Candida zeylanoides</i>
	<i>Thiobacillus ferrooxydans</i>	90 <i>Cladophialophora carrionii</i>
	<i>Thiomonas cuprina</i>	<i>Coccidioides immitis</i>
35	<i>Trabulsiella guamensis</i>	<i>Coprinus cinereus</i>
	<i>Treponema pallidum</i>	<i>Cryptococcus albidus</i>
	<i>Ureaplasma urealyticum</i>	<i>Cryptococcus humicolus</i>
	<i>Veillonella parvula</i>	95 <i>Cryptococcus neoformans</i>
	<i>Vibrio alginolyticus</i>	<i>Cunninghamella bertholletiae</i>
40	<i>Vibrio anguillarum</i>	<i>Curvularia lunata</i>
	<i>Vibrio cholerae</i>	<i>Emericella nidulans</i>
	<i>Wolinella succinogenes</i>	<i>Exophiala jeikei</i>
	<i>Xanthomonas citri</i>	100 <i>Eremothecium gossypii</i>
	<i>Xanthomonas oryzae</i>	<i>Fonsecaea pedrosoi</i>
45	<i>Xenorhabdus bovienii</i>	<i>Fusarium oxysporum</i>
	<i>Xenorhabdus nematophilus</i>	<i>Geotrichum</i> sp.
	<i>Yersinia bercovieri</i>	<i>Histoplasma capsulatum</i>
	<i>Yersinia enterocolitica</i>	105 <i>Issatchenkia orientalis</i>
	<i>Yersinia frederiksenii</i>	<i>Kluyveromyces lactis</i>
50	<i>Yersinia intermedia</i>	<i>Malassezia furfur</i>
	<i>Yersinia pestis</i>	<i>Malassezia pachydermatis</i>
	<i>Yersinia pseudotuberculosis</i>	<i>Malbranchea filamentosa</i>
	<i>Yersinia rohdei</i>	110 <i>Metschnikowia pulcherrima</i>
	<i>Yokenella regensburgei</i>	<i>Microsporum audouinii</i>
55	<i>Zoogloea ramigera</i>	<i>Mucor circinelloides</i>
		<i>Neurospora crassa</i>
	Fungal species	<i>Paecilomyces lilacinus</i>
		115 <i>Paracoccidioides brasiliensis</i>
		<i>Penicillium mameffei</i>
60	<i>Absidia corymbifera</i>	<i>Phialophora verrucosa</i>
	<i>Absidia glauca</i>	<i>Pichia anomala</i>
	<i>Alternaria alternata</i>	
	<i>Arxula adeninivorans</i>	

Table 4. Non-limiting example of microbial species for which *tuf* and/or *atpD* and/or *recA* sequences are used in the present invention (continued).

Fungal species (continued)

5	<i>Piedraia hortai</i>	<i>Trypanosoma brucei</i> subsp. <i>brucei</i>
	<i>Podospora anserina</i>	<i>Trypanosoma congolense</i>
	<i>Puccinia graminis</i>	65 <i>Trypanosoma cruzi</i>
	<i>Pseudallescheria boydii</i>	
10	<i>Rhizomucor racemosus</i>	
	<i>Rhizopus oryzae</i>	
	<i>Rhodotorula minuta</i>	
	<i>Rhodotorula mucilaginosa</i>	
	<i>Saccharomyces cerevisiae</i>	
15	<i>Saksenaea vasiformis</i>	
	<i>Schizosaccharomyces pombe</i>	
	<i>Scopulariopsis koningii</i>	
	<i>Sporobolomyces salmonicolor</i>	
	<i>Sporothrix schenckii</i>	
20	<i>Stephanoascus ciferrii</i>	
	<i>Syncephalastrum racemosum</i>	
	<i>Trichoderma reesei</i>	
	<i>Trichophyton mentagrophytes</i>	
	<i>Trichophyton tonsurans</i>	
25	<i>Trichosporon cutaneum</i>	
	<i>Ustilago maydis</i>	
	<i>Wangiella dermatitidis</i>	
	<i>Yarrowia lipolytica</i>	
30	Parasitical species	
	<i>Babesia bigemina</i>	
	<i>Babesia bovis</i>	
	<i>Babesia microti</i>	
35	<i>Blastocystis hominis</i>	
	<i>Crithidia fasciculata</i>	
	<i>Cryptosporidium parvum</i>	
	<i>Entamoeba histolytica</i>	
	<i>Giardia lamblia</i>	
40	<i>Kentrophoros</i> sp.	
	<i>Leishmania aethiopica</i>	
	<i>Leishmania amazonensis</i>	
	<i>Leishmania braziliensis</i>	
	<i>Leishmania donovani</i>	
45	<i>Leishmania infantum</i>	
	<i>Leishmania enriettii</i>	
	<i>Leishmania gerbilli</i>	
	<i>Leishmania guyanensis</i>	
	<i>Leishmania hertigi</i>	
50	<i>Leishmania major</i>	
	<i>Leishmania mexicana</i>	
	<i>Leishmania tarentolae</i>	
	<i>Leishmania tropica</i>	
	<i>Neospora caninum</i>	
55	<i>Onchocerca volvulus</i>	
	<i>Plasmodium berghei</i>	
	<i>Plasmodium falciparum</i>	
	<i>Plasmodium knowlesi</i>	
	<i>Porphyra purpurea</i>	
60	<i>Toxoplasma gondii</i>	
	<i>Treponema pallidum</i>	
	<i>Trichomonas vaginalis</i>	

Table 5. Antibiotic resistance genes selected for diagnostic purposes.

Genes	Antibiotics	Bacteria ¹	ACCESSION NO.	SEQ ID NO. (genes)
5	<i>aac(3)-Ib</i> ²	Aminoglycosides	<i>Enterobacteriaceae</i> <i>Pseudomonads</i>	L06157
	<i>aac(3)-IIb</i> ²	Aminoglycosides	<i>Enterobacteriaceae</i> , <i>Pseudomonads</i>	M97172
10	<i>aac(3)-IVa</i> ²	Aminoglycosides	<i>Enterobacteriaceae</i>	X01385
	<i>aac(3)-VIa</i> ²	Aminoglycosides	<i>Enterobacteriaceae</i> , <i>Pseudomonads</i>	M88012
	<i>aac(2)-Ia</i> ²	Aminoglycosides	<i>Enterobacteriaceae</i> , <i>Pseudomonads</i>	X04555
15	<i>aac(6)-aph(2'')</i> ²	Aminoglycosides	<i>Enterococcus</i> sp., <i>Staphylococcus</i> sp.	83-86 ³
	<i>aac(6)-Ia</i> ²	Aminoglycosides	<i>Enterobacteriaceae</i> , <i>Pseudomonads</i>	M18967
	<i>aac(6)-Ic</i> ²	Aminoglycosides	<i>Enterobacteriaceae</i> , <i>Pseudomonads</i>	M94066
20	<i>aac(6)-IIa</i> ²	Aminoglycosides	<i>Pseudomonads</i>	112 ⁴
	<i>aadB</i> [<i>ant(2'')-Ia</i> ²]	Aminoglycosides	<i>Enterobacteriaceae</i>	53-54 ³
	<i>aacC1</i> [<i>aac(3)-Ia</i> ²]	Aminoglycosides	<i>Pseudomonads</i>	55-56 ³
	<i>aacC2</i> [<i>aac(3)-IIa</i> ²]	Aminoglycosides	<i>Pseudomonads</i>	57-58 ³
25	<i>aacC3</i> [<i>aac(3)-III</i> ²]	Aminoglycosides	<i>Pseudomonads</i>	59-60 ³
	<i>aacA4</i> [<i>aac(6)-Ib</i> ²]	Aminoglycosides	<i>Pseudomonads</i>	65-66 ³
	<i>ant(3'')-Ia</i> ²	Aminoglycosides	<i>Enterobacteriaceae</i> , <i>Enterococcus</i> sp., <i>Staphylococcus</i> sp.	X02340 M10241
30	<i>ant(4'')-Ia</i> ²	Aminoglycosides	<i>Staphylococcus</i> sp.	V01282
	<i>aph(3'')-Ia</i> ²	Aminoglycosides	<i>Enterobacteriaceae</i> , <i>Pseudomonads</i>	J01839
	<i>aph(3'')-IIa</i> ²	Aminoglycosides	<i>Enterobacteriaceae</i> , <i>Pseudomonads</i>	V00618
35	<i>aph(3'')-IIIa</i> ²	Aminoglycosides	<i>Enterococcus</i> sp., <i>Staphylococcus</i> sp.	V01547
	<i>aph(3'')-VIa</i> ²	Aminoglycosides	<i>Enterobacteriaceae</i> , <i>Pseudomonads</i>	X07753
40	<i>rrs</i> ²	Streptomycin	<i>M. tuberculosis</i>	L15307 S62531
	<i>rpsL</i> ²	Streptomycin	<i>M. tuberculosis</i> , <i>M. avium</i> complex	X80120 U14749 X70995 L08011
45	<i>blaOXA</i> ^{5,6}	β -lactams	<i>Enterobacteriaceae</i> , <i>Pseudomonads</i>	110 ⁴
	<i>blaROB</i> ⁵	β -lactams	<i>Haemophilus</i> sp.	45-48 ³
	<i>blaSHV</i> ^{5,6}	β -lactams	<i>Pasteurella</i> sp.	41-44 ³
50	<i>blaTEM</i> ^{5,6}	β -lactams	<i>Enterobacteriaceae</i> , <i>Pseudomonas aeruginosa</i>	37-40 ³
	<i>blaTEM</i> ^{5,6}	β -lactams	<i>Enterobacteriaceae</i> , <i>Neisseria</i> sp., <i>Haemophilus</i> sp.	
55	<i>blaCARB</i> ⁵	β -lactams	<i>Pseudomonas</i> sp., <i>Enterobacteriaceae</i>	J05162 S46063 M69058

Table 5. Antibiotic resistance genes selected for diagnostic purposes (continued).

Table 5.					
G n s	Antibiotics	Bacteria ¹	ACCESSION NO.	SEQ ID NO. (genes)	
5					
	<i>bla</i> _{CTX-M-1} ⁵	<i>Enterobacteriaceae</i>	X92506		
	<i>bla</i> _{CTX-M-2} ⁵	<i>Enterobacteriaceae</i>	X92507		
	<i>bla</i> _{CMY-2} ⁷	<i>Enterobacteriaceae</i>	X91840		
	<i>bla</i> _{PER-1} ⁵	<i>Enterobacteriaceae</i> , <i>Pseudomonadaceae</i>	Z21957		
10					
	<i>bla</i> _{PER-2} ⁷	<i>Enterobacteriaceae</i>	X93314		
	<i>bla</i> _{IMP} ⁵	<i>Enterobacteriaceae</i> , <i>Pseudomonas aeruginosa</i>	AJ223604		
	<i>bla</i> _Z ¹²	<i>Enterococcus</i> sp., <i>Staphylococcus</i> sp.		111 ⁴	
15					
	<i>mecA</i> ¹²	<i>Staphylococcus</i> sp.		97-98 ³	
	<i>penA</i> ¹³	<i>Neisseria gonorrhoeae</i>	X54021		
	<i>pbp1a</i> ¹³	<i>Streptococcus pneumoniae</i>		SEE TABLE 7	
20			M20527 X67872 AB006868 AB006874 X67873 AB006878 AB006875 AB006877 AB006879 AF046237 AF046235 AF026431 AF046232 AF046233 AF046236 X67871 Z49095 AF046234 AB006873 X67866 X67868 AB006870 AB006869 AB006872 X67870 AB006871 X67867 X67869 AB006876 AF046230 AF046238 Z49094		
25					
30					
35					
40					
45					
50					
	<i>pbp2b</i> ¹³	<i>Streptococcus pneumoniae</i>	X16022 M25516 M25518 M25515 U20071 U20084 U20082 U20067 U20079 Z22185 U20072	SEE TABLE 7	
55					
60					

Table 5. Antibiotic resistance genes selected for diagnostic purposes (continued).

Genes	Antibiotics	Bacteria ¹	ACCESSION NO.	SEQ ID NO. (genes)
5 <i>pbp2b</i> ¹³	β -lactams	<i>Streptococcus pneumoniae</i>	U20083 U20081 M25522 U20075 U20070 U20077 U20068 Z22184 U20069 U20078 M25521 M25525 M25519 Z21981 M25523 M25526 M25524 Z22230 U20073 U20080 U20074 U20076 M25520 M25517	
10				
15				
20				
25				
30 <i>pbp2x</i> ¹³	β -lactams	<i>Streptococcus pneumoniae</i>	X16367 X65135 AB011204 AB011209 AB011199 AB011200 AB011201 AB011202 AB011198 AB011208 AB011205 AB015852 AB011210 AB015849 AB015850 AB015851 AB015847 AB015846 AB011207 AB015848 Z49096	SEE TABLE 7
35				
40				
45				
50				
<i>int</i>	β -lactams, trimethoprim	<i>Enterobacteriaceae</i> ,		99-102 ³
<i>sul</i>	aminoglycosides, antiseptic, chloramphenicol	<i>Pseudomonads</i>		103-106 ³
55 <i>ermA</i> ¹⁴	Macrolides, lincosamides, streptogramin B	<i>Staphylococcus</i> sp.		113 ⁴
60 <i>ermB</i> ¹⁴	Macrolides, lincosamides, streptogramin B	<i>Enterobacteriaceae</i> , <i>Staphylococcus</i> sp. <i>Enterococcus</i> sp. <i>Streptococcus</i> sp.		114 ⁴
65				

Table 5. Antibiotic resistance genes selected for diagnostic purposes (continued).

Genes	Antibiotics	Bacteria ¹	ACCESSION NO.	SEQ ID NO. (genes)
5 <i>ermC</i> ¹⁴	Macrolides, lincosamides, streptogramin B	<i>Enterobacteriaceae</i> , <i>Staphylococcus</i> sp.		115 ⁴
10 <i>ereA</i> ¹²	Macrolides	<i>Enterobacteriaceae</i> , <i>Staphylococcus</i> sp.	M11277	
<i>ereB</i> ¹²	Macrolides	<i>Enterobacteriaceae</i> , <i>Staphylococcus</i> sp.	A15097	
<i>msrA</i> ¹²	Macrolides	<i>Staphylococcus</i> sp.		77-80 ³
15 <i>mtr</i> ⁸	Macrolides	<i>Neisseria gonorrhoeae</i>	S42418 S40252 S42417 S40251 Z25796 U14993 Q51007 Q51006 Q51073 AF037040 AF037041	
20				
25 <i>mefA</i> , <i>mefE</i> ⁸	Macrolides	<i>Streptococcus</i> sp.	U70055 U83667 D16251	
<i>mphA</i> ⁸	Macrolides	<i>Enterobacteriaceae</i> , <i>Staphylococcus</i> sp.		
30 <i>linA/linA'</i> ⁹	Lincosamides	<i>Staphylococcus</i> sp.	J03947 M14039	
<i>linB</i> ¹⁰	Lincosamides	<i>Enterococcus faecium</i>	AF110130	
<i>rma</i> ¹¹	Macrolides	<i>Mycobacterium</i> <i>avium</i> complex	U74494	
35 <i>vga</i> ¹⁵	Streptogramin	<i>Staphylococcus</i> sp.		89-90 ³
<i>vgb</i> ¹⁵	Streptogramin	<i>Staphylococcus</i> sp.	M36022	
<i>vat</i> ¹⁵	Streptogramin	<i>Staphylococcus</i> sp.		87-88 ³
<i>vatB</i> ¹⁵	Streptogramin	<i>Staphylococcus</i> sp.	U19456 L38809	
40 <i>satA</i> ¹⁵	Streptogramin	<i>Enterococcus faecium</i>		81-82 ³
<i>ileS</i> ¹²	Mupirocin	<i>Staphylococcus aureus</i>	X74219	
<i>mupA</i> ¹²	Mupirocin	<i>Staphylococcus aureus</i>	X75439	
45 <i>gyrA</i> ¹⁶	Quinolones	Gram-positive and gram-negative bacteria	X95718 X06744 X57174 X16817 X71437 AF065152 AF060881 D32252	
50				
<i>parC/grfA</i> ¹⁶	Quinolones	Gram-positive and gram-negative bacteria	AB005036 AF056287 X95717 AF129764 AB017811 AF065152	
55				
60				

Table 5. Antibiotic resistance genes selected for diagnostic purposes (continued).

Genes	Antibiotics	Bacteria ¹	ACCESSION NO.	SEQ ID NO. (genes)
5				
<i>parE/grlB</i> ¹⁶	Quinolones	Gram-positive bacteria	X95717 AF065153 AF058920	
10				
<i>norA</i> ¹⁶	Quinolones	<i>Staphylococcus</i> sp.	D90119 M80252 M97169	
<i>mexR (nalB)</i> ¹⁶	Quinolones	<i>Pseudomonas aeruginosa</i>	U23763	
<i>nfxB</i> ¹⁶	Quinolones	<i>Pseudomonas aeruginosa</i>	X65646	
15				
<i>cat</i> ¹²	Chloramphenicol	Gram-positive and gram-negative bacteria	M55620 X15100 A24651 M28717 A00568 A00569 X74948 Y00723 A24362 A00569 M93113 M62822 M58516	
20				
25				
<i>rpoB</i> ¹⁷	Rifampin	<i>Mycobacterium tuberculosis</i>	AF055891 AF055892 S71246 L27989 AF055893	
30				
<i>inhA</i> ¹⁷	Isoniazid	<i>Mycobacterium tuberculosis</i>	AF106077 U02492	
35				
<i>katG</i> ¹⁷	Isoniazid	<i>Mycobacterium tuberculosis</i>	U40593 U06259 U06260 U06261 U06262 U40594 U40595	
40				
<i>ahpC</i> ¹⁷	Isoniazid	<i>Mycobacterium tuberculosis</i>	U43812 U57761 U24085 U16243 U58030 U18264 U68480 U59967	
45				
<i>embB</i> ¹⁷	Ethambutol	<i>Mycobacterium tuberculosis</i>	U68480	
<i>pnca</i> ¹⁷	Pyrazinamide	<i>Mycobacterium tuberculosis</i>	U59967	
50				
<i>vanA</i> ¹²	Vancomycin	<i>Enterococcus</i> sp.		67-70 ³ SEE TABLE 7
<i>vanB</i> ¹²	Vancomycin	<i>Enterococcus</i> sp.		116 ⁴
<i>vanC1</i> ¹²	Vancomycin	<i>Enterococcus gallinarum</i>		117 ⁴ SEE TABLE 7
55				
<i>vanC2</i> ¹²	Vancomycin	<i>Enterococcus casseliflavus</i>	U94521 U94522 U94523 U94524 U94525 L29638	SEE TABLE 7
60				

Table 5. Antibiotic resistance genes selected for diagnostic purposes (continued).

Genes	Antibiotics	Bacteria ¹	ACCESSION NO.	SEQ ID NO. (genes)
5 <i>vanC3</i> 12	Vancomycin	<i>Enterococcus flavescens</i>	L29639 U72706 L29640	SEE TABLE 7
10 <i>vanD</i> 18	Vancomycin	<i>Enterococcus faecium</i>	AF130997	
<i>tetB</i> 19	Tetracycline	Gram-negative bacteria	J01830	
<i>tetM</i> 19	Tetracycline	Gram-negative and Gram-positive bacteria	X52632	
15 <i>sulII</i> 20	Sulfonamides	Gram-negative bacteria	D37827 M36657 AF017389 AF017391	
<i>dhfrIa</i> 20	Trimethoprim	Gram-negative bacteria	AJ238350 X17477	
20 <i>dhfrIb</i> 20	Trimethoprim	Gram-negative bacteria	Z50805 Z50804	
<i>dhfrV</i> 20	Trimethoprim	Gram-negative bacteria	X12868	
<i>dhfrVII</i> 20	Trimethoprim	Gram-negative bacteria	U31119	
<i>dhfrVIII</i> 20	Trimethoprim	Gram-negative bacteria	U10186	
25 <i>dhfrIX</i> 20	Trimethoprim	Gram-negative bacteria	X57730	
<i>dhfrXII</i> 20	Trimethoprim	Gram-negative bacteria	Z21672	
<i>dfrA</i> 20	Trimethoprim	<i>Staphylococcus</i> sp.	AF045472 U40259 AF051916	
30	<p>1 Bacteria having high incidence for the specified antibiotic resistance gene. The presence of the antibiotic resistance genes in other bacteria is not excluded.</p> <p>2 Shaw, K. J., P. N. Rather, R. S. Hare, and G. H. Miller. 1993. Molecular genetics of aminoglycoside resistance genes and familial relationships of the aminoglycoside-modifying enzymes. <i>Microbiol. Rev.</i> 57:138-163.</p> <p>3 Antibiotic resistance genes from our co-pending US patent no. 6,001,564 for which we have selected PCR primer pairs.</p> <p>4 These SEQ ID NOs. refer to a previous patent (application WO98/20157).</p> <p>5 Bush, K., G.A. Jacoby and A. Medeiros. 1995. A functional classification scheme for β-lactamase and its correlation with molecular structure. <i>Antimicrob. Agents. Chemother.</i> 39:1211-1233.</p> <p>6 Nucleotide mutations in <i>blaSHV</i>, <i>blaTEM</i>, and <i>blaOXA</i>, are associated with extended-spectrum β-lactamase or inhibitor-resistant β-lactamase.</p> <p>7 Bauerfeind, A., Y. Chong, and K. Lee. 1998. Plasmid-encoded AmpC beta-lactamases: how far have we gone 10 years after discovery? <i>Yonsei Med. J.</i> 39:520-525.</p> <p>8 Sutcliffe, J., T. Grebe, A. Tait-Kamradt, and L. Wondrack. 1996. Detection of erythromycin-resistant determinants by PCR. <i>Antimicrob. Agent Chemother.</i> 40:2562-2566.</p> <p>9 Leclerc, R., A., Brisson-Noël, J. Duval, and P. Courvalin. 1991. Phenotypic expression and genetic heterogeneity of lincosamide inactivation in <i>Staphylococcus</i> sp. <i>Antimicrob. Agents. Chemother.</i> 31:1887-1891.</p> <p>10 Bozdogan, B., L. Berrezouga, M.-S. Kuo, D. A. Yurek, K. A. Farley, B. J. Stockman, and R. Leclercq. 1999. A new gene, <i>linB</i>, conferring resistance to lincosamides by nucleotidylation in <i>Enterococcus faecium</i> HM1025. <i>Antimicrob. Agents. Chemother.</i> 43:925-929.</p> <p>11 Cockerill III, F.R. 1999. Genetic methods for assessing antimicrobial resistance. <i>Antimicrob. Agents. Chemother.</i> 43:199-212.</p> <p>12 Tenover, F. C., T. Popovic, and O. Olsvik. 1996. Genetic methods for detecting antibacterial resistance genes. pp. 1368-1378. In Murray, P. R., E. J. Baron, M. A. Pfaller, F. C. Tenover, R. H. Tenover (eds). <i>Manual of clinical microbiology</i>. 6th ed., ASM Press, Washington, D.C. USA</p> <p>13 Dowson, C. G., T. J. Tracey, and B. G. Spratt. 1994. Origin and molecular epidemiology of penicillin-</p>			

- binding-protein-mediated resistance to β -lactam antibiotics. Trends Molec. Microbiol. 2: 361-366.
- 14 Jensen, L. B., N. Frimodt-Møller, F. M. Aarestrup. 1999. Presence of *erm* gene classes in Gram-positive bacteria of animal and human origin in Denmark. FEMS Microbiol. 170:151-158.
 - 15 Thal, L. A., and M. J. Zervos. 1999. Occurrence and epidemiology of resistance to virginimycin and streptogramins. J. Antimicrob. Chemother. 43:171-176.
 - 16 Martinez J. L., A. Alonso, J. M. Gomez-Gomez, and F. Baquero. 1998. Quinolone resistance by mutations in chromosomal gyrase genes. Just the tip of the iceberg? J. Antimicrob. Chemother. 42:683-688.
 - 17 Cockerill III, F.R. 1999. Genetic methods for assessing antimicrobial resistance. Antimicrob. Agents. Chemother. 43:199-212.
 - 18 Casadewall, B. and P. Courvalin. 1999 Characterization of the *vanD* glycopeptide resistance gene cluster from *Enterococcus faecium* BM 4339. J. Bacteriol. 181:3644-3648.
 - 19 Roberts, M.C. 1999. Genetic mobility and distribution of tetracycline resistance determinants. Ciba Found. Symp. 207:206-222.
 - 20 Huovinen, P., L. Sundström, G. Swedberg, and O. Sköld. 1995. Trimethoprim and sulfonamide resistance. Antimicrob. Agent Chemother. 39:279-289.

Table 6. List of bacterial toxins selected for diagnostic purposes.

	Organism	Toxin	Accession number
5	<i>Actinobacillus actinomycetemcomitans</i>	Cytotoxic distending toxin (<i>cdtA</i> , <i>cdtB</i> , <i>cdtC</i>) Leukotoxin (<i>ltxA</i>)	AF006830 M27399
	<i>Actinomyces pyogenes</i>	Hemolysin (pyolysin)	U84782
	<i>Aeromonas hydrophila</i>	Aerolysin (<i>aerA</i>) Haemolysin (<i>hlyA</i>) Cytotoxic enterotoxin (<i>aif</i>)	M16495 U81555 L77573
10	<i>Bacillus anthracis</i>	Anthrax toxin (<i>cya</i>)	M23179
	<i>Bacillus cereus</i>	Enterotoxin (<i>bceT</i>) Enterotoxigenic hemolysin BL Non-haemolytic enterotoxins A,B and C (<i>nhe</i>)	D17312 AF192766, AF192767 AJ237785 Y19005
15	<i>Bacillus mycoides</i>	Hemolytic enterotoxin HBL	AJ243150 to AJ243153
	<i>Bacillus pseudomycoides</i>	Hemolytic enterotoxin HBL	AJ243154 to AJ243156
	<i>Bacteroides fragilis</i>	Enterotoxin (<i>bftP</i>) Matrix metalloprotease/enterotoxin (<i>fragilysin</i>) Metalloprotease toxin-2	U67735 S75344, AF038459 U90931 AF081785 AF056297
20		Metalloprotease toxin-3	
	<i>Bordetella bronchiseptica</i>	Adenylate cyclase hemolysin (<i>cyaA</i>) Dermonecrotic toxin (<i>dnt</i>)	Z37112, U22953 U59687 AB020025
25	<i>Bordetella pertussis</i>	Pertussis toxin (S1 subunit, <i>tox</i>)	AJ006151 AJ006153 AJ006155 AJ006157 AJ006159 AJ007363 M14378, M16494 AJ007364 M13223 X16347 18323 U10527
30		Patents: EP0322533-A 2 05jul89 EP0322115-A 5 28jun89 EP0396964-A 1 14nov90 JP1987228286-A 1 7oct87	
35		Adenyl cyclase (<i>cya</i>) Dermonecrotic toxin (<i>dnt</i>)	
	<i>Campylobacter jejuni</i>	Cytotoxic distending toxin (<i>cdtA</i> , <i>cdtB</i> , <i>cdtC</i>)	U51121
	<i>Citrobacter freundii</i>	Shiga-like toxin (<i>stx-IIcA</i>)	X67514, S53206
40	<i>Clostridium botulinum</i>	Botulinum toxin (BoNT) The A,B,E and F serotypes are neurotoxic for humans The other serotypes have not been considered	X52066, X52088 X73423 M30196 X70814 X70819 X71343 Z11934 X70817 M81186 X70818 X70815 X62089 X62883 S76749 X81714 X70816 X70820 X70281 L35496 M92906
50		Partial sequences (<200 bp) have not been considered	
55			
60	<i>Clostridium difficile</i>	A toxin (enterotoxin) (<i>tcdA</i>)	AB012304 AF053400 Y12618 X51797 X17194 M30307
65			

Table 6. List of bacterial toxins selected for diagnostic purposes (continued).

Organism	Toxin	Accession number
<i>Clostridium difficile</i>	B toxin (cytotoxin) (<i>toxB</i>)	Z23277
		X53138
<i>Clostridium perfringens</i>	Alpha (phospholipase C) (<i>cpe</i>)	L43545
		L43546
		L43547
		L43548
		X13608
		X17300
		D10248
		L13198
		X83275
		L77965
		AJ000766
		M98037
<i>Clostridium sordellii</i>	Enterotoxin (<i>cpe</i>)	X81849
		X71844
		Y16009
		AF037328
		AF037329
		AF037330
		M80837
		M95206
		X60694
		X73562
		D45904
		M36704
<i>Clostridium tetani</i>	Epsilon toxin (<i>etxD</i>)	X82638
		X06214
		X04436
		X00703
<i>Corynebacterium diphtheriae</i>	Cytotoxin L	
<i>Corynebacterium pseudotuberculosis</i>	Tetanus toxin	
<i>Eikenella corrodens</i>	Diphtheriae toxin	
<i>Enterobacter cloacae</i>	Phospholipase C	A21336
<i>Enterococcus faecalis</i>	Lysine decarboxylase (<i>cadA</i>)	U89166
<i>Escherichia coli</i> (EHEC)	Shiga-like toxin II	Z50754, U33502
<i>Escherichia coli</i> (EHEC)	Cytolysin B (<i>cytB</i>)	M38052
<i>Escherichia coli</i> (EHEC)	Hemolysin toxin (<i>hlyA</i> and <i>ehxA</i>)	AF043471
		X94129
		X79839
		X86087
		AB011549
		AF074613
		X81418
		M14107
		M10133
		M12863
		X81417
		X81416
<i>Escherichia coli</i> (EHEC)	Shiga-like (Vero cytotoxin) (<i>stx</i>)	X81415
		Z36900
		L11078
		L04539
		L11079
		X65949
		M21534
		M29153
		Z37725
		Z36901
		X61283
		AB017524
<i>Escherichia coli</i> (EHEC)	Contains the sequences for both the A and B subunits	U72191
<i>Escherichia coli</i> (EHEC)	Patent: JP 1985227681-A/1	
<i>Escherichia coli</i> (EHEC)	Patent: WO 9011351-A 2	

Table 6. List of bacterial toxins selected for diagnostic purposes (continued).

Organism	Toxin	Accession number
5	<i>Escherichia coli</i> (ETEC) Enterotoxin (heat-labile) (e/fB) Patents: EP 0145486-A 5 WO 9313202-A 42 JP 1986005097-A JP 1992320675-A Enterotoxin (heat-stable) (astA) (estA1)	M17874
		M17873
		J01605
		AB011677
		L11241
10		M58746
		M29255
		V00612
		J01831
		U03293
15	<i>Escherichia coli</i> (other) Cytolethal-distending toxin (cdt) (3 genes) Cytotoxic necrotizing factor 1 (cnf1) Microcin 24 (mtfS) Autotransporter enterotoxin (Pet) (cytotoxin)	U04208
		U89305
		U42629
		U47048
		AF056581
20	<i>Haemophilus ducreyi</i> <i>Helicobacter pylori</i> Cytolethal distending toxin (cdtA, cdtB, cdtC) Vacuolating toxin (vacA)	U53215
		U07145
		U80067
		U80068
		AF077938
25		AF077939
		AF077940
		AF077941
		AF057703
		X15127
30	<i>Legionella pneumophila</i> <i>Listeria monocytogenes</i> Structural toxin protein (rtxA) Listeriolysin O (lisa, hlyA)	M24199
		X60035
		U25452
		U25443
		U25446
35		U25449
	<i>Pasteurella multocida</i> Mitogenic toxin (dermonecrotic toxin)	X57775, Z28388
		X51512
		X52478
		M30186
40	<i>Proteus mirabilis</i> <i>Pseudomonas aeruginosa</i> <i>Salmonella typhimurium</i> Hemolysin (hpmA) Cytotoxin (Enterotoxin A) Calmodulin-sensitive adenylate cyclase toxin (cya) Cytolysin (salmolysin) (slyA) Enterotoxin (stn)	X14956
		AF060869
		U03842
		L16014
		M22618
45	<i>Serratia marcescens</i> <i>Shigella dysenteriae</i> type 1 Hemolysin (shlA) Shiga toxin (2 subunits) (stxA and stxB)	X07903, M32511
		M19437
		M24352, M21947
		Z54211
		Z47381
50	<i>Shigella flexneri</i> ShET2 enterotoxin (senA) Enterotoxin 1 (set1A and set1B) Hemolysin E (hlyE, clyA, sheA)	U35656
		AF200955
		AJ132761
		L01270
		D42143
55	<i>Shigella sonnei</i> <i>Sphingomonas paucimobilis</i> <i>Staphylococcus aureus</i> Beta-hemolysin (hlyA) Gamma-hemolysin (hlg2) Enterotoxin Enterotoxin A (sea)	L01055
		U93688
		L22565, L22566
		M18970
		M11118
60	Enterotoxin B Enterotoxin C1 (entC1) Enterotoxin C2 (entC2) Enterotoxin C3 (entC3) Enterotoxin D (sed) Enterotoxin E	X05815
		P34071
		X51661
		M94872
		M21319

Table 6. List of bacterial toxins selected for diagnostic purposes (continued).

	Organism	Toxin	Accession number
5	<i>Staphylococcus aureus</i>	Enterotoxin G (<i>seg</i>) Enterotoxin H (<i>seh</i>) Enterotoxin I (<i>sei</i>) Enterotoxin J Exfoliative toxin A (ETA) (Epidermolytic toxin A)	AF064773 U11702 AF064774 AF053140 M17347 M17357 L25372, M20371 M17348, M13775
10		Exfoliative toxin B (ETB) Leukocidin R (F and S component, <i>lukF</i> and <i>lukS</i>) (Hemolysin B and C)	X64389, S53213 X72700 L01055
15		Toxic shock syndrome toxin 1 (TSST-1) (alpha toxin) (alpha hemolysin)	X01645 M90536 J02615 U93688
20	<i>Staphylococcus epidermidis</i> <i>Staphylococcus intermedius</i>	Delta toxin (<i>hld</i>) Enterotoxin 1 Leukocidin R (F and S component, <i>lukF</i> and <i>lukS</i>) (synergohymenotropic toxin)	AF068634 U91526 X79188
25	<i>Streptococcus pneumoniae</i> <i>Streptococcus pyogenes</i>	Pneumolysin <i>Streptococcus pyrogenes</i> exotoxin A (<i>speA</i>)	X52474 X61560 (and 19 others) X03929 U40453, M19350
30		Pyrogenic exotoxin B (<i>speB</i>)	U63134 M86905, M35110
35	<i>Vibrio cholerae</i>	Cholerae toxin (<i>ctxA</i> and <i>ctxB</i> subunits) <u>Patents:</u> JP 1995008279-A 1 EP 0368819-A 12 (<i>ctxB</i>) WO 9313202-A 45 (<i>ctxA</i>)	X00171 X78390 X58786 X58785, S55782 D30052 D30053 K02679 AF175708
40		Accessory cholera enterotoxin (<i>ace</i>) Heat-stable enterotoxin (<i>stx</i>) <i>Zonula occludens</i> toxin (<i>zot</i>)	Z22569, AF175708 X74108, M85198 M97591, L03220 M83563, AF175708
	<i>Vibrio parahaemolyticus</i>	Thermostable direct hemolysin (<i>tdh</i>)	S67841
	<i>Vibrio vulnificus</i>	Cytolysin (<i>vvhA</i>)	M34670
45	<i>Yersinia enterocolitica</i>	Heat-stable enterotoxin (<i>ystI</i>) Heat-stable enterotoxin type B (<i>ystB</i>) Heat-stable enterotoxin type C (<i>ystC</i>)	U09235, X65999 D88145 D63578
	<i>Yersinia kristensenii</i>	Enterotoxin	X69218
50	<i>Yersinia pestis</i>	Toxin	X92727

Table 7. Origin of the sequences in the sequence listing.

SEQ ID NO.	Bacterial, fungal or parasitological species	Source	Comments*
5	1 <i>Acinetobacter baumannii</i>	This patent	tuf
	2 <i>Actinomyces meyeri</i>	This patent	tuf
	3 <i>Aerococcus viridans</i>	This patent	tuf
	4 <i>Achromobacter xylosoxidans</i> subsp. <i>denitrificans</i>	This patent	tuf
	5 <i>Anaerorhabdus furcosus</i>	This patent	tuf
10	6 <i>Bacillus anthracis</i>	This patent	tuf
	7 <i>Bacillus cereus</i>	This patent	tuf
	8 <i>Bacteroides distasonis</i>	This patent	tuf
	9 <i>Enterococcus casseliflavus</i>	This patent	tuf
	10 <i>Staphylococcus saprophyticus</i>	This patent	tuf
15	11 <i>Bacteroides ovatus</i>	This patent	tuf
	12 <i>Bartonella henselae</i>	This patent	tuf
	13 <i>Bifidobacterium adolescentis</i>	This patent	tuf
	14 <i>Bifidobacterium dentium</i>	This patent	tuf
	15 <i>Brucella abortus</i>	This patent	tuf
20	16 <i>Burkholderia cepacia</i>	This patent	tuf
	17 <i>Cedecea davisae</i>	This patent	tuf
	18 <i>Cedecea neteri</i>	This patent	tuf
	19 <i>Cedecea lapagei</i>	This patent	tuf
	20 <i>Chlamydia pneumoniae</i>	This patent	tuf
25	21 <i>Chlamydia psittaci</i>	This patent	tuf
	22 <i>Chlamydia trachomatis</i>	This patent	tuf
	23 <i>Chryseobacterium meningosepticum</i>	This patent	tuf
	24 <i>Citrobacter amalonaticus</i>	This patent	tuf
	25 <i>Citrobacter braakii</i>	This patent	tuf
30	26 <i>Citrobacter koseri</i>	This patent	tuf
	27 <i>Citrobacter farmeri</i>	This patent	tuf
	28 <i>Citrobacter freundii</i>	This patent	tuf
	29 <i>Citrobacter sedlakii</i>	This patent	tuf
	30 <i>Citrobacter werkmanii</i>	This patent	tuf
35	31 <i>Citrobacter youngae</i>	This patent	tuf
	32 <i>Clostridium perfringens</i>	This patent	tuf
	33 <i>Comamonas acidovorans</i>	This patent	tuf
	34 <i>Corynebacterium bovis</i>	This patent	tuf
	35 <i>Corynebacterium cervicis</i>	This patent	tuf
40	36 <i>Corynebacterium flavesces</i>	This patent	tuf
	37 <i>Corynebacterium kutscheri</i>	This patent	tuf
	38 <i>Corynebacterium minutissimum</i>	This patent	tuf
	39 <i>Corynebacterium mycetoides</i>	This patent	tuf
	40 <i>Corynebacterium pseudogenitalium</i>	This patent	tuf
45	41 <i>Corynebacterium renale</i>	This patent	tuf
	42 <i>Corynebacterium ulcerans</i>	This patent	tuf
	43 <i>Corynebacterium urealyticum</i>	This patent	tuf
	44 <i>Corynebacterium xerosis</i>	This patent	tuf
	45 <i>Coxiella burnetii</i>	This patent	tuf
50	46 <i>Edwardsiella hoshinae</i>	This patent	tuf
	47 <i>Edwardsiella tarda</i>	This patent	tuf
	48 <i>Elkenella corrodens</i>	This patent	tuf
	49 <i>Enterobacter aerogenes</i>	This patent	tuf
	50 <i>Enterobacter agglomerans</i>	This patent	tuf
55	51 <i>Enterobacter amnigenus</i>	This patent	tuf
	52 <i>Enterobacter asburiae</i>	This patent	tuf
	53 <i>Enterobacter cancerogenus</i>	This patent	tuf
	54 <i>Enterobacter cloacae</i>	This patent	tuf
	55 <i>Enterobacter gergoviae</i>	This patent	tuf
60	56 <i>Enterobacter hormaechei</i>	This patent	tuf
	57 <i>Enterobacter sakazakii</i>	This patent	tuf
	58 <i>Enterococcus casseliflavus</i>	This patent	tuf
	59 <i>Enterococcus cecorum</i>	This patent	tuf
	60 <i>Enterococcus dispar</i>	This patent	tuf
65	61 <i>Enterococcus durans</i>	This patent	tuf

Table 7. Origin of the sequences in the sequence listing (continued).

SEQ ID NO.	Bacterial, fungal or parasitical species	Source	Comments*
5	62 <i>Enterococcus faecalis</i>	This patent	tuf
	63 <i>Enterococcus faecalis</i>	This patent	tuf
	64 <i>Enterococcus faecium</i>	This patent	tuf
	65 <i>Enterococcus flavescens</i>	This patent	tuf
	66 <i>Enterococcus gallinarum</i>	This patent	tuf
10	67 <i>Enterococcus hirae</i>	This patent	tuf
	68 <i>Enterococcus mundtii</i>	This patent	tuf
	69 <i>Enterococcus pseudoavium</i>	This patent	tuf
	70 <i>Enterococcus raffinosus</i>	This patent	tuf
	71 <i>Enterococcus saccharolyticus</i>	This patent	tuf
15	72 <i>Enterococcus solitarius</i>	This patent	tuf
	73 <i>Enterococcus casseliflavus</i>	This patent	tuf (C)
	74 <i>Staphylococcus saprophyticus</i>	This patent	unknown
	75 <i>Enterococcus flavescens</i>	This patent	tuf (C)
	76 <i>Enterococcus gallinarum</i>	This patent	tuf (C)
20	77 <i>Ehrlichia canis</i>	This patent	tuf
	78 <i>Escherichia coli</i>	This patent	tuf
	79 <i>Escherichia fergusonii</i>	This patent	tuf
	80 <i>Escherichia hermannii</i>	This patent	tuf
	81 <i>Escherichia vulneris</i>	This patent	tuf
25	82 <i>Eubacterium lentum</i>	This patent	tuf
	83 <i>Eubacterium nodatum</i>	This patent	tuf
	84 <i>Ewingella americana</i>	This patent	tuf
	85 <i>Francisella tularensis</i>	This patent	tuf
	86 <i>Fusobacterium nucleatum</i> subsp. <i>polymorphum</i>	This patent	tuf
30	87 <i>Gemella haemolysans</i>	This patent	tuf
	88 <i>Gemella morbillorum</i>	This patent	tuf
	89 <i>Haemophilus actinomycetemcomitans</i>	This patent	tuf
	90 <i>Haemophilus aphrophilus</i>	This patent	tuf
	91 <i>Haemophilus ducreyi</i>	This patent	tuf
35	92 <i>Haemophilus haemolyticus</i>	This patent	tuf
	93 <i>Haemophilus parahaemolyticus</i>	This patent	tuf
	94 <i>Haemophilus parainfluenzae</i>	This patent	tuf
	95 <i>Haemophilus paraphrophilus</i>	This patent	tuf
	96 <i>Haemophilus segnis</i>	This patent	tuf
40	97 <i>Hafnia alvei</i>	This patent	tuf
	98 <i>Kingella kingae</i>	This patent	tuf
	99 <i>Klebsiella omithinolytica</i>	This patent	tuf
	100 <i>Klebsiella oxytoca</i>	This patent	tuf
	101 <i>Klebsiella planticola</i>	This patent	tuf
45	102 <i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	This patent	tuf
	103 <i>Klebsiella pneumoniae pneumoniae</i>	This patent	tuf
	104 <i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	This patent	tuf
	105 <i>Kluyvera ascorbata</i>	This patent	tuf
	106 <i>Kluyvera cryocrescens</i>	This patent	tuf
50	107 <i>Kluyvera georgiana</i>	This patent	tuf
	108 <i>Lactobacillus casei</i> subsp. <i>casei</i>	This patent	tuf
	109 <i>Lactococcus lactis</i> subsp. <i>lactis</i>	This patent	tuf
	110 <i>Lectercia adecarboxylata</i>	This patent	tuf
	111 <i>Legionella micdadei</i>	This patent	tuf
55	112 <i>Legionella pneumophila</i> subsp. <i>pneumophila</i>	This patent	tuf
	113 <i>Lemnorella grimonii</i>	This patent	tuf
	114 <i>Lemnorella richardii</i>	This patent	tuf
	115 <i>Leptospira interrogans</i>	This patent	tuf
	116 <i>Megamonas hypermegale</i>	This patent	tuf
60	117 <i>Mitsuokella multacidus</i>	This patent	tuf
	118 <i>Mobiluncus curtisii</i> subsp. <i>holmesii</i>	This patent	tuf
	119 <i>Moellerella wisconsensis</i>	This patent	tuf
	120 <i>Moraxella catarrhalis</i>	This patent	tuf
	121 <i>Morganella morganii</i> subsp. <i>morganii</i>	This patent	tuf
65	122 <i>Mycobacterium tuberculosis</i>	This patent	tuf

Table 7. Origin of the sequences in the sequence listing (continued).

SEQ ID NO.	Bacterial, fungal or parasitological species	Source	Comments*
5	123 <i>Neisseria cinerea</i>	This patent	tuf
	124 <i>Neisseria elongata</i> subsp. <i>elongata</i>	This patent	tuf
	125 <i>Neisseria flavescens</i>	This patent	tuf
	126 <i>Neisseria gonorrhoeae</i>	This patent	tuf
	127 <i>Neisseria lactamica</i>	This patent	tuf
10	128 <i>Neisseria meningitidis</i>	This patent	tuf
	129 <i>Neisseria mucosa</i>	This patent	tuf
	130 <i>Neisseria sicca</i>	This patent	tuf
	131 <i>Neisseria subflava</i>	This patent	tuf
	132 <i>Neisseria weaveri</i>	This patent	tuf
15	133 <i>Ochrobactrum anthropi</i>	This patent	tuf
	134 <i>Pantoea agglomerans</i>	This patent	tuf
	135 <i>Pantoea dispersa</i>	This patent	tuf
	136 <i>Pasteurella multocida</i>	This patent	tuf
	137 <i>Peptostreptococcus anaerobius</i>	This patent	tuf
20	138 <i>Peptostreptococcus asaccharolyticus</i>	This patent	tuf
	139 <i>Peptostreptococcus prevotii</i>	This patent	tuf
	140 <i>Porphyromonas asaccharolytica</i>	This patent	tuf
	141 <i>Porphyromonas gingivalis</i>	This patent	tuf
	142 <i>Pragia fontium</i>	This patent	tuf
25	143 <i>Prevotella melaninogenica</i>	This patent	tuf
	144 <i>Prevotella oralis</i>	This patent	tuf
	145 <i>Propionibacterium acnes</i>	This patent	tuf
	146 <i>Proteus mirabilis</i>	This patent	tuf
	147 <i>Proteus penneri</i>	This patent	tuf
30	148 <i>Proteus vulgaris</i>	This patent	tuf
	149 <i>Providencia alcalifaciens</i>	This patent	tuf
	150 <i>Providencia rettgeri</i>	This patent	tuf
	151 <i>Providencia rustigianii</i>	This patent	tuf
	152 <i>Providencia stuartii</i>	This patent	tuf
35	153 <i>Pseudomonas aeruginosa</i>	This patent	tuf
	154 <i>Pseudomonas fluorescens</i>	This patent	tuf
	155 <i>Pseudomonas stutzeri</i>	This patent	tuf
	156 <i>Psychrobacter phenylpyruvicum</i>	This patent	tuf
	157 <i>Rahnella aquatilis</i>	This patent	tuf
40	158 <i>Salmonella choleraesuis</i> subsp. <i>arizonae</i>	This patent	tuf
	159 <i>Salmonella choleraesuis</i> subsp. <i>choleraesuis</i>	This patent	tuf
	serotype Choleraesuis		
	160 <i>Salmonella choleraesuis</i> subsp. <i>diarizonae</i>	This patent	tuf
	161 <i>Salmonella choleraesuis</i> subsp. <i>choleraesuis</i>	This patent	tuf
45	serotype Heidelberg		
	162 <i>Salmonella choleraesuis</i> subsp. <i>houtenae</i>	This patent	tuf
	163 <i>Salmonella choleraesuis</i> subsp. <i>indica</i>	This patent	tuf
	164 <i>Salmonella choleraesuis</i> subsp. <i>salamae</i>	This patent	tuf
	165 <i>Salmonella choleraesuis</i> subsp. <i>choleraesuis</i> serotype Typhi	This patent	tuf
50	166 <i>Serratia fonticola</i>	This patent	tuf
	167 <i>Serratia liquefaciens</i>	This patent	tuf
	168 <i>Serratia marcescens</i>	This patent	tuf
	169 <i>Serratia odorifera</i>	This patent	tuf
	170 <i>Serratia plymuthica</i>	This patent	tuf
55	171 <i>Serratia rubidaea</i>	This patent	tuf
	172 <i>Shigella boydii</i>	This patent	tuf
	173 <i>Shigella dysenteriae</i>	This patent	tuf
	174 <i>Shigella flexneri</i>	This patent	tuf
	175 <i>Shigella sonnei</i>	This patent	tuf
60	176 <i>Staphylococcus aureus</i>	This patent	tuf
	177 <i>Staphylococcus aureus</i>	This patent	tuf
	178 <i>Staphylococcus aureus</i>	This patent	tuf
	179 <i>Staphylococcus aureus</i>	This patent	tuf
	180 <i>Staphylococcus aureus</i> subsp. <i>aureus</i>	This patent	tuf
65	181 <i>Staphylococcus auricularis</i>	This patent	tuf
	182 <i>Staphylococcus capitis</i> subsp. <i>capitis</i>	This patent	tuf

Table 7. Origin of the sequences in the sequence listing (continued).

SEQ ID NO.	Bacterial, fungal or parasitological species	Source	Comments*
5	183 <i>Macrococcus caseolyticus</i>	This patent	tuf
	184 <i>Staphylococcus cohnii</i>	This patent	tuf
	185 <i>Staphylococcus epidermidis</i>	This patent	tuf
	186 <i>Staphylococcus haemolyticus</i>	This patent	tuf
	187 <i>Staphylococcus warneri</i>	This patent	tuf
10	188 <i>Staphylococcus haemolyticus</i>	This patent	tuf
	189 <i>Staphylococcus haemolyticus</i>	This patent	tuf
	190 <i>Staphylococcus haemolyticus</i>	This patent	tuf
	191 <i>Staphylococcus hominis</i> subsp. <i>hominis</i>	This patent	tuf
	192 <i>Staphylococcus warneri</i>	This patent	tuf
15	193 <i>Staphylococcus hominis</i>	This patent	tuf
	194 <i>Staphylococcus hominis</i>	This patent	tuf
	195 <i>Staphylococcus hominis</i>	This patent	tuf
	196 <i>Staphylococcus hominis</i>	This patent	tuf
	197 <i>Staphylococcus lugdunensis</i>	This patent	tuf
20	198 <i>Staphylococcus saprophyticus</i>	This patent	tuf
	199 <i>Staphylococcus saprophyticus</i>	This patent	tuf
	200 <i>Staphylococcus saprophyticus</i>	This patent	tuf
	201 <i>Staphylococcus sciuri</i> subsp. <i>sciuri</i>	This patent	tuf
	202 <i>Staphylococcus warneri</i>	This patent	tuf
25	203 <i>Staphylococcus warneri</i>	This patent	tuf
	204 <i>Bifidobacterium longum</i>	This patent	tuf
	205 <i>Stenotrophomonas maltophilia</i>	This patent	tuf
	206 <i>Streptococcus acidominimus</i>	This patent	tuf
	207 <i>Streptococcus agalactiae</i>	This patent	tuf
30	208 <i>Streptococcus agalactiae</i>	This patent	tuf
	209 <i>Streptococcus agalactiae</i>	This patent	tuf
	210 <i>Streptococcus agalactiae</i>	This patent	tuf
	211 <i>Streptococcus anginosus</i>	This patent	tuf
	212 <i>Streptococcus bovis</i>	This patent	tuf
35	213 <i>Streptococcus anginosus</i>	This patent	tuf
	214 <i>Streptococcus cricetus</i>	This patent	tuf
	215 <i>Streptococcus cristatus</i>	This patent	tuf
	216 <i>Streptococcus downei</i>	This patent	tuf
	217 <i>Streptococcus dysgalactiae</i>	This patent	tuf
40	218 <i>Streptococcus equi</i> subsp. <i>equi</i>	This patent	tuf
	219 <i>Streptococcus ferus</i>	This patent	tuf
	220 <i>Streptococcus gordonii</i>	This patent	tuf
	221 <i>Streptococcus anginosus</i>	This patent	tuf
	222 <i>Streptococcus macacae</i>	This patent	tuf
45	223 <i>Streptococcus gordonii</i>	This patent	tuf
	224 <i>Streptococcus mutans</i>	This patent	tuf
	225 <i>Streptococcus parasanguinis</i>	This patent	tuf
	226 <i>Streptococcus rattus</i>	This patent	tuf
	227 <i>Streptococcus sanguinis</i>	This patent	tuf
50	228 <i>Streptococcus sobrinus</i>	This patent	tuf
	229 <i>Streptococcus suis</i>	This patent	tuf
	230 <i>Streptococcus uberis</i>	This patent	tuf
	231 <i>Streptococcus vestibularis</i>	This patent	tuf
	232 <i>Tatumella ptyseos</i>	This patent	tuf
55	233 <i>Trabulsiella guamensis</i>	This patent	tuf
	234 <i>Veillonella parvula</i>	This patent	tuf
	235 <i>Yersinia enterocolitica</i>	This patent	tuf
	236 <i>Yersinia frederiksenii</i>	This patent	tuf
	237 <i>Yersinia intermedia</i>	This patent	tuf
60	238 <i>Yersinia pestis</i>	This patent	tuf
	239 <i>Yersinia pseudotuberculosis</i>	This patent	tuf
	240 <i>Yersinia rohdei</i>	This patent	tuf
	241 <i>Yokenella regensburgi</i>	This patent	tuf
	242 <i>Achromobacter xylosoxidans</i> subsp. <i>denitrificans</i>	This patent	atpD
65	243 <i>Acinetobacter baumannii</i>	This patent	atpD
	244 <i>Acinetobacter lwoffii</i>	This patent	atpD

Table 7. Origin of the sequences in the sequence listing (continued).

SEQ ID NO.	Bacterial, fungal or parasitical species	Sourc	Comments*
5	245 <i>Staphylococcus saprophyticus</i>	This patent	atpD
	246 <i>Alcaligenes faecalis</i>	This patent	atpD
	247 <i>Bacillus anthracis</i>	This patent	atpD
	248 <i>Bacillus cereus</i>	This patent	atpD
	249 <i>Bacteroides distasonis</i>	This patent	atpD
10	250 <i>Bacteroides ovatus</i>	This patent	atpD
	251 <i>Leclercia adecarboxylata</i>	This patent	atpD
	252 <i>Stenotrophomonas maltophilia</i>	This patent	atpD
	253 <i>Bartonella henselae</i>	This patent	atpD
	254 <i>Bifidobacterium adolescentis</i>	This patent	atpD
15	255 <i>Brucella abortus</i>	This patent	atpD
	256 <i>Cedecea davisae</i>	This patent	atpD
	257 <i>Cedecea lapagei</i>	This patent	atpD
	258 <i>Cedecea neteri</i>	This patent	atpD
	259 <i>Chryseobacterium meningosepticum</i>	This patent	atpD
20	260 <i>Citrobacter amalonaticus</i>	This patent	atpD
	261 <i>Citrobacter braakii</i>	This patent	atpD
	262 <i>Citrobacter koseri</i>	This patent	atpD
	263 <i>Citrobacter farmeri</i>	This patent	atpD
	264 <i>Citrobacter freundii</i>	This patent	atpD
25	265 <i>Citrobacter koseri</i>	This patent	atpD
	266 <i>Citrobacter sedlakii</i>	This patent	atpD
	267 <i>Citrobacter werkmanii</i>	This patent	atpD
	268 <i>Citrobacter youngae</i>	This patent	atpD
	269 <i>Clostridium innocuum</i>	This patent	atpD
30	270 <i>Clostridium perfringens</i>	This patent	atpD
	272 <i>Corynebacterium diphtheriae</i>	This patent	atpD
	273 <i>Corynebacterium pseudodiphtheriticum</i>	This patent	atpD
	274 <i>Corynebacterium ulcerans</i>	This patent	atpD
	275 <i>Corynebacterium urealyticum</i>	This patent	atpD
35	276 <i>Coxiella burnetii</i>	This patent	atpD
	277 <i>Edwardsiella hoshinae</i>	This patent	atpD
	278 <i>Edwardsiella tarda</i>	This patent	atpD
	279 <i>Eikenella corrodens</i>	This patent	atpD
	280 <i>Enterobacter agglomerans</i>	This patent	atpD
40	281 <i>Enterobacter amnigenus</i>	This patent	atpD
	282 <i>Enterobacter asburiae</i>	This patent	atpD
	283 <i>Enterobacter cancerogenus</i>	This patent	atpD
	284 <i>Enterobacter cloacae</i>	This patent	atpD
	285 <i>Enterobacter gergoviae</i>	This patent	atpD
45	286 <i>Enterobacter hormaechei</i>	This patent	atpD
	287 <i>Enterobacter sakazakii</i>	This patent	atpD
	288 <i>Enterococcus avium</i>	This patent	atpD
	289 <i>Enterococcus casseliflavus</i>	This patent	atpD
	290 <i>Enterococcus durans</i>	This patent	atpD
50	291 <i>Enterococcus faecalis</i>	This patent	atpD
	292 <i>Enterococcus faecium</i>	This patent	atpD
	293 <i>Enterococcus gallinarum</i>	This patent	atpD
	294 <i>Enterococcus saccharolyticus</i>	This patent	atpD
	295 <i>Escherichia fergusonii</i>	This patent	atpD
55	296 <i>Escherichia hermannii</i>	This patent	atpD
	297 <i>Escherichia vulneris</i>	This patent	atpD
	298 <i>Eubacterium lentum</i>	This patent	atpD
	299 <i>Ewingella americana</i>	This patent	atpD
	300 <i>Francisella tularensis</i>	This patent	atpD
60	301 <i>Fusobacterium gonidiaformans</i>	This patent	atpD
	302 <i>Fusobacterium necrophorum</i> subsp. <i>necrophorum</i>	This patent	atpD
	303 <i>Fusobacterium nucleatum</i> subsp. <i>polymorphum</i>	This patent	atpD
	304 <i>Gardnerella vaginalis</i>	This patent	atpD
	305 <i>Gemella haemolysans</i>	This patent	atpD
65	306 <i>Gemella morbillorum</i>	This patent	atpD

Table 7. Origin of the sequences in the sequence listing (continued).

SEQ ID NO.	Bacterial, fungal or parasitical species	Source	Comments*
5	307 <i>Haemophilus ducreyi</i>	This patent	atpD
	308 <i>Haemophilus haemolyticus</i>	This patent	atpD
	309 <i>Haemophilus parahaemolyticus</i>	This patent	atpD
	310 <i>Haemophilus parainfluenzae</i>	This patent	atpD
	311 <i>Hafnia alvei</i>	This patent	atpD
10	312 <i>Kingella kingae</i>	This patent	atpD
	313 <i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	This patent	atpD
	314 <i>Klebsiella ornithinolytica</i>	This patent	atpD
	315 <i>Klebsiella oxytoca</i>	This patent	atpD
	316 <i>Klebsiella planticola</i>	This patent	atpD
15	317 <i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	This patent	atpD
	318 <i>Kluyvera ascorbata</i>	This patent	atpD
	319 <i>Kluyvera cryocrescens</i>	This patent	atpD
	320 <i>Kluyvera georgiana</i>	This patent	atpD
	321 <i>Lactobacillus acidophilus</i>	This patent	atpD
20	322 <i>Legionella pneumophila</i> subsp. <i>pneumophila</i>	This patent	atpD
	323 <i>Lerninorella grimonii</i>	This patent	atpD
	324 <i>Listeria monocytogenes</i>	This patent	atpD
	325 <i>Micrococcus lylae</i>	This patent	atpD
	326 <i>Moellerella wisconsensis</i>	This patent	atpD
25	327 <i>Moraxella catarrhalis</i>	This patent	atpD
	328 <i>Moraxella osloensis</i>	This patent	atpD
	329 <i>Morganella morganii</i> subsp. <i>morganii</i>	This patent	atpD
	330 <i>Pantoea agglomerans</i>	This patent	atpD
	331 <i>Pantoea dispersa</i>	This patent	atpD
30	332 <i>Pasteurella multocida</i>	This patent	atpD
	333 <i>Pragia fontium</i>	This patent	atpD
	334 <i>Proteus mirabilis</i>	This patent	atpD
	335 <i>Proteus vulgaris</i>	This patent	atpD
	336 <i>Providencia alcalifaciens</i>	This patent	atpD
35	337 <i>Providencia rettgeri</i>	This patent	atpD
	338 <i>Providencia rustigianii</i>	This patent	atpD
	339 <i>Providencia stuartii</i>	This patent	atpD
	340 <i>Psychrobacter phenylpyruvicus</i>	This patent	atpD
	341 <i>Rahnella aquatilis</i>	This patent	atpD
40	342 <i>Salmonella choleraesuis</i> subsp. <i>arizonae</i>	This patent	atpD
	343 <i>Salmonella choleraesuis</i> subsp. <i>choleraesuis</i>	This patent	atpD
	serotype <i>Choleraesuis</i>		
	344 <i>Salmonella choleraesuis</i> subsp. <i>diarizonae</i>	This patent	atpD
	345 <i>Salmonella choleraesuis</i> subsp. <i>houtenae</i>	This patent	atpD
45	346 <i>Salmonella choleraesuis</i> subsp. <i>indica</i>	This patent	atpD
	347 <i>Salmonella choleraesuis</i> subsp. <i>choleraesuis</i>	This patent	atpD
	serotype <i>Paratyphi A</i>		
	348 <i>Salmonella choleraesuis</i> subsp. <i>choleraesuis</i>	This patent	atpD
	serotype <i>Paratyphi B</i>		
50	349 <i>Salmonella choleraesuis</i> subsp. <i>salamae</i>	This patent	atpD
	350 <i>Salmonella choleraesuis</i> subsp. <i>choleraesuis</i> serotype <i>Typhi</i>	This patent	atpD
	351 <i>Salmonella choleraesuis</i> subsp. <i>choleraesuis</i>	This patent	atpD
	serotype <i>Typhimurium</i>		
	352 <i>Salmonella choleraesuis</i> subsp. <i>choleraesuis</i>	This patent	atpD
55	serotype <i>Virchow</i>		
	353 <i>Serratia ficaria</i>	This patent	atpD
	354 <i>Serratia fonticola</i>	This patent	atpD
	355 <i>Serratia grimesii</i>	This patent	atpD
	356 <i>Serratia liquefaciens</i>	This patent	atpD
60	357 <i>Serratia marcescens</i>	This patent	atpD
	358 <i>Serratia odorifera</i>	This patent	atpD
	359 <i>Serratia plymuthica</i>	This patent	atpD
	360 <i>Serratia rubidaea</i>	This patent	atpD
	361 <i>Pseudomonas putida</i>	This patent	atpD
65	362 <i>Shigella boydii</i>	This patent	atpD
	363 <i>Shigella dysenteriae</i>	This patent	atpD

Tabl 7. Origin of the sequences in the sequence listing (continued).

SEQ ID NO.	Bacterial, fungal or parasitical species	Source	Comments*
5	364 <i>Shigella flexn ri</i>	This patent	atpD
	365 <i>Shigella sonn i</i>	This patent	atpD
	366 <i>Staphylococcus aureus</i>	This patent	atpD
	367 <i>Staphylococcus auricularis</i>	This patent	atpD
	368 <i>Staphylococcus capitis</i> subsp. <i>capitis</i>	This patent	atpD
10	369 <i>Staphylococcus cohnii</i>	This patent	atpD
	370 <i>Staphylococcus epidermidis</i>	This patent	atpD
	371 <i>Staphylococcus haemolyticus</i>	This patent	atpD
	372 <i>Staphylococcus hominis</i> subsp. <i>hominis</i>	This patent	atpD
	373 <i>Staphylococcus hominis</i>	This patent	atpD
15	374 <i>Staphylococcus lugdunensis</i>	This patent	atpD
	375 <i>Staphylococcus saprophyticus</i>	This patent	atpD
	376 <i>Staphylococcus simulans</i>	This patent	atpD
	377 <i>Staphylococcus warneri</i>	This patent	atpD
	378 <i>Streptococcus acidominimus</i>	This patent	atpD
20	379 <i>Streptococcus agalactiae</i>	This patent	atpD
	380 <i>Streptococcus agalactiae</i>	This patent	atpD
	381 <i>Streptococcus agalactiae</i>	This patent	atpD
	382 <i>Streptococcus agalactiae</i>	This patent	atpD
	383 <i>Streptococcus agalactiae</i>	This patent	atpD
25	384 <i>Streptococcus dysgalactiae</i>	This patent	atpD
	385 <i>Streptococcus equi</i> subsp. <i>equi</i>	This patent	atpD
	386 <i>Streptococcus anginosus</i>	This patent	atpD
	387 <i>Streptococcus salivarius</i>	This patent	atpD
	388 <i>Streptococcus suis</i>	This patent	atpD
30	389 <i>Streptococcus uberis</i>	This patent	atpD
	390 <i>Tatumella ptyseos</i>	This patent	atpD
	391 <i>Trabulsiella guamensis</i>	This patent	atpD
	392 <i>Yersinia bercovieri</i>	This patent	atpD
	393 <i>Yersinia enterocolitica</i>	This patent	atpD
35	394 <i>Yersinia frederiksenii</i>	This patent	atpD
	395 <i>Yersinia intermedia</i>	This patent	atpD
	396 <i>Yersinia pseudotuberculosis</i>	This patent	atpD
	397 <i>Yersinia rohdei</i>	This patent	atpD
	398 <i>Yokenella regensburgei</i>	This patent	tuf (EF-1)
40	399 <i>Yarrowia lipolytica</i>	This patent	tuf (EF-1)
	400 <i>Absidia corymbifera</i>	This patent	tuf (EF-1)
	401 <i>Alternaria alternata</i>	This patent	tuf (EF-1)
	402 <i>Aspergillus flavus</i>	This patent	tuf (EF-1)
	403 <i>Aspergillus fumigatus</i>	This patent	tuf (EF-1)
45	404 <i>Aspergillus fumigatus</i>	This patent	tuf (EF-1)
	405 <i>Aspergillus niger</i>	This patent	tuf (EF-1)
	406 <i>Blastoschizomyces capitatus</i>	This patent	tuf (EF-1)
	407 <i>Candida albicans</i>	This patent	tuf (EF-1)
	408 <i>Candida albicans</i>	This patent	tuf (EF-1)
50	409 <i>Candida albicans</i>	This patent	tuf (EF-1)
	410 <i>Candida albicans</i>	This patent	tuf (EF-1)
	411 <i>Candida albicans</i>	This patent	tuf (EF-1)
	412 <i>Candida dubliniensis</i>	This patent	tuf (EF-1)
	413 <i>Candida catenulata</i>	This patent	tuf (EF-1)
55	414 <i>Candida dubliniensis</i>	This patent	tuf (EF-1)
	415 <i>Candida dubliniensis</i>	This patent	tuf (EF-1)
	416 <i>Candida famata</i>	This patent	tuf (EF-1)
	417 <i>Candida glabrata</i>	This patent	tuf (EF-1)
	418 <i>Candida guilliermondii</i>	This patent	tuf (EF-1)
60	419 <i>Candida haemulonii</i>	This patent	tuf (EF-1)
	420 <i>Candida inconspicua</i>	This patent	tuf (EF-1)
	421 <i>Candida kefyr</i>	This patent	tuf (EF-1)
	422 <i>Candida krusei</i>	This patent	tuf (EF-1)
	423 <i>Candida lambica</i>	This patent	tuf (EF-1)
65	424 <i>Candida lusitanae</i>	This patent	tuf (EF-1)
	425 <i>Candida norvegensis</i>	This patent	tuf (EF-1)

Table 7. Origin of the sequences in the sequence listing (continued).

SEQ ID NO.	Bacterial, fungal or parasitological species	Source	Comments*
5	426 <i>Candida parapsilosis</i>	This patent	tuf (EF-1)
	427 <i>Candida rugosa</i>	This patent	tuf (EF-1)
	428 <i>Candida sphaerica</i>	This patent	tuf (EF-1)
	429 <i>Candida tropicalis</i>	This patent	tuf (EF-1)
	430 <i>Candida utilis</i>	This patent	tuf (EF-1)
10	431 <i>Candida viswanathii</i>	This patent	tuf (EF-1)
	432 <i>Candida zeylanoides</i>	This patent	tuf (EF-1)
	433 <i>Coccidioides immitis</i>	This patent	tuf (EF-1)
	434 <i>Cryptococcus albidus</i>	This patent	tuf (EF-1)
	435 <i>Exophiala jeanselmei</i>	This patent	tuf (EF-1)
15	436 <i>Fusarium oxysporum</i>	This patent	tuf (EF-1)
	437 <i>Geotrichum</i> sp.	This patent	tuf (EF-1)
	438 <i>Histoplasma capsulatum</i>	This patent	tuf (EF-1)
	439 <i>Issatchenkia orientalis kudrjanzev</i>	This patent	tuf (EF-1)
	440 <i>Malassezia furfur</i>	This patent	tuf (EF-1)
20	441 <i>Malassezia pachydermatis</i>	This patent	tuf (EF-1)
	442 <i>Malbranchea filamentosa</i>	This patent	tuf (EF-1)
	443 <i>Metschnikowia pulcherrima</i>	This patent	tuf (EF-1)
	444 <i>Paecilomyces lilacinus</i>	This patent	tuf (EF-1)
	445 <i>Paracoccidioides brasiliensis</i>	This patent	tuf (EF-1)
25	446 <i>Penicillium mameffei</i>	This patent	tuf (EF-1)
	447 <i>Pichia anomala</i>	This patent	tuf (EF-1)
	448 <i>Pichia anomala</i>	This patent	tuf (EF-1)
	449 <i>Pseudallescheria boydii</i>	This patent	tuf (EF-1)
	450 <i>Rhizopus oryzae</i>	This patent	tuf (EF-1)
30	451 <i>Rhodotorula minuta</i>	This patent	tuf (EF-1)
	452 <i>Sporobolomyces salmonicolor</i>	This patent	tuf (EF-1)
	453 <i>Sporothrix schenckii</i>	This patent	tuf (EF-1)
	454 <i>Stephanoascus ciferrii</i>	This patent	tuf (EF-1)
	455 <i>Trichophyton mentagrophytes</i>	This patent	tuf (EF-1)
35	456 <i>Trichosporon cutaneum</i>	This patent	tuf (EF-1)
	457 <i>Wangiella dermatitidis</i>	This patent	tuf (EF-1)
	458 <i>Aspergillus fumigatus</i>	This patent	atpD
	459 <i>Blastoschizomyces capitatus</i>	This patent	atpD
	460 <i>Candida albicans</i>	This patent	atpD
40	461 <i>Candida dubliniensis</i>	This patent	atpD
	462 <i>Candida famata</i>	This patent	atpD
	463 <i>Candida glabrata</i>	This patent	atpD
	464 <i>Candida guilliermondii</i>	This patent	atpD
	465 <i>Candida haemulonii</i>	This patent	atpD
45	466 <i>Candida inconspicua</i>	This patent	atpD
	467 <i>Candida kefyr</i>	This patent	atpD
	468 <i>Candida krusei</i>	This patent	atpD
	469 <i>Candida lambica</i>	This patent	atpD
	470 <i>Candida lusitanae</i>	This patent	atpD
50	471 <i>Candida norvegensis</i>	This patent	atpD
	472 <i>Candida parapsilosis</i>	This patent	atpD
	473 <i>Candida rugosa</i>	This patent	atpD
	474 <i>Candida sphaerica</i>	This patent	atpD
	475 <i>Candida tropicalis</i>	This patent	atpD
55	476 <i>Candida utilis</i>	This patent	atpD
	477 <i>Candida viswanathii</i>	This patent	atpD
	478 <i>Candida zeylanoides</i>	This patent	atpD
	479 <i>Coccidioides immitis</i>	This patent	atpD
	480 <i>Cryptococcus albidus</i>	This patent	atpD
60	481 <i>Fusarium oxysporum</i>	This patent	atpD
	482 <i>Geotrichum</i> sp.	This patent	atpD
	483 <i>Histoplasma capsulatum</i>	This patent	atpD
	484 <i>Malassezia furfur</i>	This patent	atpD
	485 <i>Malassezia pachydermatis</i>	This patent	atpD
65	486 <i>Metschnikowia pulcherrima</i>	This patent	atpD
	487 <i>Penicillium mameffei</i>	This patent	atpD

Table 7. Origin of the sequences in the sequence listing (continued).

SEQ ID NO.	Bacterial, fungal or parasitical species	Source	Comments*
5	488 <i>Pichia anomala</i>	This patent	atpD
	489 <i>Pichia anomala</i>	This patent	atpD
	490 <i>Rhodotorula minuta</i>	This patent	atpD
	491 <i>Rhodotorula mucilaginosa</i>	This patent	atpD
	492 <i>Sporobolomyces salmonicolor</i>	This patent	atpD
10	493 <i>Sporothrix schenckii</i>	This patent	atpD
	494 <i>Stephanoascus ciferrii</i>	This patent	atpD
	495 <i>Trichophyton mentagrophytes</i>	This patent	atpD
	496 <i>Wangiella dermatitidis</i>	This patent	atpD
	497 <i>Yarrowia lipolytica</i>	This patent	tuf (M)
15	498 <i>Aspergillus fumigatus</i>	This patent	tuf (M)
	499 <i>Blastoschizomyces capitatus</i>	This patent	tuf (M)
	500 <i>Candida rugosa</i>	This patent	tuf (M)
	501 <i>Coccidioides immitis</i>	This patent	tuf (M)
	502 <i>Fusarium oxysporum</i>	This patent	tuf (M)
20	503 <i>Histoplasma capsulatum</i>	This patent	tuf (M)
	504 <i>Paracoccidioides brasiliensis</i>	This patent	tuf (M)
	505 <i>Penicillium marneffei</i>	This patent	tuf (M)
	506 <i>Pichia anomala</i>	This patent	tuf (M)
	507 <i>Trichophyton mentagrophytes</i>	This patent	tuf (M)
25	508 <i>Yarrowia lipolytica</i>	This patent	tuf (EF-1)
	509 <i>Babesia bigemina</i>	This patent	tuf (EF-1)
	510 <i>Babesia bovis</i>	This patent	tuf (EF-1)
	511 <i>Crithidia fasciculata</i>	This patent	tuf (EF-1)
	512 <i>Entamoeba histolytica</i>	This patent	tuf (EF-1)
30	513 <i>Giardia lamblia</i>	This patent	tuf (EF-1)
	514 <i>Leishmania tropica</i>	This patent	tuf (EF-1)
	515 <i>Leishmania aethiopica</i>	This patent	tuf (EF-1)
	516 <i>Leishmania tropica</i>	This patent	tuf (EF-1)
	517 <i>Leishmania donovani</i>	This patent	tuf (EF-1)
35	518 <i>Leishmania infantum</i>	This patent	tuf (EF-1)
	519 <i>Leishmania enriettii</i>	This patent	tuf (EF-1)
	520 <i>Leishmania gerbilli</i>	This patent	tuf (EF-1)
	521 <i>Leishmania hertigi</i>	This patent	tuf (EF-1)
	522 <i>Leishmania major</i>	This patent	tuf (EF-1)
40	523 <i>Leishmania amazonensis</i>	This patent	tuf (EF-1)
	524 <i>Leishmania mexicana</i>	This patent	tuf (EF-1)
	525 <i>Leishmania tarentolae</i>	This patent	tuf (EF-1)
	526 <i>Leishmania tropica</i>	This patent	tuf (EF-1)
	527 <i>Neospora caninum</i>	This patent	tuf (EF-1)
45	528 <i>Trichomonas vaginalis</i>	This patent	tuf (EF-1)
	529 <i>Trypanosoma brucei</i> subsp. <i>brucei</i>	This patent	atpD
	530 <i>Crithidia fasciculata</i>	This patent	atpD
	531 <i>Leishmania tropica</i>	This patent	atpD
	532 <i>Leishmania aethiopica</i>	This patent	atpD
50	533 <i>Leishmania donovani</i>	This patent	atpD
	534 <i>Leishmania infantum</i>	This patent	atpD
	535 <i>Leishmania gerbilli</i>	This patent	atpD
	536 <i>Leishmania hertigi</i>	This patent	atpD
	537 <i>Leishmania major</i>	This patent	atpD
55	538 <i>Leishmania amazonensis</i>	WO98/20157	tuf
	607 <i>Enterococcus faecalis</i>	WO98/20157	tuf
	608 <i>Enterococcus faecium</i>	WO98/20157	tuf
	609 <i>Enterococcus gallinarum</i>	Database	tuf
	610 <i>Haemophilus influenzae</i>	WO98/20157	tuf
60	611 <i>Staphylococcus epidermidis</i>	This patent	tuf
	612 <i>Salmonella choleraesuis</i> subsp. <i>choleraesuis</i>	This patent	tuf
	serotype Paratyphi A		
	613 <i>Serratia ficaria</i>	This patent	tuf
	614 <i>Enterococcus malodoratus</i>	This patent	tuf (C)
65	615 <i>Enterococcus durans</i>	This patent	tuf (C)
	616 <i>Enterococcus pseudoavium</i>	This patent	tuf (C)

Table 7. Origin of the sequences in the sequence listing (continued).

SEQ ID NO.	Bacterial, fungal or parasitical species	Source	Comments*
5	617 <i>Enterococcus dispar</i>	This patent	tuf (C)
	618 <i>Enterococcus avium</i>	This patent	tuf (C)
	619 <i>Saccharomyces cerevisiae</i>	Database	tuf (M)
	621 <i>Enterococcus faecium</i>	This patent	tuf (C)
	622 <i>Saccharomyces cerevisiae</i>	This patent	tuf (EF-1)
10	623 <i>Cryptococcus neoformans</i>	This patent	tuf (EF-1)
	624 <i>Candida albicans</i>	This patent	tuf (EF-1)
	662 <i>Corynebacterium diphtheriae</i>	WO98/20157	tuf
	663 <i>Candida catenulata</i>	This patent	atpD
	665 <i>Saccharomyces cerevisiae</i>	Database	tuf (EF-1)
15	666 <i>Saccharomyces cerevisiae</i>	Database	atpD
	667 <i>Trypanosoma cruzi</i>	This patent	atpD
	668 <i>Corynebacterium glutamicum</i>	Database	tuf
	669 <i>Escherichia coli</i>	Database	atpD
	670 <i>Helicobacter pylori</i>	Database	atpD
20	671 <i>Clostridium acetobutylicum</i>	Database	atpD
	672 <i>Cytophaga lytica</i>	Database	atpD
	673 <i>Ehrlichia risticii</i>	This patent	atpD
	674 <i>Vibrio cholerae</i>	This patent	atpD
	675 <i>Vibrio cholerae</i>	This patent	tuf
25	676 <i>Leishmania enriettii</i>	This patent	atpD
	677 <i>Babesia microti</i>	This patent	tuf (EF-1)
	678 <i>Cryptococcus neoformans</i>	This patent	atpD
	679 <i>Cryptococcus neoformans</i>	This patent	atpD
	680 <i>Cunninghamella bertholletiae</i>	This patent	atpD
30	684 <i>Candida tropicalis</i>	Database	atpD (V)
	685 <i>Enterococcus hirae</i>	Database	atpD (V)
	686 <i>Chlamydia pneumoniae</i>	Database	atpD (V)
	687 <i>Halobacterium salinarum</i>	Database	atpD (V)
	688 Human	Database	atpD (V)
35	689 <i>Plasmodium falciparum</i>	Database	atpD (V)
	690 <i>Saccharomyces cerevisiae</i>	Database	atpD (V)
	691 <i>Schizosaccharomyces pombe</i>	Database	atpD (V)
	692 <i>Trypanosoma congolense</i>	Database	atpD (V)
	693 <i>Thermus thermophilus</i>	Database	atpD (V)
40	698 <i>Escherichia coli</i>	Database	tuf
	709 <i>Borrelia burgdorferi</i>	genome project	atpD (V)
	710 <i>Treponema pallidum</i>	genome project	atpD (V)
	711 <i>Chlamydia trachomatis</i>	genome project	atpD (V)
	712 <i>Enterococcus faecalis</i>	genome project	atpD (V)
45	713 <i>Methanosarcina barkeri</i>	Database	atpD (V)
	714 <i>Methanococcus jannaschii</i>	Database	atpD (V)
	715 <i>Porphyromonas gingivalis</i>	genome project	atpD (V)
	716 <i>Streptococcus pneumoniae</i>	genome project	atpD (V)
	717 <i>Burkholderia mallei</i>	This patent	tuf
50	718 <i>Burkholderia pseudomallei</i>	This patent	tuf
	719 <i>Clostridium beijerinckii</i>	This patent	tuf
	720 <i>Clostridium innocuum</i>	This patent	tuf
	721 <i>Clostridium novyi</i>	This patent	tuf
	722 <i>Clostridium septicum</i>	This patent	tuf
55	723 <i>Clostridium tertium</i>	This patent	tuf
	724 <i>Clostridium tetani</i>	This patent	tuf
	725 <i>Enterococcus malodoratus</i>	This patent	tuf
	726 <i>Enterococcus sulfureus</i>	This patent	tuf
	727 <i>Lactococcus garvieae</i>	This patent	tuf
60	728 <i>Mycoplasma pirum</i>	This patent	tuf
	729 <i>Mycoplasma salivarium</i>	This patent	tuf
	730 <i>Neisseria polysacchara</i>	This patent	tuf
	731 <i>Salmonella choleraesuis</i> subsp. <i>choleraesuis</i> serotype Enteritidis	This patent	tuf
65			

Table 7. Origin of the sequences in the sequence listing (continued).

SEQ ID NO.	Bacterial, fungal or parasitical species	Source	Comments*
5	732 <i>Salmonella choleraesuis</i> subsp. <i>choleraesuis</i> serotype Gallinarum	This patent	tuf
	733 <i>Salmonella choleraesuis</i> subsp. <i>choleraesuis</i> serotype Paratyphi B	This patent	tuf
	734 <i>Salmonella choleraesuis</i> subsp. <i>choleraesuis</i> serotype Virchow	This patent	tuf
10	735 <i>Serratia grimesii</i>	This patent	tuf
	736 <i>Clostridium difficile</i>	This patent	atpD
	737 <i>Burkholderia pseudomallei</i>	This patent	atpD
	738 <i>Clostridium bifermentans</i>	This patent	atpD
15	739 <i>Clostridium beijerinckii</i>	This patent	atpD
	740 <i>Clostridium difficile</i>	This patent	atpD
	741 <i>Clostridium ramosum</i>	This patent	atpD
	742 <i>Clostridium septicum</i>	This patent	atpD
	743 <i>Clostridium tertium</i>	This patent	atpD
20	744 <i>Comamonas acidovorans</i>	This patent	atpD
	745 <i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	This patent	atpD
	746 <i>Neisseria canis</i>	This patent	atpD
	747 <i>Neisseria cinerea</i>	This patent	atpD
	748 <i>Neisseria cuniculi</i>	This patent	atpD
25	749 <i>Neisseria elongata</i> subsp. <i>elongata</i>	This patent	atpD
	750 <i>Neisseria flavescens</i>	This patent	atpD
	751 <i>Neisseria gonorrhoeae</i>	This patent	atpD
	752 <i>Neisseria gonorrhoeae</i>	This patent	atpD
	753 <i>Neisseria lactamica</i>	This patent	atpD
30	754 <i>Neisseria meningitidis</i>	This patent	atpD
	755 <i>Neisseria mucosa</i>	This patent	atpD
	756 <i>Neisseria subflava</i>	This patent	atpD
	757 <i>Neisseria weaveri</i>	This patent	atpD
	758 <i>Neisseria animalis</i>	This patent	atpD
35	759 <i>Proteus penneri</i>	This patent	atpD
	760 <i>Salmonella choleraesuis</i> subsp. <i>choleraesuis</i> serotype Enteritidis	This patent	atpD
	761 <i>Yersinia pestis</i>	This patent	atpD
	762 <i>Burkholderia mallei</i>	This patent	atpD
40	763 <i>Clostridium sordellii</i>	This patent	atpD
	764 <i>Clostridium novyi</i>	This patent	atpD
	765 <i>Clostridium botulinum</i>	This patent	atpD
	766 <i>Clostridium histolyticum</i>	This patent	atpD
	767 <i>Peptostreptococcus prevotii</i>	This patent	atpD
45	768 <i>Absidia corymbifera</i>	This patent	atpD
	769 <i>Alternaria alternata</i>	This patent	atpD
	770 <i>Aspergillus flavus</i>	This patent	atpD
	771 <i>Mucor circinelloides</i>	This patent	atpD
	772 <i>Piedraia hortai</i>	This patent	atpD
50	773 <i>Pseudallescheria boydii</i>	This patent	atpD
	774 <i>Rhizopus oryzae</i>	This patent	atpD
	775 <i>Scopulariopsis koningii</i>	This patent	atpD
	776 <i>Trichophyton mentagrophytes</i>	This patent	atpD
	777 <i>Trichophyton tonsurans</i>	This patent	atpD
55	778 <i>Trichosporon cutaneum</i>	This patent	tuf (EF-1)
	779 <i>Cladophialophora carrionii</i>	This patent	tuf (EF-1)
	780 <i>Cunninghamella bertholletiae</i>	This patent	tuf (EF-1)
	781 <i>Curvularia lunata</i>	This patent	tuf (EF-1)
	782 <i>Fonsecaea pedrosoli</i>	This patent	tuf (EF-1)
60	783 <i>Microsporium audouinii</i>	This patent	tuf (EF-1)
	784 <i>Mucor circinelloides</i>	This patent	tuf (EF-1)
	785 <i>Phialophora verrucosa</i>	This patent	tuf (EF-1)
	786 <i>Saksenaea vasiformis</i>	This patent	tuf (EF-1)
	787 <i>Syncephalastrum racemosum</i>	This patent	tuf (EF-1)
65	788 <i>Trichophyton tonsurans</i>	This patent	tuf (EF-1)
	789 <i>Trichophyton mentagrophytes</i>	This patent	tuf (EF-1)

Table 7. Origin of the sequences in the sequence listing (continued).

SEQ ID NO.	Bacterial,fungal or parasitcal species	Source	Comments*
5	790 <i>Bipolaris hawaiiensis</i>	This patent	tuf (EF-1)
	791 <i>Aspergillus fumigatus</i>	This patent	tuf (M)
	792 <i>Trichophyton mentagrophytes</i>	This patent	tuf (M)
	827 <i>Clostridium novyi</i>	This patent	atpD (V)
	828 <i>Clostridium difficile</i>	This patent	atpD (V)
10	829 <i>Clostridium septicum</i>	This patent	atpD (V)
	830 <i>Clostridium botulinum</i>	This patent	atpD (V)
	831 <i>Clostridium perfringens</i>	This patent	atpD (V)
	832 <i>Clostridium tetani</i>	This patent	atpD (V)
	833 <i>Streptococcus pyogenes</i>	Database	atpD (V)
15	834 <i>Babesia bovis</i>	This patent	atpD (V)
	835 <i>Cryptosporidium parvum</i>	This patent	atpD (V)
	836 <i>Leishmania infantum</i>	This patent	atpD (V)
	837 <i>Leishmania major</i>	This patent	atpD (V)
	838 <i>Leishmania tarentolae</i>	This patent	atpD (V)
20	839 <i>Trypanosoma brucei</i>	This patent	atpD (V)
	840 <i>Trypanosoma cruzi</i>	This patent	tuf (EF-1)
	841 <i>Trypanosoma cruzi</i>	This patent	tuf (EF-1)
	842 <i>Trypanosoma cruzi</i>	This patent	tuf (EF-1)
	843 <i>Babesia bovis</i>	This patent	tuf (M)
25	844 <i>Leishmania aethiopica</i>	This patent	tuf (M)
	845 <i>Leishmania amazonensis</i>	This patent	tuf (M)
	846 <i>Leishmania donovani</i>	This patent	tuf (M)
	847 <i>Leishmania infantum</i>	This patent	tuf (M)
	848 <i>Leishmania enriettii</i>	This patent	tuf (M)
30	849 <i>Leishmania gerbilli</i>	This patent	tuf (M)
	850 <i>Leishmania major</i>	This patent	tuf (M)
	851 <i>Leishmania mexicana</i>	This patent	tuf (M)
	852 <i>Leishmania tarentolae</i>	This patent	tuf (M)
	853 <i>Trypanosoma cruzi</i>	This patent	tuf (M)
35	854 <i>Trypanosoma cruzi</i>	This patent	tuf (M)
	855 <i>Trypanosoma cruzi</i>	This patent	tuf (M)
	856 <i>Babesia bigemina</i>	This patent	atpD
	857 <i>Babesia bovis</i>	This patent	atpD
	858 <i>Babesia microti</i>	This patent	atpD
40	859 <i>Leishmania guyanensis</i>	This patent	atpD
	860 <i>Leishmania mexicana</i>	This patent	atpD
	861 <i>Leishmania tropica</i>	This patent	atpD
	862 <i>Leishmania tropica</i>	This patent	atpD
	863 <i>Bordetella pertussis</i>	Database	tuf
45	864 <i>Trypanosoma brucei</i>	Database	tuf (EF-1)
	865 <i>Cryptosporidium parvum</i>	This patent	tuf (EF-1)
	866 <i>Staphylococcus saprophyticus</i>	This patent	atpD
	867 <i>Zoogloea ramigera</i>	This patent	atpD
	868 <i>Staphylococcus saprophyticus</i>	This patent	tuf
50	869 <i>Enterococcus casseliflavus</i>	This patent	tuf
	870 <i>Enterococcus casseliflavus</i>	This patent	tuf
	871 <i>Enterococcus flavescens</i>	This patent	tuf
	872 <i>Enterococcus gallinarum</i>	This patent	tuf
	873 <i>Enterococcus gallinarum</i>	This patent	tuf
55	874 <i>Staphylococcus haemolyticus</i>	This patent	tuf
	875 <i>Staphylococcus epidermidis</i>	This patent	tuf
	876 <i>Staphylococcus epidermidis</i>	This patent	tuf
	877 <i>Staphylococcus epidermidis</i>	This patent	tuf
	878 <i>Staphylococcus epidermidis</i>	This patent	tuf
60	879 <i>Enterococcus gallinarum</i>	This patent	tuf
	880 <i>Pseudomonas aeruginosa</i>	This patent	tuf
	881 <i>Enterococcus casseliflavus</i>	This patent	tuf
	882 <i>Enterococcus casseliflavus</i>	This patent	tuf
	883 <i>Enterococcus faecalis</i>	This patent	tuf
65	884 <i>Enterococcus faecalis</i>	This patent	tuf
	885 <i>Enterococcus faecium</i>	This patent	tuf

Table 7. Origin of the sequences in the sequence listing (continued).

SEQ ID NO.	Bacterial, fungal or parasitical species	Source	Comments*
5	886 <i>Enterococcus faecium</i>	This patent	tuf
	887 <i>Zoogloea ramigera</i>	This patent	tuf
	888 <i>Enterococcus faecalis</i>	This patent	tuf
	889 <i>Aspergillus fumigatus</i>	This patent	atpD
	890 <i>Penicillium mameffe</i>	This patent	atpD
10	891 <i>Paecilomyces lilacinus</i>	This patent	atpD
	892 <i>Penicillium mameffe</i>	This patent	atpD
	893 <i>Sporothrix schenckii</i>	This patent	atpD
	894 <i>Malbranchea filamentosa</i>	This patent	atpD
	895 <i>Paecilomyces lilacinus</i>	This patent	atpD
15	896 <i>Aspergillus niger</i>	This patent	atpD
	897 <i>Aspergillus fumigatus</i>	This patent	tuf (EF-1)
	898 <i>Penicillium mameffe</i>	This patent	tuf (EF-1)
	899 <i>Piedraia hortai</i>	This patent	tuf (EF-1)
	900 <i>Paecilomyces lilacinus</i>	This patent	tuf (EF-1)
20	901 <i>Paracoccidioides brasiliensis</i>	This patent	tuf (EF-1)
	902 <i>Sporothrix schenckii</i>	This patent	tuf (EF-1)
	903 <i>Penicillium mameffe</i>	This patent	tuf (EF-1)
	904 <i>Curvularia lunata</i>	This patent	tuf (M)
	905 <i>Aspergillus niger</i>	This patent	tuf (M)
25	906 <i>Bipolaris hawaiiensis</i>	This patent	tuf (M)
	907 <i>Aspergillus flavus</i>	This patent	tuf (M)
	908 <i>Alternaria alternata</i>	This patent	tuf (M)
	909 <i>Penicillium mameffe</i>	This patent	tuf (M)
	910 <i>Penicillium mameffe</i>	This patent	tuf (M)
30	918 <i>Escherichia coli</i>	Database	recA
	929 <i>Bacteroides fragilis</i>	This patent	atpD (V)
	930 <i>Bacteroides distasonis</i>	This patent	atpD (V)
	931 <i>Porphyromonas asaccharolytica</i>	This patent	atpD (V)
	932 <i>Listeria monocytogenes</i>	This patent	tuf
35	939 <i>Saccharomyces cerevisiae</i>	Database	recA (Rad51)
	940 <i>Saccharomyces cerevisiae</i>	Database	recA (Dmc1)
	941 <i>Cryptococcus humicola</i>	This patent	atpD
	942 <i>Escherichia coli</i>	This patent	atpD
	943 <i>Escherichia coli</i>	This patent	atpD
40	944 <i>Escherichia coli</i>	This patent	atpD
	945 <i>Escherichia coli</i>	This patent	atpD
	946 <i>Neisseria polysaccharea</i>	This patent	atpD
	947 <i>Neisseria sicca</i>	This patent	atpD
	948 <i>Streptococcus mitis</i>	This patent	atpD
45	949 <i>Streptococcus mitis</i>	This patent	atpD
	950 <i>Streptococcus mitis</i>	This patent	atpD
	951 <i>Streptococcus oralis</i>	This patent	atpD
	952 <i>Streptococcus pneumoniae</i>	This patent	atpD
	953 <i>Streptococcus pneumoniae</i>	This patent	atpD
50	954 <i>Streptococcus pneumoniae</i>	This patent	atpD
	955 <i>Streptococcus pneumoniae</i>	This patent	atpD
	956 <i>Babesia microti</i>	This patent	atpD (V)
	957 <i>Entamoeba histolytica</i>	This patent	atpD (V)
	958 <i>Fusobacterium nucleatum</i> subsp. <i>polymorphum</i>	This patent	atpD (V)
55	959 <i>Leishmania aethiopica</i>	This patent	atpD (V)
	960 <i>Leishmania tropica</i>	This patent	atpD (V)
	961 <i>Leishmania guyanensis</i>	This patent	atpD (V)
	962 <i>Leishmania donovani</i>	This patent	atpD (V)
	963 <i>Leishmania hertigi</i>	This patent	atpD (V)
60	964 <i>Leishmania mexicana</i>	This patent	atpD (V)
	965 <i>Leishmania tropica</i>	This patent	atpD (V)
	966 <i>Peptostreptococcus anaerobius</i>	This patent	atpD (V)
	967 <i>Bordetella pertussis</i>	This patent	tuf
	968 <i>Bordetella pertussis</i>	This patent	tuf
65	969 <i>Enterococcus columbae</i>	This patent	tuf

Table 7. Origin of the sequences in the sequence listing (continued).

SEQ ID NO.	Bacterial, fungal or parasitological species	Source	Comments*
5	970 <i>Enterococcus flavescens</i>	This patent	tuf
	971 <i>Streptococcus pneumoniae</i>	This patent	tuf
	972 <i>Escherichia coli</i>	This patent	tuf
	973 <i>Escherichia coli</i>	This patent	tuf
	974 <i>Escherichia coli</i>	This patent	tuf
10	975 <i>Escherichia coli</i>	This patent	tuf
	976 <i>Mycobacterium avium</i>	This patent	tuf
	977 <i>Streptococcus pneumoniae</i>	This patent	tuf
	978 <i>Mycobacterium gordonae</i>	This patent	tuf
	979 <i>Streptococcus pneumoniae</i>	This patent	tuf
15	980 <i>Mycobacterium tuberculosis</i>	This patent	tuf
	981 <i>Staphylococcus warneri</i>	This patent	tuf
	982 <i>Streptococcus mitis</i>	This patent	tuf
	983 <i>Streptococcus mitis</i>	This patent	tuf
	984 <i>Streptococcus mitis</i>	This patent	tuf
20	985 <i>Streptococcus oralis</i>	This patent	tuf
	986 <i>Streptococcus pneumoniae</i>	This patent	tuf
	987 <i>Enterococcus hirae</i>	This patent	tuf (C)
	988 <i>Enterococcus mundtii</i>	This patent	tuf (C)
	989 <i>Enterococcus raffinosus</i>	This patent	tuf (C)
25	990 <i>Bacillus anthracis</i>	This patent	recA
	991 <i>Prevotella melaninogenica</i>	This patent	recA
	992 <i>Enterococcus casseliflavus</i>	This patent	tuf
	993 <i>Streptococcus pyogenes</i>	Database	speA
	1002 <i>Streptococcus pyogenes</i>	genome project	tuf
30	1003 <i>Bacillus cereus</i>	This patent	recA
	1004 <i>Streptococcus pneumoniae</i>	This patent	pbp1a
	1005 <i>Streptococcus pneumoniae</i>	This patent	pbp1a
	1006 <i>Streptococcus pneumoniae</i>	This patent	pbp1a
	1007 <i>Streptococcus pneumoniae</i>	This patent	pbp1a
35	1008 <i>Streptococcus pneumoniae</i>	This patent	pbp1a
	1009 <i>Streptococcus pneumoniae</i>	This patent	pbp1a
	1010 <i>Streptococcus pneumoniae</i>	This patent	pbp1a
	1011 <i>Streptococcus pneumoniae</i>	This patent	pbp1a
	1012 <i>Streptococcus pneumoniae</i>	This patent	pbp1a
40	1013 <i>Streptococcus pneumoniae</i>	This patent	pbp1a
	1014 <i>Streptococcus pneumoniae</i>	This patent	pbp1a
	1015 <i>Streptococcus pneumoniae</i>	This patent	pbp1a
	1016 <i>Streptococcus pneumoniae</i>	This patent	pbp1a
	1017 <i>Streptococcus pneumoniae</i>	This patent	pbp1a
45	1018 <i>Streptococcus pneumoniae</i>	This patent	pbp1a
	1019 <i>Streptococcus pneumoniae</i>	This patent	pbp2b
	1020 <i>Streptococcus pneumoniae</i>	This patent	pbp2b
	1021 <i>Streptococcus pneumoniae</i>	This patent	pbp2b
	1022 <i>Streptococcus pneumoniae</i>	This patent	pbp2b
50	1023 <i>Streptococcus pneumoniae</i>	This patent	pbp2b
	1024 <i>Streptococcus pneumoniae</i>	This patent	pbp2b
	1025 <i>Streptococcus pneumoniae</i>	This patent	pbp2b
	1026 <i>Streptococcus pneumoniae</i>	This patent	pbp2b
	1027 <i>Streptococcus pneumoniae</i>	This patent	pbp2b
55	1028 <i>Streptococcus pneumoniae</i>	This patent	pbp2b
	1029 <i>Streptococcus pneumoniae</i>	This patent	pbp2b
	1030 <i>Streptococcus pneumoniae</i>	This patent	pbp2b
	1031 <i>Streptococcus pneumoniae</i>	This patent	pbp2b
	1032 <i>Streptococcus pneumoniae</i>	This patent	pbp2b
60	1033 <i>Streptococcus pneumoniae</i>	This patent	pbp2b
	1034 <i>Streptococcus pneumoniae</i>	This patent	pbp2x
	1035 <i>Streptococcus pneumoniae</i>	This patent	pbp2x
	1036 <i>Streptococcus pneumoniae</i>	This patent	pbp2x
65	1037 <i>Streptococcus pneumoniae</i>	This patent	pbp2x

Table 7. Origin of the sequences in the sequence listing (continued).

SEQ ID NO.	Bacterial, fungal or parasitical species	Source	Comments*
5	1038 <i>Streptococcus pneumoniae</i>	This patent	pbp2x
	1039 <i>Streptococcus pneumoniae</i>	This patent	pbp2x
	1040 <i>Streptococcus pneumoniae</i>	This patent	pbp2x
	1041 <i>Streptococcus pneumoniae</i>	This patent	pbp2x
	1042 <i>Streptococcus pneumoniae</i>	This patent	pbp2x
10	1043 <i>Streptococcus pneumoniae</i>	This patent	pbp2x
	1044 <i>Streptococcus pneumoniae</i>	This patent	pbp2x
	1045 <i>Streptococcus pneumoniae</i>	This patent	pbp2x
	1046 <i>Streptococcus pneumoniae</i>	This patent	pbp2x
	1047 <i>Streptococcus pneumoniae</i>	This patent	pbp2x
15	1048 <i>Streptococcus pneumoniae</i>	This patent	pbp2x
	1049 <i>Enterococcus faecium</i>	This patent	vanA
	1050 <i>Enterococcus gallinarum</i>	This patent	vanA
	1051 <i>Enterococcus faecium</i>	This patent	vanA
	1052 <i>Enterococcus faecium</i>	This patent	vanA
20	1053 <i>Enterococcus faecium</i>	This patent	vanA
	1054 <i>Enterococcus faecalis</i>	This patent	vanA
	1055 <i>Enterococcus gallinarum</i>	This patent	vanA
	1056 <i>Enterococcus faecium</i>	This patent	vanA
	1057 <i>Enterococcus flavescens</i>	This patent	vanA
25	1058 <i>Enterococcus gallinarum</i>	This patent	vanC1
	1059 <i>Enterococcus gallinarum</i>	This patent	vanC1
	1060 <i>Enterococcus casseliflavus</i>	This patent	vanC2
	1061 <i>Enterococcus casseliflavus</i>	This patent	vanC2
	1062 <i>Enterococcus casseliflavus</i>	This patent	vanC2
30	1063 <i>Enterococcus casseliflavus</i>	This patent	vanC2
	1064 <i>Enterococcus flavescens</i>	This patent	vanC3
	1065 <i>Enterococcus flavescens</i>	This patent	vanC3
	1066 <i>Enterococcus flavescens</i>	This patent	vanC3
	1067 <i>Enterococcus faecium</i>	This patent	vanXY
35	1068 <i>Enterococcus faecium</i>	This patent	vanXY
	1069 <i>Enterococcus faecium</i>	This patent	vanXY
	1070 <i>Enterococcus faecalis</i>	This patent	vanXY
	1071 <i>Enterococcus gallinarum</i>	This patent	vanXY
	1072 <i>Enterococcus faecium</i>	This patent	vanXY
40	1073 <i>Enterococcus flavescens</i>	This patent	vanXY
	1074 <i>Enterococcus faecium</i>	This patent	vanXY
	1075 <i>Enterococcus gallinarum</i>	This patent	vanXY
	1076 <i>Escherichia coli</i>	Database	stx ₁
	1077 <i>Escherichia coli</i>	Database	stx ₂
45	1093 <i>Staphylococcus saprophyticus</i>	This patent	unknown
	1117 <i>Enterococcus faecium</i>	Database	vanB
	1138 <i>Enterococcus gallinarum</i>	Database	vanC1
	1139 <i>Enterococcus faecium</i>	Database	vanA
	1140 <i>Enterococcus casseliflavus</i>	Database	vanC2
50	1141 <i>Enterococcus faecium</i>	Database	vanHAXY
	1169 <i>Streptococcus pneumoniae</i>	Database	pbp1a
	1172 <i>Streptococcus pneumoniae</i>	Database	pbp2b
	1173 <i>Streptococcus pneumoniae</i>	Database	pbp2x
	1178 <i>Staphylococcus aureus</i>	Database	mecA
55	1183 <i>Streptococcus pneumoniae</i>	Database	hexA
	1184 <i>Streptococcus pneumoniae</i>	This patent	hexA
	1185 <i>Streptococcus pneumoniae</i>	This patent	hexA
	1186 <i>Streptococcus pneumoniae</i>	This patent	hexA
	1187 <i>Streptococcus pneumoniae</i>	This patent	hexA

Table 7. Origin of the sequences in the sequence listing (continued).

SEQ ID NO.	Bacterial, fungal or parasitical species	Source	Comments*
5	1188 <i>Streptococcus oralis</i>	This patent	<i>hexA</i>
	1189 <i>Streptococcus mitis</i>	This patent	<i>hexA</i>
	1190 <i>Streptococcus mitis</i>	This patent	<i>hexA</i>
	1191 <i>Streptococcus mitis</i>	This patent	<i>hexA</i>
	1198 <i>Staphylococcus saprophyticus</i>	This patent	unknown
10	1215 <i>Streptococcus pyogenes</i>	Database	<i>PCP</i>
	1230 <i>Escherichia coli</i>	Database	<i>tuf</i> (EF-G)
	1242 <i>Enterococcus faecium</i>	Database	<i>ddl</i>
	1243 <i>Enterococcus faecalis</i>	Database	<i>mtlF</i> , <i>mtlD</i>
15	1244 <i>Staphylococcus aureus</i> subsp. <i>aureus</i>	This patent	unknown

* *tuf* indicates *tuf* sequences, *tuf* (C) indicates *tuf* sequences divergent from main (usually A and B) copies of the elongation factor-Tu, *tuf* (EF-1) indicates *tuf* sequences of the eukaryotic type (elongation factor 1 α), *tuf* (M) indicates *tuf* sequences from organellar (mostly mitochondrial) origin.

atpD indicates *atpD* sequences of the F-type, *atpD* (V) indicates *atpD* sequences of the V-type.

recA indicates *recA* sequences, *recA*(Rad51) indicates *rad51* sequences or homologs and *recA*(Dmc1) indicates *dmc1* sequences or homologs.

speA indicates *speA* sequences.

hexA indicates *hexA* sequences.

mecA indicates *mecA* sequences.

vanA indicates *vanA* sequences, *vanB* indicates *vanB* sequences, *vanC1* indicates *vanC1* sequences, *vanC2* indicates *vanC2* sequences, *vanC3* indicates *vanC3* sequences, *vanXY* indicates *vanXY* sequences, *vanHAXY* indicates *vanHAXY* sequences.

pbp1a indicates *pbp1a* sequences, *pbp2b* indicates *pbp2b* sequences, *pbp2x* indicates *pbp2x* sequences.

pcp indicates *pcp* sequences.

stx₁ indicates *stx₁* sequences, *stx₂* indicates *stx₂* sequences.

unknown indicates an unknown gene.

Table 8. Bacterial species used to test the specificity of the *Streptococcus agalactiae*-specific amplification primers derived from *tuf* sequences.

	Strain	Reference number	Strain	Reference number
5	<i>Streptococcus acidominimus</i>	ATCC 51726	<i>Bacteroides caccae</i>	ATCC 43185
	<i>Streptococcus agalactiae</i>	ATCC 12403	<i>Bacteroides vulgatus</i>	ATCC 8482
	<i>Streptococcus agalactiae</i>	ATCC 12973	<i>Bacteroides fragilis</i>	ATCC 25285
10	<i>Streptococcus agalactiae</i>	ATCC 13813	<i>Candida albicans</i>	ATCC 11006
	<i>Streptococcus agalactiae</i>	ATCC 27591	<i>Clostridium innocuum</i>	ATCC 14501
	<i>Streptococcus agalactiae</i>	CDCs 1073	<i>Clostridium ramosum</i>	ATCC 25582
	<i>Streptococcus anginosus</i>	ATCC 27335	<i>Lactobacillus casei</i> subsp. <i>casei</i>	ATCC 393
	<i>Streptococcus anginosus</i>	ATCC 33397	<i>Clostridium septicum</i>	ATCC 12464
15	<i>Streptococcus bovis</i>	ATCC 33317	<i>Corynebacterium cervicis</i>	NCTC 10604
	<i>Streptococcus anginosus</i>	ATCC 27823	<i>Corynebacterium genitalium</i>	ATCC 33031
	<i>Streptococcus cricetus</i>	ATCC 19642	<i>Corynebacterium urealyticum</i>	ATCC 43042
	<i>Streptococcus cristatus</i>	ATCC 51100	<i>Enterococcus faecalis</i>	ATCC 29212
	<i>Streptococcus downei</i>	ATCC 33748	<i>Enterococcus faecium</i>	ATCC 19434
20	<i>Streptococcus dysgalactiae</i>	ATCC 43078	<i>Eubacterium lentum</i>	ATCC 43055
	<i>Streptococcus equi</i> subsp. <i>equi</i>	ATCC 9528	<i>Eubacterium nodatum</i>	ATCC 33099
	<i>Streptococcus ferus</i>	ATCC 33477	<i>Gardnerella vaginalis</i>	ATCC 14018
	<i>Streptococcus gordonii</i>	ATCC 10558	<i>Lactobacillus acidophilus</i>	ATCC 4356
	<i>Streptococcus macacae</i>	ATCC 35911	<i>Lactobacillus crispatus</i>	ATCC 33820
25	<i>Streptococcus mitis</i>	ATCC 49456	<i>Lactobacillus gasseri</i>	ATCC 33323
	<i>Streptococcus mutans</i>	ATCC 25175	<i>Lactobacillus johnsonii</i>	ATCC 33200
	<i>Streptococcus oralis</i>	ATCC 35037	<i>Lactococcus lactis</i> subsp. <i>lactis</i>	ATCC 19435
	<i>Streptococcus parasanguinis</i>	ATCC 15912	<i>Lactococcus lactis</i> subsp. <i>lactis</i>	ATCC 11454
	<i>Streptococcus parauberis</i>	DSM 6631	<i>Listeria innocua</i>	ATCC 33090
30	<i>Streptococcus pneumoniae</i>	ATCC 27336	<i>Micrococcus luteus</i>	ATCC 9341
	<i>Streptococcus pyogenes</i>	ATCC 19615	<i>Escherichia coli</i>	ATCC 25922
	<i>Streptococcus rattus</i>	ATCC 19645	<i>Micrococcus lylae</i>	ATCC 27566
	<i>Streptococcus salivarius</i>	ATCC 7073	<i>Porphyromonas asaccharolytica</i>	ATCC 25260
	<i>Streptococcus sanguinis</i>	ATCC 10556	<i>Prevotella corporis</i>	ATCC 33547
35	<i>Streptococcus sobrinus</i>	ATCC 27352	<i>Prevotella melanogenica</i>	ATCC 25845
	<i>Streptococcus suis</i>	ATCC 43765	<i>Staphylococcus aureus</i>	ATCC 13301
	<i>Streptococcus uberis</i>	ATCC 19436	<i>Staphylococcus epidermidis</i>	ATCC 14990
	<i>Streptococcus vestibularis</i>	ATCC 49124	<i>Staphylococcus saprophyticus</i>	ATCC 15305
40				

Tabl 9. Bacterial sp cies used to test the specificity of the *Streptococcus agalactiae*-specific amplification primers derived from *atpD* sequences.

	Strain	Reference number	Strain	Reference number
5	<i>Streptococcus acidominimus</i>	ATCC 51726	<i>Streptococcus gordonii</i>	ATCC 10558
	<i>Streptococcus agalactiae</i>	ATCC 12400	<i>Streptococcus macacae</i>	ATCC 35911
	<i>Streptococcus agalactiae</i>	ATCC 12403	<i>Streptococcus mitis</i>	ATCC 49456
10	<i>Streptococcus agalactiae</i>	ATCC 12973	<i>Streptococcus mutans</i>	ATCC 25175
	<i>Streptococcus agalactiae</i>	ATCC 13813	<i>Streptococcus oralis</i>	ATCC 35037
	<i>Streptococcus agalactiae</i>	ATCC 27591	<i>Streptococcus parasanguinis</i>	ATCC 15912
	<i>Streptococcus agalactiae</i>	CDCs-1073	<i>Streptococcus parauberis</i>	DSM 6631
	<i>Streptococcus anginosus</i>	ATCC 27335	<i>Streptococcus pneumoniae</i>	ATCC 27336
15	<i>Streptococcus anginosus</i>	ATCC 27823	<i>Streptococcus pyogenes</i>	ATCC 19615
	<i>Streptococcus bovis</i>	ATCC 33317	<i>Streptococcus rattii</i>	ATCC 19645
	<i>Streptococcus cricetus</i>	ATCC 19642	<i>Streptococcus salivarius</i>	ATCC 7073
	<i>Streptococcus cristatus</i>	ATCC 51100	<i>Streptococcus sanguinis</i>	ATCC 10556
	<i>Streptococcus downei</i>	ATCC 33748	<i>Streptococcus sobrinus</i>	ATCC 27352
20	<i>Streptococcus dysgalactiae</i>	ATCC 43078	<i>Streptococcus suis</i>	ATCC 43765
	<i>Streptococcus equi</i> subsp. <i>equi</i>	ATCC 9528	<i>Streptococcus uberis</i>	ATCC 19436
	<i>Streptococcus ferus</i>	ATCC 33477	<i>Streptococcus vestibularis</i>	ATCC 49124

Table 10. Bacterial species used to test the specificity of the *Enterococcus*-specific amplification primers derived from *tufS* sequences.

	Strain	Reference number	Strain	Reference number
5	Gram-positive species (n=74)			
	<i>Abiotrophia adiacens</i>	ATCC 49176	<i>Listeria innocua</i>	ATCC 33090
	<i>Abiotrophia defectiva</i>	ATCC 49175	<i>Listeria ivanovii</i>	ATCC 19119
	<i>Bacillus cereus</i>	ATCC 14579	<i>Listeria monocytogenes</i>	ATCC 15313
	<i>Bacillus subtilis</i>	ATCC 27370	<i>Listeria seeligeri</i>	ATCC 35967
10	<i>Bifidobacterium adolescentis</i>	ATCC 27534	<i>Micrococcus luteus</i>	ATCC 9341
	<i>Bifidobacterium breve</i>	ATCC 15700	<i>Pediococcus acidilacti</i>	ATCC 33314
	<i>Bifidobacterium dentium</i>	ATCC 27534	<i>Pediococcus pentosaceus</i>	ATCC 33316
	<i>Bifidobacterium longum</i>	ATCC 15707	<i>Peptococcus niger</i>	ATCC 27731
	<i>Clostridium perfringens</i>	ATCC 3124	<i>Peptostreptococcus anaerobius</i>	ATCC 27337
15	<i>Clostridium septicum</i>	ATCC 12464	<i>Peptostreptococcus indolicus</i>	ATCC 29247
	<i>Corynebacterium aquaticus</i>	ATCC 14665	<i>Peptostreptococcus micros</i>	ATCC 33270
	<i>Corynebacterium pseudodiphtheriticum</i>	ATCC 10700	<i>Propionibacterium acnes</i>	ATCC 6919
	<i>Enterococcus avium</i>	ATCC 14025	<i>Staphylococcus aureus</i>	ATCC 43300
20	<i>Enterococcus casseliflavus</i>	ATCC 25788	<i>Staphylococcus capitis</i>	ATCC 27840
	<i>Enterococcus cecorum</i>	ATCC 43199	<i>Staphylococcus epidermidis</i>	ATCC 14990
	<i>Enterococcus columbae</i>	ATCC 51263	<i>Staphylococcus haemolyticus</i>	ATCC 29970
	<i>Enterococcus dispar</i>	ATCC 51266	<i>Staphylococcus hominis</i>	ATCC 27844
	<i>Enterococcus durans</i>	ATCC 19432	<i>Staphylococcus lugdunensis</i>	ATCC 43809
25	<i>Enterococcus faecalis</i>	ATCC 29212	<i>Staphylococcus saprophyticus</i>	ATCC 15305
	<i>Enterococcus faecium</i>	ATCC 19434	<i>Staphylococcus simulans</i>	ATCC 27848
	<i>Enterococcus flavescens</i>	ATCC 49996	<i>Staphylococcus wamneri</i>	ATCC 27836
	<i>Enterococcus gallinarum</i>	ATCC 49573	<i>Streptococcus agalactiae</i>	ATCC 13813
	<i>Enterococcus hirae</i>	ATCC 8044	<i>Streptococcus anginosus</i>	ATCC 33397
30	<i>Enterococcus malodoratus</i>	ATCC 43197	<i>Streptococcus bovis</i>	ATCC 33317
	<i>Enterococcus mundtii</i>	ATCC 43186	<i>Streptococcus constellatus</i>	ATCC 27823
	<i>Enterococcus pseudoavium</i>	ATCC 49372	<i>Streptococcus cristatus</i>	ATCC 51100
	<i>Enterococcus raffinosus</i>	ATCC 49427	<i>Streptococcus intermedius</i>	ATCC 27335
	<i>Enterococcus saccharolyticus</i>	ATCC 43076	<i>Streptococcus mitis</i>	ATCC 49456
35	<i>Enterococcus solitarius</i>	ATCC 49428	<i>Streptococcus mitis</i>	ATCC 3639
	<i>Enterococcus sulfureus</i>	ATCC 49903	<i>Streptococcus mutans</i>	ATCC 27175
	<i>Eubacterium lentum</i>	ATCC 49903	<i>Streptococcus parasanguinis</i>	ATCC 15912
	<i>Gemella haemolysans</i>	ATCC 10379	<i>Streptococcus pneumoniae</i>	ATCC 27736
	<i>Gemella morbillorum</i>	ATCC 27842	<i>Streptococcus pneumoniae</i>	ATCC 6303
40	<i>Lactobacillus acidophilus</i>	ATCC 4356	<i>Streptococcus pyogenes</i>	ATCC 19615
	<i>Leuconostoc mesenteroides</i>	ATCC 19225	<i>Streptococcus salivarius</i>	ATCC 7073
	<i>Listeria grayi</i>	ATCC 19120	<i>Streptococcus sanguinis</i>	ATCC 10556
	<i>Listeria grayi</i>	ATCC 19123	<i>Streptococcus suis</i>	ATCC 43765
45				

Table 10. Bacterial species used to test the specificity of the *Enterococcus* genus-specific amplification primers derived from *tuf* sequences (continued).

	Strain	Reference number	Strain	Reference number
5	Gram-negative species (n=39)			
	<i>Acidominococcus fermentans</i>	ATCC 2508	<i>Hafnia alvei</i>	ATCC 13337
	<i>Acinetobacter baumannii</i>	ATCC 19606	<i>Klebsiella oxytoca</i>	ATCC 13182
	<i>Alcaligenes faecalis</i>	ATCC 8750	<i>Meganomonas hypermegas</i>	ATCC 25560
	<i>Anaerobiospirillum</i>	ATCC 29305	<i>Mitsukoella multiacidus</i>	ATCC 27723
10	<i>succiniproducens</i>		<i>Moraxella catarrhalis</i>	ATCC 43628
	<i>Anaerorhabdus furcosus</i>	ATCC 25662	<i>Morganella morganii</i>	ATCC 25830
	<i>Bacteroides distasonis</i>	ATCC 8503	<i>Neisseria meningitidis</i>	ATCC 13077
	<i>Bacteroides thetaiotaomicron</i>	ATCC 29741	<i>Pasteurella aerogenes</i>	ATCC 27883
	<i>Bacteroides vulgatus</i>	ATCC 8482	<i>Proteus vulgaris</i>	ATCC 13315
15	<i>Bordetella pertussis</i>	LSPQ 3702	<i>Providencia alcalifaciens</i>	ATCC 9886
	<i>Bulkholderia cepacia</i>	LSPQ 2217	<i>Providencia rettgeri</i>	ATCC 9250
	<i>Butyrvibrio fibrinosolvens</i>	ATCC 19171	<i>Pseudomonas aeruginosa</i>	ATCC 27853
	<i>Cardiobacterium hominis</i>	ATCC 15826	<i>Salmonella typhimurium</i>	ATCC 14028
	<i>Citrobacter freundii</i>	ATCC 8090	<i>Serratia marcescens</i>	ATCC 13880
20	<i>Desulfovibrio vulgaris</i>	ATCC 29579	<i>Shigella flexneri</i>	ATCC 12022
	<i>Edwardsiella tarda</i>	ATCC 15947	<i>Shigella sonnei</i>	ATCC 29930
	<i>Enterobacter cloacae</i>	ATCC 13047	<i>Succinivibrio dextrinosolvens</i>	ATCC 19716
	<i>Escherichia coli</i>	ATCC 25922	<i>Tissierella praeacuta</i>	ATCC 25539
	<i>Fusobacterium russii</i>	ATCC 25533	<i>Veillonella parvula</i>	ATCC 10790
25	<i>Haemophilus influenzae</i>	ATCC 9007	<i>Yersinia enterocolitica</i>	ATCC 9610

Table 11. Microbial species for which *tuf* and/or *atpD* and/or *recA* sequences are available in public databases.

	Species	Strain	Accession number	Coding gene*
Bacteria				
	<i>Agrobacterium tumefaciens</i>		X99673	<i>tuf</i>
	<i>Agrobacterium tumefaciens</i>		X99673	<i>tuf</i> (EF-G)
5	<i>Agrobacterium tumefaciens</i>		X99674	<i>tuf</i>
	<i>Anacystis nidulans</i>	PCC 6301	X17442	<i>tuf</i>
	<i>Aquifex aeolicus</i>	VF5	AE000669	<i>tuf</i>
	<i>Aquifex aeolicus</i>	VF5	AE000669	<i>tuf</i> (EF-G)
	<i>Aquifex pyrophilus</i>		Genome project ²	<i>tuf</i> (EF-G)
10	<i>Aquifex pyrophilus</i>		Y15787	<i>tuf</i>
	<i>Archaeoglobus fulgidus</i>		Genome project ²	<i>tuf</i> (EF-G)
	<i>Bacillus halodurans</i>	C-125	AB017508	<i>tuf</i>
	<i>Bacillus halodurans</i>	C-125	AB017508	<i>tuf</i> (EF-G)
	<i>Bacillus stearothermophilus</i>	CCM 2184	AJ000260	<i>tuf</i>
15	<i>Bacillus subtilis</i>	168	D64127	<i>tuf</i>
	<i>Bacillus subtilis</i>	168	D64127	<i>tuf</i> (EF-G)
	<i>Bacillus subtilis</i>	DSM 10	Z99104	<i>tuf</i>
	<i>Bacteroides forsythus</i>	ATCC 43037	AB035466	<i>tuf</i>
	<i>Bacteroides fragilis</i>	DSM 1151	- ¹	<i>tuf</i>
20	<i>Bordetella bronchiseptica</i>	RB50	Genome project ²	<i>tuf</i>
	<i>Bordetella pertussis</i>	Tohama 1	Genome project ²	<i>tuf</i>
	<i>Borrelia burgdorferi</i>	B31	U78193	<i>tuf</i>
	<i>Borrelia burgdorferi</i>		AE001155	<i>tuf</i> (EF-G)
	<i>Brevibacterium linens</i>	DSM 20425	X76863	<i>tuf</i>
25	<i>Buchnera aphidicola</i>	Ap	Y12307	<i>tuf</i>
	<i>Campylobacter jejuni</i>	NCTC 11168	Y17167	<i>tuf</i>
	<i>Chlamydia pneumoniae</i>	CWL029	AE001592	<i>tuf</i>
	<i>Chlamydia pneumoniae</i>	CWL029	AE001639	<i>tuf</i> (EF-G)
	<i>Chlamydia trachomatis</i>		M74221	<i>tuf</i>
30	<i>Chlamydia trachomatis</i>	D/UW-3/CX	AE001317	<i>tuf</i> (EF-G)
	<i>Chlamydia trachomatis</i>	D/UW-3/CX	AE001305	<i>tuf</i>
	<i>Chlamydia trachomatis</i>	F/IC-Cal-13	L22216	<i>tuf</i>
	<i>Chlorobium vibrioforme</i>	DSM 263	X77033	<i>tuf</i>
	<i>Chloroflexus aurantiacus</i>	DSM 636	X76865	<i>tuf</i>
35	<i>Clostridium acetobutylicum</i>	ATCC 824	Genome project ²	<i>tuf</i>
	<i>Clostridium difficile</i>	630	Genome project ²	<i>tuf</i>
	<i>Corynebacterium glutamicum</i>	ASO 19	X77034	<i>tuf</i>
	<i>Corynebacterium glutamicum</i>	MJ-233	E09634	<i>tuf</i>
	<i>Coxiella burnetii</i>	Nine Mile phase I	AF136604	<i>tuf</i>
40	<i>Cytophaga lytica</i>	DSM 2039	X77035	<i>tuf</i>
	<i>Deinococcus radiodurans</i>	R1	AE001891	<i>tuf</i> (EF-G)
	<i>Deinococcus radiodurans</i>	R1	Genome project ²	<i>tuf</i>
	<i>Deinonema sp.</i>		- ¹	<i>tuf</i>
	<i>Eikenella corrodens</i>	ATCC 23834	Z12610	<i>tuf</i>
45	<i>Eikenella corrodens</i>	ATCC 23834	Z12610	<i>tuf</i> (EF-G)
	<i>Enterococcus faecalis</i>		Genome project ²	<i>tuf</i> (EF-G)
	<i>Escherichia coli</i>		J01690	<i>tuf</i>
	<i>Escherichia coli</i>		J01717	<i>tuf</i>
	<i>Escherichia coli</i>		X00415	<i>tuf</i> (EF-G)
50	<i>Escherichia coli</i>		X57091	<i>tuf</i>
	<i>Escherichia coli</i>	K-12 MG1655	U00006	<i>tuf</i>
	<i>Escherichia coli</i>	K-12 MG1655	U00096	<i>tuf</i>
	<i>Fervidobacterium islandicum</i>	DSM 5733	Y15788	<i>tuf</i>
	<i>Fibrobacter succinogenes</i>	S85	X76866	<i>tuf</i>

Table 11. Microbial species for which *tuf* and/or *atpD* and/or *recA* sequences are available in public databases (continued).

	Species	Strain	Accession number	Coding gene*
	<i>Flavobacterium ferrugineum</i>	DSM 13524	X76867	<i>tuf</i>
	<i>Flexistipes sinusarabici</i>		X59461	<i>tuf</i>
	<i>Gloeobacter violaceus</i>	PCC 7421	U09433	<i>tuf</i>
	<i>Gloeotheca</i> sp.	PCC 6501	U09434	<i>tuf</i>
5	<i>Haemophilus actinomycetemcomitans</i>	HK1651	Genome project ²	<i>tuf</i>
	<i>Haemophilus ducreyi</i>	35000	AF087414	<i>tuf</i> (EF-G)
	<i>Haemophilus influenzae</i>	Rd	U32739	<i>tuf</i>
	<i>Haemophilus influenzae</i>	Rd	U32739	<i>tuf</i> (EF-G)
	<i>Halobacterium marismortui</i>		X16677	<i>tuf</i>
10	<i>Helicobacter pylori</i>	26695	AE000511	<i>tuf</i>
	<i>Helicobacter pylori</i>	J99	AE001539	<i>tuf</i> (EF-G)
	<i>Helicobacter pylori</i>	J99	AE001541	<i>tuf</i>
	<i>Herpetosiphon aurantiacus</i>	Hpga1	X76868	<i>tuf</i>
	<i>Lactobacillus paracasei</i>		E13922	<i>tuf</i>
15	<i>Leptospira interrogans</i>		AF115283	<i>tuf</i>
	<i>Methanobacterium thermoautotrophicum</i>	delta H	AE000877	<i>tuf</i>
	<i>Methanococcus jannaschii</i>	ATCC 43067	U67486	<i>tuf</i>
	<i>Methanococcus jannaschii</i>	DSM 2661	Genome project ²	<i>tuf</i> (EF-G)
	<i>Methanococcus vannielii</i>		X05698	<i>tuf</i>
20	<i>Micrococcus luteus</i>	IFO 3333	M17788	<i>tuf</i> (EF-G)
	<i>Micrococcus luteus</i>	IFO 3333	M17788	<i>tuf</i>
	<i>Moraxella</i> sp.	TAC II 25	AJ249258	<i>tuf</i>
	<i>Mycobacterium avium</i>	104	Genome project ²	<i>tuf</i>
	<i>Mycobacterium bovis</i>	AF2122/97	Genome project ²	<i>tuf</i>
25	<i>Mycobacterium leprae</i>		L13276	<i>tuf</i>
	<i>Mycobacterium leprae</i>		Z14314	<i>tuf</i>
	<i>Mycobacterium leprae</i>		Z14314	<i>tuf</i> (EF-G)
	<i>Mycobacterium leprae</i>	Thai 53	D13869	<i>tuf</i>
	<i>Mycobacterium tuberculosis</i>	Erdmann	S40925	<i>tuf</i>
30	<i>Mycobacterium tuberculosis</i>	H37Rv	AL021943	<i>tuf</i> (EF-G)
	<i>Mycobacterium tuberculosis</i>	H37Rv	Z84395	<i>tuf</i>
	<i>Mycobacterium tuberculosis</i>	y42	AD000005	<i>tuf</i>
	<i>Mycoplasma capricolum</i>	PG-31	X16462	<i>tuf</i>
	<i>Mycoplasma genitalium</i>	G37	U39732	<i>tuf</i>
35	<i>Mycoplasma genitalium</i>	G37	Genome project ²	<i>tuf</i> (EF-G)
	<i>Mycoplasma hominis</i>		X57136	<i>tuf</i>
	<i>Mycoplasma hominis</i>	PG21	M57675	<i>tuf</i>
	<i>Mycoplasma pneumoniae</i>	M129	AE000019	<i>tuf</i>
	<i>Mycoplasma pneumoniae</i>	M129	AE000058	<i>tuf</i> (EF-G)
40	<i>Neisseria gonorrhoeae</i>	MS11	L36380	<i>tuf</i>
	<i>Neisseria gonorrhoeae</i>	MS11	L36380	<i>tuf</i> (EF-G)
	<i>Neisseria meningitidis</i>		Genome project ²	<i>tuf</i> (EF-G)
	<i>Neisseria meningitidis</i>	Z2491	Genome project ²	<i>tuf</i>
	<i>Peptococcus niger</i>	DSM 20745	X76869	<i>tuf</i>
45	<i>Porphyromonas gingivalis</i>	W83	Genome project ²	<i>tuf</i>
	<i>Phormidium ectocarpi</i>	PCC 7375	U09443	<i>tuf</i>
	<i>Planobispora rosea</i>	ATCC 53773	U67308	<i>tuf</i>
	<i>Plectonema boryanum</i>	PCC 73110	U09444	<i>tuf</i>
	<i>Porphyromonas gingivalis</i>	W83	Genome project ²	<i>tuf</i>
50	<i>Porphyromonas gingivalis</i>	FDC 381	AB035461	<i>tuf</i>
	<i>Porphyromonas gingivalis</i>	W83	AB035462	<i>tuf</i>
	<i>Porphyromonas gingivalis</i>	SUNY 1021	AB035463	<i>tuf</i>
	<i>Porphyromonas gingivalis</i>	A7A1-28	AB035464	<i>tuf</i>
	<i>Porphyromonas gingivalis</i>	ATCC 33277	AB035465	<i>tuf</i>
55	<i>Porphyromonas gingivalis</i>	ATCC 33277	AB035471	<i>tuf</i> (EF-G)

Tabl 11. Microbial species for which *tuf* and/or *atpD* and/or *recA* sequences are available in public databases (continued).

	Species	Strain	Accession number	Coding gene*
	<i>Prochlorothrix hollandica</i>		U09445	<i>tuf</i>
	<i>Pseudomonas aeruginosa</i>	PAO-1	Genome project ²	<i>tuf</i>
	<i>Pyrococcus abyssi</i>	Orsay	AJ248285	<i>tuf</i>
	<i>Rickettsia prowazekii</i>	Madrid E	AJ235272	<i>tuf</i>
5	<i>Rickettsia prowazekii</i>	Madrid E	Z54171	<i>tuf</i> (EF-G)
	<i>Salmonella typhimurium</i>		X64591	<i>tuf</i> (EF-G)
	<i>Salmonella typhimurium</i>	LT2 trpE91	X55116	<i>tuf</i>
	<i>Salmonella typhimurium</i>	LT2 trpE91	X55117	<i>tuf</i>
	<i>Serpulina hyodysenteriae</i>	B204	U51635	<i>tuf</i>
10	<i>Serratia marcescens</i>		AF058451	<i>tuf</i>
	<i>Shewanella putida</i>		Genome project ²	<i>tuf</i>
	<i>Shewanella putrefaciens</i>	DSM 50426	-1	<i>tuf</i>
	<i>Shewanella putrefaciens</i>	MR-1	Genome project ²	<i>tuf</i>
	<i>Spirochaeta aurantia</i>	DSM 1902	X76874	<i>tuf</i>
15	<i>Staphylococcus aureus</i>		AJ237696	<i>tuf</i> (EF-G)
	<i>Stigmatella aurantiaca</i>	DW4	X82820	<i>tuf</i>
	<i>Stigmatella aurantiaca</i>	Sg a1	X76870	<i>tuf</i>
	<i>Streptococcus mutans</i>	GS-5 Kuramitsu	U75481	<i>tuf</i>
	<i>Streptococcus mutans</i>	UAB159	Genome project ²	<i>tuf</i>
20	<i>Streptococcus oralis</i>	NTCC 11427	P331701	<i>tuf</i>
	<i>Streptococcus pyogenes</i>		Genome project ²	<i>tuf</i> (EF-G)
	<i>Streptococcus pyogenes</i>	M1-GAS	Genome project ²	<i>tuf</i>
	<i>Streptomyces aureofaciens</i>	ATCC 10762	AF007125	<i>tuf</i>
	<i>Streptomyces cinnamomeus</i>	Tue89	X98831	<i>tuf</i>
25	<i>Streptomyces coelicolor</i>	A3(2)	AL031013	<i>tuf</i> (EF-G)
	<i>Streptomyces coelicolor</i>	M145	X77039	<i>tuf</i>
	<i>Streptomyces collinus</i>	BSM 40733	S79408	<i>tuf</i>
	<i>Streptomyces netropsis</i>	Tu1063	AF153618	<i>tuf</i>
	<i>Streptomyces ramocissimus</i>		X67057	<i>tuf</i>
30	<i>Streptomyces ramocissimus</i>		X67057	<i>tuf</i> (EF-G)
	<i>Synechococcus</i> sp.		X17442	<i>tuf</i> (EF-G)
	<i>Synechocystis</i> sp.		X65159	<i>tuf</i> (EF-G)
	<i>Synechocystis</i> sp.	PCC 6803	D90913	<i>tuf</i>
	<i>Taxobacter occealus</i>	Myx 2105	X77036	<i>tuf</i>
35	<i>Thermoplasma acidophilum</i>	DSM 1728	X53866	<i>tuf</i>
	<i>Thermotoga maritima</i>		Genome project ²	<i>tuf</i> (EF-G)
	<i>Thermotoga maritima</i>		M27479	<i>tuf</i>
	<i>Thermus aquaticus</i>	EP 00276	X66322	<i>tuf</i>
	<i>Thermus thermophilus</i>	HB8	X16278	<i>tuf</i> (EF-G)
40	<i>Thermus thermophilus</i>	HB8	X05977	<i>tuf</i>
	<i>Thermus thermophilus</i>	HB8	X06657	<i>tuf</i>
	<i>Thiomonas cuprina</i>	DSM 5495	U78300	<i>tuf</i>
	<i>Thiomonas cuprina</i>	DSM 5495	U78300	<i>tuf</i> (EF-G)
	<i>Thiomonas cuprina</i>	Hoe5	X76871	<i>tuf</i>
45	<i>Treponema pallidum</i>		AE001202	<i>tuf</i>
	<i>Treponema pallidum</i>		AE001248	<i>tuf</i> (EF-G)
	<i>Streptomyces ramocissimus</i>		X67058	<i>tuf</i>
	<i>Ureaplasma urealyticum</i>	ATCC 33697	Z34275	<i>tuf</i>
	<i>Vibrio cholerae</i>	N16961	TIGR2	<i>tuf</i>
50	<i>Wolinella succinogenes</i>	DSM 1740	X76872	<i>tuf</i>
	<i>Yersinia pestis</i>	CO-92	Genome project ²	<i>tuf</i>
Fungi				
55	<i>Absidia glauca</i>	CBS 101.48	X54730	<i>tuf</i> (EF-1)

Table 11. Microbial species for which *tuf* and/or *atpD* and/or *recA* sequences are available in public databases (continued).

	Species	Strain	Accession number	Coding gene*
	<i>Arxula adeninivorans</i>	Ls3	Z47379	<i>tuf</i> (EF-1)
	<i>Aspergillus oryzae</i>	KBN616	AB007770	<i>tuf</i> (EF-1)
	<i>Aureobasidium pullulans</i>	R106	U19723	<i>tuf</i> (EF-1)
	<i>Candida albicans</i>	SC5314	M29934	<i>tuf</i> (EF-1)
5	<i>Candida albicans</i>	SC5314	M29935	<i>tuf</i> (EF-1)
	<i>Cryptococcus neoformans</i>	B3501	U81803	<i>tuf</i> (EF-1)
	<i>Cryptococcus neoformans</i>	M1-106	U81804	<i>tuf</i> (EF-1)
	<i>Eremothecium gossypii</i>	ATCC 10895	X73978	<i>tuf</i> (EF-1)
	<i>Fusarium oxysporum</i>	NRRL 26037	AF008498	<i>tuf</i> (EF-1)
10	<i>Histoplasma capsulatum</i>	186AS	U14100	<i>tuf</i> (EF-1)
	<i>Podospora anserina</i>		X74799	<i>tuf</i> (EF-1)
	<i>Puccinia graminis</i>	race 32	X73529	<i>tuf</i> (EF-1)
	<i>Rhizomucor racemosus</i>	ATCC 1216B	X17475	<i>tuf</i> (EF-1)
	<i>Rhizomucor racemosus</i>	ATCC 1216B	J02605	<i>tuf</i> (EF-1)
15	<i>Rhizomucor racemosus</i>	ATCC 1216B	X17476	<i>tuf</i> (EF-1)
	<i>Rhodotorula mucilaginosa</i>		AF016239	<i>tuf</i> (EF-1)
	<i>Saccharomyces cerevisiae</i>		K00428	<i>tuf</i> (M)
	<i>Saccharomyces cerevisiae</i>		M59369	<i>tuf</i> (EF-G)
	<i>Saccharomyces cerevisiae</i>		X00779	<i>tuf</i> (EF-1)
20	<i>Saccharomyces cerevisiae</i>		X01638	<i>tuf</i> (EF-1)
	<i>Schizosaccharomyces pombe</i>		U42189	<i>tuf</i> (EF-1)
	<i>Trichoderma reesei</i>	QM9414	Z23012	<i>tuf</i> (EF-1)
	<i>Yarrowia lipolytica</i>		AF054510	<i>tuf</i> (EF-1)
25	Parasites			
	<i>Blastocystis hominis</i>	HE87-1	D64080	<i>tuf</i> (EF-1)
	<i>Eimeria tenella</i>	LS18	A1755521	<i>tuf</i> (EF-1)
	<i>Giardia lamblia</i>		D14342	<i>tuf</i> (EF-1)
30	<i>Kentrophoros</i> sp.		AF056101	<i>tuf</i> (EF-1)
	<i>Leishmania amazonensis</i>	IFLA/BR/67/PH8	M92653	<i>tuf</i> (EF-1)
	<i>Leishmania braziliensis</i>		U72244	<i>tuf</i> (EF-1)
	<i>Onchocerca volvulus</i>		M64333	<i>tuf</i> (EF-1)
	<i>Porphyra purpurea</i>	Avonport	U08844	<i>tuf</i> (EF-1)
35	<i>Plasmodium berghei</i>	ANKA	AJ224150	<i>tuf</i> (EF-1)
	<i>Plasmodium falciparum</i>	K1	X60488	<i>tuf</i> (EF-1)
	<i>Plasmodium knowlesi</i>	line H	AJ224153	<i>tuf</i> (EF-1)
	<i>Toxoplasma gondii</i>	RH	Y11431	<i>tuf</i> (EF-1)
	<i>Trypanosoma cruzi</i>	Y	L76077	<i>tuf</i> (EF-1)
40	<i>Trypanosoma brucei</i>	LVH/75/ USAMRU-K/18	U10562	<i>tuf</i> (EF-1)
	Human and plants			
	<i>Arabidopsis thaliana</i>	Columbia	X89227	<i>tuf</i> (EF-1)
45	<i>Glycine max</i>	Ceresia	X89058	<i>tuf</i> (EF-1)
	<i>Glycine max</i>	Ceresia	Y15107	<i>tuf</i> (EF-1)
	<i>Glycine max</i>	Ceresia	Y15108	<i>tuf</i> (EF-1)
	<i>Glycine max</i>	Maple Arrow	X66062	<i>tuf</i> (EF-1)
	<i>Homo sapiens</i>		X03558	<i>tuf</i> (EF-1)
50	<i>Pyramimonas disomata</i>		AB008010	<i>tuf</i>
	Bacteria			
	<i>Acetobacterium woodii</i>	DSM 1030	U10505	<i>atpD</i>
55	<i>Bacillus firmus</i>	OF4	M60117	<i>atpD</i>

Table 11. Microbial species for which *tuf* and/ or *atpD* and/or *recA* sequences are available in public databases (continued).

	Species	Strain	Accession number	Coding gene*
	<i>Bacillus megaterium</i>	QM B1551	M20255	<i>atpD</i>
	<i>Bacillus stearothermophilus</i>		D38058	<i>atpD</i>
	<i>Bacillus stearothermophilus</i>	IFO1035	D38060	<i>atpD</i>
	<i>Bacillus subtilis</i>	168	Z28592	<i>atpD</i>
5	<i>Bacteroides fragilis</i>	DSM 2151	M22247	<i>atpD</i>
	<i>Bordetella bronchiseptica</i>	RB50	Genome project ²	<i>atpD</i>
	<i>Bordetella pertussis</i>	Tohama 1	Genome project ²	<i>atpD</i>
	<i>Borrelia burgdorferi</i>	B31	AE001122	<i>atpD</i> (V)
	<i>Burkholderia cepacia</i>	DSM50181	X76877	<i>atpD</i>
10	<i>Campylobacter jejuni</i>	NCTC 11168	Genome project ²	<i>atpD</i>
	<i>Chlamydia pneumoniae</i>		Genome project ²	<i>atpD</i> (V)
	<i>Chlamydia trachomatis</i>	MoPn	Genome project ²	<i>atpD</i> (V)
	<i>Chlorobium vibrioforme</i>	DSM 263	X76873	<i>atpD</i>
	<i>Citrobacter freundii</i>	JEO503	AF037156	<i>atpD</i>
15	<i>Clostridium acetobutylicum</i>	ATCC 824	Genome project ²	<i>atpD</i>
	<i>Clostridium acetobutylicum</i>	DSM 792	AF101055	<i>atpD</i>
	<i>Clostridium difficile</i>	630	Genome project ²	<i>atpD</i>
	<i>Corynebacterium glutamicum</i>	ASO 19	X76875	<i>atpD</i>
	<i>Corynebacterium glutamicum</i>	MJ-233	E09634	<i>atpD</i>
20	<i>Cytophaga lytica</i>	DSM 2039	M22535	<i>atpD</i>
	<i>Enterobacter aerogenes</i>	DSM 30053	- ³	<i>atpD</i>
	<i>Enterococcus faecalis</i>		M90060	<i>atpD</i>
	<i>Enterococcus faecalis</i>	V583	Genome project ²	<i>atpD</i> (V)
	<i>Enterococcus hirae</i>	ATCC 9790	D17462	<i>atpD</i> (V)
25	<i>Escherichia coli</i>		J01594	<i>atpD</i>
	<i>Escherichia coli</i>		M25464	<i>atpD</i>
	<i>Escherichia coli</i>		V00267	<i>atpD</i>
	<i>Escherichia coli</i>		V00311	<i>atpD</i>
	<i>Escherichia coli</i>	K12 MG1655	L10328	<i>atpD</i>
30	<i>Flavobacterium ferrugineum</i>	DSM 13524	- ³	<i>atpD</i>
	<i>Haemophilus actinomycetemcomitans</i>		Genome project ²	<i>atpD</i>
	<i>Haemophilus influenzae</i>	Rd	U32730	<i>atpD</i>
	<i>Halobacterium salinarum</i>		S56356	<i>atpD</i> (V)
	<i>Haloferax volcanii</i>	WR 340	X79516	<i>atpD</i>
35	<i>Helicobacter pylori</i>	NCTC 11638	AF004014	<i>atpD</i>
	<i>Helicobacter pylori</i>	26695	Genome project ²	<i>atpD</i>
	<i>Helicobacter pylori</i>	J99	Genome project ²	<i>atpD</i>
	<i>Lactobacillus casei</i>	DSM 20021	X64542	<i>atpD</i>
	<i>Methanococcus jannaschii</i>	DSM 2661	U67477	<i>atpD</i> (V)
40	<i>Methanosarcina barkeri</i>	DSM 800	J04836	<i>atpD</i> (V)
	<i>Moorella thermoacetica</i>	ATCC 39073	U64318	<i>atpD</i>
	<i>Mycobacterium avium</i>	104	Genome project ²	<i>atpD</i>
	<i>Mycobacterium bovis</i>	AF2122/97	Genome project ²	<i>atpD</i>
	<i>Mycobacterium leprae</i>		U15186	<i>atpD</i>
45	<i>Mycobacterium tuberculosis</i>	H37Rv	Z73419	<i>atpD</i>
	<i>Mycoplasma gallisepticum</i>		X64256	<i>atpD</i>
	<i>Mycoplasma genitalium</i>	G37	U39725	<i>atpD</i>
	<i>Mycoplasma pneumoniae</i>	M129	U43738	<i>atpD</i>
	<i>Neisseria gonorrhoeae</i>	FA 1090	Genome project ²	<i>atpD</i>
50	<i>Neisseria meningitidis</i>	Z2491	Genome project ²	<i>atpD</i>
	<i>Pectinatus frisingensis</i>	DSM 20465	X64543	<i>atpD</i>
	<i>Peptococcus niger</i>	DSM 20475	X76878	<i>atpD</i>
	<i>Pirellula marina</i>	IFAM 1313	X57204	<i>atpD</i>
	<i>Porphyromonas gingivalis</i>	W83	Genome project ²	<i>atpD</i> (V)
55	<i>Propionigenium modestum</i>	DSM 2376	X58461	<i>atpD</i>

Table 11. Microbial species for which *tuf* and/ or *atpD* and/or *recA* sequences are available in public databases (continued).

	Species	Strain	Accession number	Coding gene*
	<i>Pseudomonas aeruginosa</i>	PAO1	Genome project ²	<i>atpD</i>
	<i>Pseudomonas putida</i>		Genome project ²	<i>atpD</i>
	<i>Rhodobacter capsulatus</i>	B100	X99599	<i>atpD</i>
	<i>Rhodospirillum rubrum</i>		X02499	<i>atpD</i>
5	<i>Rickettsia prowazekii</i>	F-12	AF036246	<i>atpD</i>
	<i>Rickettsia prowazekii</i>	Madrid	Genome project ²	<i>atpD</i>
	<i>Ruminococcus albus</i>	7ATCC	AB006151	<i>atpD</i>
	<i>Salmonella choleraesuis</i>	S83769	AF037146	<i>atpD</i>
	subsp. <i>arizonae</i>			
10	<i>Salmonella choleraesuis</i>	u24	AF037147	<i>atpD</i>
	subsp. <i>arizonae</i>			
	<i>Salmonella bongori</i>	JEO4162	AF037155	<i>atpD</i>
	<i>Salmonella bongori</i>	BR1859	AF037154	<i>atpD</i>
	<i>Salmonella choleraesuis</i>	DS210/89	AF037149	<i>atpD</i>
15	subsp. <i>diarizonae</i>			
	<i>Salmonella choleraesuis</i>	JEO307	AF037148	<i>atpD</i>
	subsp. <i>diarizonae</i>			
	<i>Salmonella choleraesuis</i>	S109671	AF037150	<i>atpD</i>
	subsp. <i>diarizonae</i>			
20	<i>Salmonella choleraesuis</i> subsp.	K228	AF037140	<i>atpD</i>
	<i>choleraesuis</i> serotype Dublin			
	<i>Salmonella choleraesuis</i> subsp.	K771	AF037139	<i>atpD</i>
	<i>choleraesuis</i> serotype Dublin			
	<i>Salmonella choleraesuis</i>	S84366	AF037151	<i>atpD</i>
25	subsp. <i>houtenae</i>			
	<i>Salmonella choleraesuis</i>	S84098	AF037152	<i>atpD</i>
	subsp. <i>houtenae</i>			
	<i>Salmonella choleraesuis</i>	BR2047	AF037153	<i>atpD</i>
	subsp. <i>indica</i>			
30	<i>Salmonella choleraesuis</i> subsp.	Div36-86	AF037142	<i>atpD</i>
	<i>choleraesuis</i> serotype Infantis			
	<i>Salmonella choleraesuis</i>	NSC72	AF037144	<i>atpD</i>
	subsp. <i>salamae</i>			
	<i>Salmonella choleraesuis</i>	S114655	AF037145	<i>atpD</i>
35	subsp. <i>salamae</i>			
	<i>Salmonella choleraesuis</i> subsp.	Div95-86	AF037143	<i>atpD</i>
	<i>choleraesuis</i> serotype Tennessee			
	<i>Salmonella choleraesuis</i> subsp.	LT2	AF037141	<i>atpD</i>
	<i>choleraesuis</i> serotype Typhimurium			
40	<i>Shewanella putida</i>		Genome project ²	<i>atpD</i>
	<i>Shewanella putrefaciens</i>	MR-1	Genome project ²	<i>atpD</i>
	<i>Stigmatella aurantiaca</i>	Sga1	X76879	<i>atpD</i>
	<i>Streptococcus bovis</i>	JB-1	AB009314	<i>atpD</i>
	<i>Streptococcus mutans</i>	GS-5	U31170	<i>atpD</i>
45	<i>Streptococcus mutans</i>	UAB159	Genome project ²	<i>atpD</i>
	<i>Streptococcus pneumoniae</i>	Type 4	Genome project ²	<i>atpD</i> (V)
	<i>Streptococcus pneumoniae</i>	Type 4	Genome project ²	<i>atpD</i>
	<i>Streptococcus pyogenes</i>		Genome project ²	<i>atpD</i> (V)
	<i>Streptococcus pyogenes</i>		Genome project ²	<i>atpD</i>
50	<i>Streptococcus sanguinis</i>	M1-GAS	Genome project ²	<i>atpD</i>
	<i>Streptococcus sanguinis</i>	10904	AF001955	<i>atpD</i>
	<i>Streptomyces lividans</i>	1326	Z22606	<i>atpD</i>
	<i>Thermus thermophilus</i>	HB8	D63799	<i>atpD</i> (V)
	<i>Thiobacillus ferrooxidans</i>	ATCC 33020	M81087	<i>atpD</i>
	<i>Treponema pallidum</i>	Nichols	AE001228	<i>atpD</i> (V)
55	<i>Vibrio alginolyticus</i>		X16050	<i>atpD</i>

Table 11. Microbial species for which *tuf* and/or *atpD* and/or *recA* sequences are available in public databases (continued).

	Species	Strain	Accession number	Coding gene*
	<i>Vibrio cholerae</i>	N16961	Genome project ²	<i>atpD</i>
	<i>Wolinella succinogenes</i>	DSM 1470	X76880	<i>atpD</i>
	<i>Yersinia enterocolitica</i>	NCTC 10460	AF037157	<i>atpD</i>
	<i>Yersinia pestis</i>	CO-92	Genome project ²	<i>atpD</i>
5	Fungi			
	<i>Candida tropicalis</i>		M64984	<i>atpD</i> (V)
	<i>Kluyveromyces lactis</i>	2359/152	U37764	<i>atpD</i>
10	<i>Neurospora crassa</i>		X53720	<i>atpD</i>
	<i>Saccharomyces cerevisiae</i>		M12082	<i>atpD</i>
	<i>Saccharomyces cerevisiae</i>	X2180-1A	J05409	<i>atpD</i> (V)
	<i>Schizosaccharomyces pombe</i>	972 h-	S47814	<i>atpD</i> (V)
	<i>Schizosaccharomyces pombe</i>	972 h-	M57956	<i>atpD</i>
15	Parasites			
	<i>Giardia lamblia</i>	WB	U18938	<i>atpD</i>
	<i>Plasmodium falciparum</i>	3D7	L08200	<i>atpD</i> (V)
20	<i>Trypanosoma congolense</i>	IL3000	Z25814	<i>atpD</i> (V)
	Human and plants			
	<i>Homo sapiens</i>		L09234	<i>atpD</i> (V)
25	<i>Homo sapiens</i>		M27132	<i>atpD</i>
	Bacteria			
	<i>Acetobacter aceti</i>	no. 1023	S60630	<i>recA</i>
30	<i>Acetobacter altoacetigenes</i>	MH-24	E05290	<i>recA</i>
	<i>Acetobacter polyoxogenes</i>	NBI 1028	D13183	<i>recA</i>
	<i>Acholeplasma laidlawii</i>	8195	M81465	<i>recA</i>
	<i>Acidiphilium facilis</i>	ATCC 35904	D16538	<i>recA</i>
	<i>Acidothermus cellulolyticus</i>	ATCC 43068	AJ006705	<i>recA</i>
35	<i>Acinetobacter calcoaceticus</i>	BD413/ADP1	L26100	<i>recA</i>
	<i>Aeromonas salmonicida</i>	A449	U83688	<i>recA</i>
	<i>Agrobacterium tumefaciens</i>	C58	L07902	<i>recA</i>
	<i>Allochrocatium vinosum</i>		AJ000677	<i>recA</i>
	<i>Aquifex aeolicus</i>	VF5	AE000775	<i>recA</i>
40	<i>Aquifex pyrophilus</i>	Kol5a	L23135	<i>recA</i>
	<i>Azotobacter vinelandii</i>		S96898	<i>recA</i>
	<i>Bacillus stearothermophilus</i>	10	Genome project ²	<i>recA</i>
	<i>Bacillus subtilis</i>	PB1831	U87792	<i>recA</i>
	<i>Bacillus subtilis</i>	168	Z99112	<i>recA</i>
45	<i>Bacteroides fragilis</i>		M63029	<i>recA</i>
	<i>Bifidobacterium breve</i>	NCFB 2258	AF094756	<i>recA</i>
	<i>Blastochloris viridis</i>	DSM 133	AF022175	<i>recA</i>
	<i>Bordetella pertussis</i>	165	X53457	<i>recA</i>
	<i>Borrelia burgdorferi</i>	Sh-2-82	U23457	<i>recA</i>
50	<i>Borrelia burgdorferi</i>	B31	AE001124	<i>recA</i>
	<i>Brevibacterium flavum</i>	MJ-233	E10390	<i>recA</i>
	<i>Brucella abortus</i>	2308	L00679	<i>recA</i>
	<i>Burkholderia cepacia</i>	ATCC 17616	U70431	<i>recA</i>
	<i>Campylobacter jejuni</i>	81-176	U03121	<i>recA</i>
55	<i>Chlamydia trachomatis</i>	L2	U16739	<i>recA</i>

Table 11. Microbial species for which *tuf* and/or *atpD* and/or *recA* sequences are available in public databases (continued).

	Species	Strain	Accession number	Coding gene*
	<i>Chloroflexus aurantiacus</i>	J-10-II	AF037259	<i>recA</i>
	<i>Clostridium acetobutylicum</i>		M94057	<i>recA</i>
	<i>Clostridium perfringens</i>	13	U61497	<i>recA</i>
	<i>Corynebacterium glutamicum</i>	AS019	U14965	<i>recA</i>
5	<i>Corynebacterium pseudotuberculosis</i>	C231	U30387	<i>recA</i>
	<i>Deinococcus radiodurans</i>	KD8301	AB005471	<i>recA</i>
	<i>Deinococcus radiodurans</i>	R1	U01876	<i>recA</i>
	<i>Enterobacter agglomerans</i>	339	L03291	<i>recA</i>
	<i>Enterococcus faecalis</i>	OGIX	M81466	<i>recA</i>
10	<i>Erwinia carotovora</i>		X55554	<i>recA</i>
	<i>Escherichia coli</i>		J01672	<i>recA</i>
	<i>Escherichia coli</i>		X55552	<i>recA</i>
	<i>Escherichia coli</i>	K-12	AE000354	<i>recA</i>
	<i>Frankia alni</i>	Arl3	AJ006707	<i>recA</i>
15	<i>Gluconobacter oxydans</i>		U21001	<i>recA</i>
	<i>Haemophilus influenzae</i>	Rd	U32687	<i>recA</i>
	<i>Haemophilus influenzae</i>	Rd	U32741	<i>recA</i>
	<i>Haemophilus influenzae</i>	Rd	L07529	<i>recA</i>
	<i>Helicobacter pylori</i>	69A	Z35478	<i>recA</i>
20	<i>Helicobacter pylori</i>	26695	AE000536	<i>recA</i>
	<i>Helicobacter pylori</i>	J99	AE001453	<i>recA</i>
	<i>Lactococcus lactis</i>	ML3	M88106	<i>recA</i>
	<i>Legionella pneumophila</i>		X55453	<i>recA</i>
	<i>Leptospira biflexa</i>	serovar patoc	U32625	<i>recA</i>
25	<i>Leptospira interrogans</i>	serovar pomona	U29169	<i>recA</i>
	<i>Magnetospirillum magnetotacticum</i>	MS-1	X17371	<i>recA</i>
	<i>Methylobacillus flagellatus</i>	MFK1	M35325	<i>recA</i>
	<i>Methylomonas clara</i>	ATCC 31226	X59514	<i>recA</i>
	<i>Mycobacterium leprae</i>		X73822	<i>recA</i>
30	<i>Mycobacterium tuberculosis</i>	H37Rv	X58485	<i>recA</i>
	<i>Mycoplasma genitalium</i>	G37	U39717	<i>recA</i>
	<i>Mycoplasma mycoides</i>	GM9	L22073	<i>recA</i>
	<i>Mycoplasma pneumoniae</i>	ATCC 29342	MPAE000033	<i>recA</i>
	<i>Mycoplasma pulmonis</i>	KD735	L22074	<i>recA</i>
35	<i>Myxococcus xanthus</i>		L40368	<i>recA</i>
	<i>Neisseria animalis</i>	NCTC 10212	U57910	<i>recA</i>
	<i>Neisseria cinerea</i>	LCDC 81-176	AJ223869	<i>recA</i>
	<i>Neisseria cinerea</i>	LNP 1646	U57906	<i>recA</i>
	<i>Neisseria cinerea</i>	NCTC 10294	AJ223871	<i>recA</i>
40	<i>Neisseria cinerea</i>	Vedros M601	AJ223870	<i>recA</i>
	<i>Neisseria elongata</i>	CCUG 2131	AJ223882	<i>recA</i>
	<i>Neisseria elongata</i>	CCUG 4165A	AJ223880	<i>recA</i>
	<i>Neisseria elongata</i>	CCUG 4557	AJ223879	<i>recA</i>
	subsp. <i>intermedia</i>			
45	<i>Neisseria elongata</i>	NCTC 10660	AJ223881	<i>recA</i>
	<i>Neisseria elongata</i>	NCTC 11050	AJ223878	<i>recA</i>
	<i>Neisseria elongata</i>	NHITCC 2376	AJ223877	<i>recA</i>
	<i>Neisseria flava</i>	Bangor 9	AJ223873	<i>recA</i>
	<i>Neisseria flavescens</i>	LNP 444	U57907	<i>recA</i>
50	<i>Neisseria gonorrhoeae</i>	CH95	U57902	<i>recA</i>
	<i>Neisseria gonorrhoeae</i>	FA19	X64842	<i>recA</i>
	<i>Neisseria gonorrhoeae</i>	MS11	X17374	<i>recA</i>
	<i>Neisseria lactamica</i>	CCUG 7757	AJ223866	<i>recA</i>
	<i>Neisseria lactamica</i>	CCUG 7852	Y11819	<i>recA</i>
55	<i>Neisseria lactamica</i>	LCDC 77-143	Y11818	<i>recA</i>

Table 11. Microbial species for which *tuf* and/or *atpD* and/or *recA* sequences are available in public databases (continued).

	Species	Strain	Accession number	Coding gene*
	<i>Neisseria lactamica</i>	LCDC 80-111	AJ223864	<i>recA</i>
	<i>Neisseria lactamica</i>	LCDC 845	AJ223865	<i>recA</i>
	<i>Neisseria lactamica</i>	NCTC 10617	U57905	<i>recA</i>
	<i>Neisseria lactamica</i>	NCTC 10618	AJ223863	<i>recA</i>
5	<i>Neisseria meningitidis</i>	44/46	X64849	<i>recA</i>
	<i>Neisseria meningitidis</i>	Bangor 13	AJ223868	<i>recA</i>
	<i>Neisseria meningitidis</i>	HF116	X64848	<i>recA</i>
	<i>Neisseria meningitidis</i>	HF130	X64844	<i>recA</i>
	<i>Neisseria meningitidis</i>	HF46	X64847	<i>recA</i>
10	<i>Neisseria meningitidis</i>	M470	X64850	<i>recA</i>
	<i>Neisseria meningitidis</i>	N94II	X64846	<i>recA</i>
	<i>Neisseria meningitidis</i>	NCTC 8249	AJ223867	<i>recA</i>
	<i>Neisseria meningitidis</i>	P63	X64845	<i>recA</i>
	<i>Neisseria meningitidis</i>	S3446	U57903	<i>recA</i>
15	<i>Neisseria meningitidis</i>	LNP 405	U57908	<i>recA</i>
	<i>Neisseria mucosa</i>	Vedros M1801	AJ223875	<i>recA</i>
	<i>Neisseria mucosa</i>	CCUG 17915	AJ223876	<i>recA</i>
	<i>Neisseria perflava</i>	LCDC 85402	AJ223862	<i>recA</i>
	<i>Neisseria perflava</i>	NCTC 4590	U57909	<i>recA</i>
20	<i>Neisseria pharyngis</i> var. <i>flava</i>	CCUG 18031	Y11815	<i>recA</i>
	<i>Neisseria polysaccharea</i>	CCUG 24845	Y11816	<i>recA</i>
	<i>Neisseria polysaccharea</i>	CCUG 24846	Y11814	<i>recA</i>
	<i>Neisseria polysaccharea</i>	INS MA 3008	Y11817	<i>recA</i>
	<i>Neisseria polysaccharea</i>	NCTC 11858	U57904	<i>recA</i>
25	<i>Neisseria sicca</i>	NRL 30016	AJ223872	<i>recA</i>
	<i>Neisseria subflava</i>	NRL 30017	AJ223874	<i>recA</i>
	<i>Paracoccus denitrificans</i>	DSM 413	U59631	<i>recA</i>
	<i>Pasteurella multocida</i>		X99324	<i>recA</i>
	<i>Porphyromonas gingivalis</i>	W83	U70054	<i>recA</i>
30	<i>Prevotella ruminicola</i>	JCM 8958	U61227	<i>recA</i>
	<i>Proteus mirabilis</i>	pG1300	X14870	<i>recA</i>
	<i>Proteus vulgaris</i>		X55555	<i>recA</i>
	<i>Pseudomonas aeruginosa</i>		X05691	<i>recA</i>
	<i>Pseudomonas aeruginosa</i>	PAM 7	X52261	<i>recA</i>
35	<i>Pseudomonas aeruginosa</i>	PAO12	D13090	<i>recA</i>
	<i>Pseudomonas cepacia</i>		D90120	<i>recA</i>
	<i>Pseudomonas fluorescens</i>	OE 28.3	M96558	<i>recA</i>
	<i>Pseudomonas putida</i>		L12684	<i>recA</i>
	<i>Pseudomonas putida</i>	PpS145	U70864	<i>recA</i>
40	<i>Rhizobium leguminosarum</i>	VF39	X59956	<i>recA</i>
	biovar <i>viciae</i>			
	<i>Rhizobium phaseoli</i>	CNPAF512	X62479	<i>recA</i>
	<i>Rhodobacter capsulatus</i>	J50	X82183	<i>recA</i>
	<i>Rhodobacter sphaeroides</i>	2.4.1	X72705	<i>recA</i>
45	<i>Rhodopseudomonas palustris</i>	N 7	D84467	<i>recA</i>
	<i>Rickettsia prowazekii</i>	Madrid E	AJ235273	<i>recA</i>
	<i>Rickettsia prowazekii</i>	Madrid E	U01959	<i>recA</i>
	<i>Serratia marcescens</i>		M22935	<i>recA</i>
	<i>Shigella flexneri</i>		X55553	<i>recA</i>
50	<i>Shigella sonnei</i>	KNIH104S	AF101227	<i>recA</i>
	<i>Sinorhizobium meliloti</i>	2011	X59957	<i>recA</i>
	<i>Staphylococcus aureus</i>		L25893	<i>recA</i>
	<i>Streptococcus aureus</i>	Challis V288	L20574	<i>recA</i>
	<i>Streptococcus mutans</i>	UA96	M81468	<i>recA</i>
55	<i>Streptococcus pneumoniae</i>		Z17307	<i>recA</i>

Table 11. Microbial species for which *tuf* and/or *atpD* and/or *recA* sequences are available in public databases (continued).

	Species	Strain	Accession number	Coding gene*
	<i>Streptococcus pneumoniae</i>	R800	Z34303	<i>recA</i>
	<i>Streptococcus pyogenes</i>	NZ131	U21934	<i>recA</i>
	<i>Streptococcus salivarius</i>		M94062	<i>recA</i>
	subsp. <i>thermophilus</i>			
5	<i>Streptomyces ambofaciens</i>	DSM 40697	Z30324	<i>recA</i>
	<i>Streptomyces coelicolor</i>	A3(2)	AL020958	<i>recA</i>
	<i>Streptomyces lividans</i>	TK24	X76076	<i>recA</i>
	<i>Streptomyces rimosus</i>	R6	X94233	<i>recA</i>
	<i>Streptomyces venezuelae</i>	ATCC10712	U04837	<i>recA</i>
10	<i>Synechococcus</i> sp.	PR6	M29495	<i>recA</i>
	<i>Thermotoga maritima</i>		L23425	<i>recA</i>
	<i>Thermus aquaticus</i>		L20095	<i>recA</i>
	<i>Thermus thermophilus</i>	HB8	D17392	<i>recA</i>
	<i>Thiobacillus ferrooxidans</i>		M26933	<i>recA</i>
15	<i>Treponema pallidum</i>	Nichols	AE001243	<i>recA</i>
	<i>Vibrio anguillarum</i>		M80525	<i>recA</i>
	<i>Vibrio cholerae</i>	017	X71969	<i>recA</i>
	<i>Vibrio cholerae</i>	2740-80	U10162	<i>recA</i>
	<i>Vibrio cholerae</i>	569B	L42384	<i>recA</i>
20	<i>Vibrio cholerae</i>	M549	AF117881	<i>recA</i>
	<i>Vibrio cholerae</i>	M553	AF117882	<i>recA</i>
	<i>Vibrio cholerae</i>	M645	AF117883	<i>recA</i>
	<i>Vibrio cholerae</i>	M793	AF117878	<i>recA</i>
	<i>Vibrio cholerae</i>	M794	AF117880	<i>recA</i>
25	<i>Vibrio cholerae</i>	M967	AF117879	<i>recA</i>
	<i>Xanthomonas citri</i>	-XW47	AF006590	<i>recA</i>
	<i>Xanthomonas oryzae</i>		AF013600	<i>recA</i>
	<i>Xenorhabdus bovienii</i>	T228/1	U87924	<i>recA</i>
	<i>Xenorhabdus nematophilus</i>	AN6	AF127333	<i>recA</i>
30	<i>Yersinia pestis</i>	231	X75336	<i>recA</i>
Fungi, parasites, human and plants				
	<i>Anabaena variabilis</i>	ATCC 29413	M29680	<i>recA</i>
35	<i>Arabidopsis thaliana</i>		U43652	<i>recA</i> (Rad51)
	<i>Candida albicans</i>		U39808	<i>recA</i> (Dmc1)
	<i>Coprinus cinereus</i>	Okayama-7	U21905	<i>recA</i> (Rad51)
	<i>Emericella nidulans</i>		Z80341	<i>recA</i> (Rad51)
	<i>Gallus gallus</i>		L09655	<i>recA</i> (Rad51)
40	<i>Homo sapiens</i>		D13804	<i>recA</i> (Rad51)
	<i>Homo sapiens</i>		D63882	<i>recA</i> (Dmc1)
	<i>Leishmania major</i>	Friedlin	AF062379	<i>recA</i> (Rad51)
	<i>Leishmania major</i>	Friedlin	AF062380	<i>recA</i> (Dmc1)
	<i>Mus musculus</i>		D58419	<i>recA</i> (Dmc1)
45	<i>Neurospora crassa</i>	74-OR23-1A	D29638	<i>recA</i> (Rad51)
	<i>Saccharomyces cerevisiae</i>		D10023	<i>recA</i> (Rad51)
	<i>Schizosaccharomyces pombe</i>		Z22691	<i>recA</i> (Rad51)
	<i>Schizosaccharomyces pombe</i>	972h-	AL021817	<i>recA</i> (Dmc1)
	<i>Tetrahymena thermophila</i>	PB9R	AF064516	<i>recA</i> (Rad51)
50	<i>Trypanosoma brucei</i>	stock 427	Y13144	<i>recA</i> (Rad51)
	<i>Ustilago maydis</i>		U62484	<i>recA</i> (Rad51)
	<i>Xenopus laevis</i>		D38488	<i>recA</i> (Rad51)
	<i>Xenopus laevis</i>		D38489	<i>recA</i> (Rad51)

55

Tabl 11. Microbial species for which *tuf* and/or *atpD* and/or *recA* sequences are available in public databases (continued).

Species	Strain	Accession number	Coding gene*
---------	--------	------------------	--------------

* *tuf* indicates *tuf* sequences

tuf (C) indicates *tuf* sequences divergent from main (usually A and B) copies of the elongation factor-Tu

tuf (EF-1) indicates *tuf* sequences of the eukaryotic type (elongation factor 1 α)

tuf (M) indicates *tuf* sequences from organellar (mostly mitochondrial) origin

atpD indicates *atpD* sequences of the F-type

atpD (V) indicates *atpD* sequences of the V-Type

recA indicates *recA* sequences

recA (Rad51) indicates *rad51* sequences or homologs

recA (Dmc1) indicates *dmc1* sequences or homologs

¹ Nucleotides sequences published in Arch. Microbiol. 1990 153:241-247

² These sequences are from the TIGR database (<http://www.tigr.org/tdb/tdb.html>)

³ Nucleotides sequences published in FEMS Microbiology Letters 1988 50:101-106

Table 12. Bacterial species used to test the specificity of the *Staphylococcus* genus-specific amplification primers derived from *tuf* sequences.

	Strain	Reference number	Strain	Reference number
5	Staphylococci species (n=27)		Other Gram-positive bacteria (n=20)	
	<i>Staphylococcus arlettae</i>	ATCC 43957	<i>Bacillus subtilis</i>	ATCC 27370
	<i>Staphylococcus aureus</i>	ATCC 35844	<i>Enterococcus avium</i>	ATCC 14025
	subsp. <i>anaerobius</i>			
10	<i>Staphylococcus aureus</i>	ATCC 43300	<i>Enterococcus durans</i>	ATCC 19432
	subsp. <i>aureus</i>			
	<i>Staphylococcus auricularis</i>	ATCC 33753	<i>Enterococcus faecalis</i>	ATCC 19433
	<i>Staphylococcus capitis</i>	ATCC 27840	<i>Enterococcus faecium</i>	ATCC 19434
	subsp. <i>capitis</i>			
15	<i>Staphylococcus caprae</i>	ATCC 35538	<i>Enterococcus flavescens</i>	ATCC 49996
	<i>Staphylococcus carnosus</i>	ATCC 51365	<i>Enterococcus gallinarum</i>	ATCC 49573
	<i>Staphylococcus chromogenes</i>	ATCC 43764	<i>Lactobacillus acidophilus</i>	ATCC 4356
	<i>Staphylococcus cohnii</i>	DSM 20260	<i>Lactococcus lactis</i>	ATCC 11454
	subsp. <i>urealyticum</i>			
20	<i>Staphylococcus delphini</i>	ATCC 49171	<i>Listeria innocua</i>	ATCC 33090
	<i>Staphylococcus epidermidis</i>	ATCC 14990	<i>Listeria ivanovii</i>	ATCC 19119
	<i>Staphylococcus equorum</i>	ATCC 43958	<i>Listeria monocytogenes</i>	ATCC 15313
	<i>Staphylococcus felis</i>	ATCC 49168	<i>Macroccoccus caseolyticus</i>	ATCC 13548
	<i>Staphylococcus gallinarum</i>	ATCC 35539	<i>Streptococcus agalactiae</i>	ATCC 13813
25	<i>Staphylococcus haemolyticus</i>	ATCC 29970	<i>Streptococcus anginosus</i>	ATCC 33397
	<i>Staphylococcus hominis</i>	ATCC 27844	<i>Streptococcus bovis</i>	ATCC 33317
	<i>Staphylococcus hyicus</i>	ATCC 11249	<i>Streptococcus mutans</i>	ATCC 25175
	<i>Staphylococcus intermedius</i>	ATCC 29663	<i>Streptococcus pneumoniae</i>	ATCC 6303
	<i>Staphylococcus kloosii</i>	ATCC 43959	<i>Streptococcus pyogenes</i>	ATCC 19615
30	<i>Staphylococcus lentus</i>	ATCC 29070	<i>Streptococcus salivarius</i>	ATCC 7073
	<i>Staphylococcus lugdunensis</i>	ATCC 43809		
	<i>Staphylococcus saprophyticus</i>	ATCC 15305		
	<i>Staphylococcus schleiferi</i>	ATCC 49545		
	subsp. <i>coagulans</i>			
35	<i>Staphylococcus sciuri</i>	ATCC 29060		
	subsp. <i>sciuri</i>			
	<i>Staphylococcus simulans</i>	ATCC 27848		
	<i>Staphylococcus warneri</i>	ATCC 27836		
	<i>Staphylococcus xylosum</i>	ATCC 29971		
40	Gram-negative bacteria (n=33)			
	<i>Acinetobacter baumannii</i>	ATCC 19606	<i>Morganella morganii</i>	ATCC 25830
	<i>Bacteroides distasonis</i>	ATCC 8503	<i>Neisseria gonorrhoeae</i>	ATCC 35201
	<i>Bacteroides fragilis</i>	ATCC 25285	<i>Neisseria meningitidis</i>	ATCC 13077
	<i>Bulkholderia cepacia</i>	ATCC 25416	<i>Proteus mirabilis</i>	ATCC 25933
45	<i>Bordetella pertussis</i>	ATCC 9797	<i>Proteus vulgaris</i>	ATCC 13315
	<i>Citrobacter freundii</i>	ATCC 8090	<i>Providencia rettgeri</i>	ATCC 9250
	<i>Enterobacter aerogenes</i>	ATCC 13048	<i>Providencia stuartii</i>	ATCC 29914
	<i>Enterobacter cloacae</i>	ATCC 13047	<i>Pseudomonas aeruginosa</i>	ATCC 27853
	<i>Escherichia coli</i>	ATCC 25922	<i>Pseudomonas fluorescens</i>	ATCC 13525
50	<i>Haemophilus influenzae</i>	ATCC 8907	<i>Salmonella choleraesuis</i>	ATCC 7001
	<i>Haemophilus parahaemolyticus</i>	ATCC 10014	<i>Salmonella typhimurium</i>	ATCC 14028
	<i>Haemophilus parainfluenzae</i>	ATCC 7901	<i>Serratia marcescens</i>	ATCC 8100
	<i>Hafnia alvei</i>	ATCC 13337	<i>Shigella flexneri</i>	ATCC 12022
	<i>Kingella indologenes</i>	ATCC 25869	<i>Shigella sonnei</i>	ATCC 29930
55	<i>Klebsiella oxytoca</i>	ATCC 13182	<i>Stenotrophomonas maltophilia</i>	ATCC 13843
	<i>Klebsiella pneumoniae</i>	ATCC 13883	<i>Yersinia enterocolitica</i>	ATCC 9610
	<i>Moraxella catarrhalis</i>	ATCC 25240		

Table 13. Bacterial species used to test the specificity of the penicillin-resistant *Streptococcus pneumoniae* amplification primers derived from *pbp1a* sequences.

Strain	Reference number	Strain	Reference number
Gram-positive species (n=67)			
<i>Abiotrophia adiacens</i>	ATCC 49175	<i>Staphylococcus hominis</i>	ATCC 27844
<i>Abiotrophia defectiva</i>	ATCC 49176	<i>Staphylococcus lugdunensis</i>	ATCC 43809
<i>Actinomyces pyogenes</i>	ATCC 19411	<i>Staphylococcus saprophyticus</i>	ATCC 15305
<i>Bacillus anthracis</i>	ATCC 4229	<i>Staphylococcus simulans</i>	ATCC 27848
<i>Bacillus cereus</i>	ATCC 14579	<i>Staphylococcus warneri</i>	ATCC 27836
<i>Bifidobacterium breve</i>	ATCC 15700	<i>Streptococcus acidominimus</i>	ATCC 51726
<i>Clostridium difficile</i>	ATCC 9689	<i>Streptococcus agalactiae</i>	ATCC 12403
<i>Enterococcus avium</i>	ATCC 14025	<i>Streptococcus anginosus</i>	ATCC 33397
<i>Enterococcus casseliflavus</i>	ATCC 25788	<i>Streptococcus bovis</i>	ATCC 33317
<i>Enterococcus dispar</i>	ATCC 51266	<i>Streptococcus constellatus</i>	ATCC 27823
<i>Enterococcus durans</i>	ATCC 19432	<i>Streptococcus cricetus</i>	ATCC 19624
<i>Enterococcus faecalis</i>	ATCC 29212	<i>Streptococcus cristatus</i>	ATCC 51100
<i>Enterococcus faecium</i>	ATCC 19434	<i>Streptococcus downei</i>	ATCC 33748
<i>Enterococcus flavescens</i>	ATCC 49996	<i>Streptococcus dysgalactiae</i>	ATCC 43078
<i>Enterococcus gallinarum</i>	ATCC 49573	<i>Streptococcus equi</i>	ATCC 9528
<i>Enterococcus hirae</i>	ATCC 8043	<i>Streptococcus ferus</i>	ATCC 33477
<i>Enterococcus mundtii</i>	ATCC 43186	<i>Streptococcus gordonii</i>	ATCC 10558
<i>Enterococcus raffinosus</i>	ATCC 49427	<i>Streptococcus intermedius</i>	ATCC 27335
<i>Lactobacillus lactis</i>	ATCC 19435	<i>Streptococcus mitis</i>	ATCC 903
<i>Lactobacillus monocytogenes</i>	ATCC 15313	<i>Streptococcus mitis</i>	LSPQ 2583
<i>Mobiluncus curtisii</i>	ATCC 35242	<i>Streptococcus mitis</i>	ATCC 49456
<i>Peptococcus niger</i>	ATCC 27731	<i>Streptococcus mutans</i>	ATCC 27175
<i>Peptostreptococcus acones</i>	ATCC 6919	<i>Streptococcus oralis</i>	ATCC 10557
<i>Peptostreptococcus anaerobius</i>	ATCC 27337	<i>Streptococcus oralis</i>	ATCC 9811
<i>Peptostreptococcus asaccharolyticus</i>	ATCC 2639	<i>Streptococcus oralis</i>	ATCC 35037
<i>Peptostreptococcus lactolyticus</i>	ATCC 51172	<i>Streptococcus parasanguinis</i>	ATCC 15912
<i>Peptostreptococcus magnus</i>	ATCC 15794	<i>Streptococcus parauberis</i>	ATCC 6631
<i>Peptostreptococcus prevotii</i>	ATCC 9321	<i>Streptococcus rattus</i>	ATCC 15912
<i>Peptostreptococcus tetradius</i>	ATCC 35098	<i>Streptococcus salivarius</i>	ATCC 7073
<i>Staphylococcus aureus</i>	ATCC 25923	<i>Streptococcus sanguinis</i>	ATCC 10556
<i>Staphylococcus capitis</i>	ATCC 27840	<i>Streptococcus suis</i>	ATCC 43765
<i>Staphylococcus epidermidis</i>	ATCC 14990	<i>Streptococcus uberis</i>	ATCC 19436
<i>Staphylococcus haemolyticus</i>	ATCC 29970	<i>Streptococcus vestibularis</i>	ATCC 49124
Gram-negative species (n=33)			
<i>Actinobacter baumannii</i>	ATCC 19606	<i>Moraxella morganii</i>	ATCC 13077
<i>Bordetella pertussis</i>	ATCC 9797	<i>Neisseria gonorrhoeae</i>	ATCC 35201
<i>Citrobacter diversus</i>	ATCC 27028	<i>Neisseria meningitidis</i>	ATCC 13077
<i>Citrobacter freundii</i>	ATCC 8090	<i>Proteus mirabilis</i>	ATCC 25933
<i>Enterobacter aerogenes</i>	ATCC 13048	<i>Proteus vulgaris</i>	ATCC 13315
<i>Enterobacter agglomerans</i>	ATCC 27155	<i>Providencia alcalifaciens</i>	ATCC 9886
<i>Enterobacter cloacae</i>	ATCC 13047	<i>Providencia rettgeri</i>	ATCC 9250
<i>Escherichia coli</i>	ATCC 25922	<i>Providencia rustigianii</i>	ATCC 33673
<i>Haemophilus ducreyi</i>	ATCC 33940	<i>Providencia stuartii</i>	ATCC 33672
<i>Haemophilus haemolyticus</i>	ATCC 33390	<i>Pseudomonas aeruginosa</i>	ATCC 35554
<i>Haemophilus influenzae</i>	ATCC 9007	<i>Pseudomonas fluorescens</i>	ATCC 13525
<i>Haemophilus parainfluenzae</i>	ATCC 7901	<i>Pseudomonas stutzeri</i>	ATCC 17588
<i>Hafnia alvei</i>	ATCC 13337	<i>Salmonella typhimurium</i>	ATCC 14028
<i>Klebsiella oxytoca</i>	ATCC 13182	<i>Serratia marcescens</i>	ATCC 13880
<i>Klebsiella pneumoniae</i>	ATCC 13883	<i>Shigella flexneri</i>	ATCC 12022
<i>Moraxella atlantae</i>	ATCC 29525	<i>Yersinia enterocolitica</i>	ATCC 9610
<i>Moraxella catarrhalis</i>	ATCC 43628		

Table 14. Bacterial species (n=104) detected by the platelet contaminants assay. Bold characters indicate the major bacterial contaminants found in platelet concentrates.

5	<i>Abiotrophia adiacens</i>	<i>Klebsiella oxytoca</i>	<i>Staphylococcus simulans</i>
	<i>Abiotrophia defectiva</i>	<i>Klebsiella pneumoniae</i>	<i>Staphylococcus warneri</i>
	<i>Acinetobacter baumannii</i>	<i>Legionella pneumophila</i>	<i>Stenotrophomonas maltophilia</i>
	<i>Acinetobacter lwoffii</i>	<i>Megamonas hypermegale</i>	80 <i>Streptococcus acidominimus</i>
	<i>Aerococcus viridans</i>	45 <i>Moraxella atlantae</i>	<i>Streptococcus agalactiae</i>
10	<i>Bacillus anthracis</i>	<i>Moraxella catarrhalis</i>	<i>Streptococcus anginosus</i>
	<i>Bacillus cereus</i>	<i>Morganella morganii</i>	<i>Streptococcus bovis</i>
	<i>Bacillus subtilis</i>	<i>Neisseria gonorrhoeae</i>	<i>Streptococcus constellatus</i>
	<i>Brucella abortus</i>	<i>Neisseria meningitidis</i>	85 <i>Streptococcus cricetus</i>
	<i>Burkholderia cepacia</i>	50 <i>Pasteurella aerogenes</i>	<i>Streptococcus cristatus</i>
15	<i>Citrobacter diversus</i>	<i>Pasteurella multocida</i>	<i>Streptococcus dysgalactiae</i>
	<i>Citrobacter freundii</i>	<i>Peptostreptococcus magnus</i>	<i>Streptococcus equi</i>
	<i>Enterobacter aerogenes</i>	<i>Proteus mirabilis</i>	<i>Streptococcus ferus</i>
	<i>Enterobacter agglomerans</i>	<i>Providencia alcalifaciens</i>	90 <i>Streptococcus gordonii</i>
	<i>Enterobacter cloacae</i>	55 <i>Providencia rettgeri</i>	<i>Streptococcus intermedius</i>
20	<i>Enterococcus avium</i>	<i>Providencia rustigianii</i>	<i>Streptococcus macacae</i>
	<i>Enterococcus casseliflavus</i>	<i>Providencia stuartii</i>	<i>Streptococcus mitis</i>
	<i>Enterococcus dispar</i>	<i>Pseudomonas aeruginosa</i>	<i>Streptococcus mutans</i>
	<i>Enterococcus durans</i>	<i>Pseudomonas fluorescens</i>	95 <i>Streptococcus oralis</i>
	<i>Enterococcus faecalis</i>	60 <i>Pseudomonas stutzeri</i>	<i>Streptococcus parasanguinis</i>
25	<i>Enterococcus faecium</i>	<i>Salmonella bongori</i>	<i>Streptococcus parauberis</i>
	<i>Enterococcus flavescens</i>	<i>Salmonella choleraesuis</i>	<i>Streptococcus pneumoniae</i>
	<i>Enterococcus gallinarum</i>	<i>Salmonella enteritidis</i>	<i>Streptococcus pyogenes</i>
	<i>Enterococcus mundtii</i>	<i>Salmonella gallinarum</i>	100 <i>Streptococcus rattii</i>
	<i>Enterococcus raffinosus</i>	65 <i>Salmonella typhimurium</i>	<i>Streptococcus salivarius</i>
30	<i>Enterococcus solitarius</i>	<i>Serratia liquefaciens</i>	<i>Streptococcus sanguinis</i>
	<i>Escherichia coli</i>	<i>Serratia marcescens</i>	<i>Streptococcus sobrinus</i>
	<i>Gemella morbillorum</i>	<i>Shigella flexneri</i>	<i>Streptococcus uberis</i>
	<i>Haemophilus ducreyi</i>	<i>Shigella sonnei</i>	105 <i>Streptococcus vestibularis</i>
	<i>Haemophilus haemolyticus</i>	70 <i>Staphylococcus aureus</i>	<i>Vibrio cholerae</i>
35	<i>Haemophilus influenzae</i>	<i>Staphylococcus capitis</i>	<i>Yersinia enterocolitica</i>
	<i>Haemophilus</i>	<i>Staphylococcus epidermidis</i>	<i>Yersinia pestis</i>
	<i>parahaemolyticus</i>	<i>Staphylococcus haemolyticus</i>	<i>Yersinia pseudotuberculosis</i>
	<i>Haemophilus parainfluenzae</i>	<i>Staphylococcus hominis</i>	
	<i>Hafnia alvei</i>	75 <i>Staphylococcus lugdunensis</i>	
40	<i>Kingella kingae</i>	<i>Staphylococcus saprophyticus</i>	

Table 15. Microorganisms identified by automated systems.

5	<i>Abiotrophia adiacens</i> (<i>Streptococcus adiacens</i>) <i>Abiotrophia defectiva</i> (<i>Streptococcus defectivus</i>) <i>Achromobacter</i> species <i>Acidaminococcus fermentans</i> <i>Acinetobacter alcaligenes</i> <i>Acinetobacter anitratus</i> <i>Acinetobacter baumannii</i>	75	<i>Alcaligenes xylosoxidans</i> subsp. <i>xylosoxidans</i> <i>Alloicoccus otitis</i> <i>Anaerobiospirillum succiniciproducens</i> <i>Anaerovibrio lipolytica</i>	150	<i>Brevibacterium</i> species <i>Brevundimonas</i> (<i>Pseudomonas</i>) <i>diminuta</i> <i>Brevundimonas</i> (<i>Pseudomonas</i>) <i>vesicularis</i> <i>Brevundimonas</i> species
10	<i>Acinetobacter calcoaceticus</i> <i>Acinetobacter calcoaceticus biovar anitratus</i> <i>Acinetobacter calcoaceticus biovar lwoffii</i>	80	<i>Arachnia propionica</i> <i>Arcanobacterium</i> (<i>Actinomyces</i>) <i>bemardiae</i> <i>Arcanobacterium</i> (<i>Actinomyces</i>) <i>pyogenes</i>	155	<i>Brochothrix thermosphacta</i> <i>Brucella abortus</i> <i>Brucella canis</i> <i>Brucella melitensis</i> <i>Brucella ovis</i>
15	<i>Acinetobacter genomospecies</i> <i>Acinetobacter haemolyticus</i> <i>Acinetobacter johnsonii</i> <i>Acinetobacter junii</i> <i>Acinetobacter lwoffii</i>	85	<i>Arcanobacterium haemolyticum</i> <i>Arcobacter cryaerophilus</i> (<i>Campylobacter cryaerophila</i>) <i>Arthrobacter globiformis</i> <i>Arthrobacter</i> species	160	<i>Brucella species</i> <i>Brucella suis</i> <i>Budvicia aquatica</i> <i>Burkholderia</i> (<i>Pseudomonas</i>) <i>cepacia</i> <i>Burkholderia</i> (<i>Pseudomonas</i>) <i>gladioli</i>
20	<i>Acinetobacter radioresistens</i> <i>Acinetobacter</i> species <i>Actinobacillus actinomycetemcomitans</i> <i>Actinobacillus capsulatus</i> <i>Actinobacillus equuli</i>	90	<i>Arxiozyma telluris</i> (<i>Torulopsis pintolopesii</i>) <i>Atopobium minutum</i> (<i>Lactobacillus minutus</i>)	165	<i>Burkholderia</i> (<i>Pseudomonas</i>) <i>mallei</i> <i>Burkholderia</i> (<i>Pseudomonas</i>) <i>pseudomallei</i> <i>Burkholderia</i> species
25	<i>Actinobacillus hominis</i> <i>Actinobacillus lignieresii</i> <i>Actinobacillus pleuropneumoniae</i> <i>Actinobacillus</i> species <i>Actinobacillus suis</i>	95	<i>Aureobacterium</i> species <i>Bacillus amyloliquefaciens</i> <i>Bacillus anthracis</i> <i>Bacillus badius</i> <i>Bacillus cereus</i>	170	<i>Buttiauxella agrestis</i> <i>Campylobacter coli</i> <i>Campylobacter concisus</i> <i>Campylobacter fetus</i> <i>Campylobacter fetus</i> subsp. <i>fetus</i> <i>Campylobacter fetus</i> subsp. <i>venerealis</i>
30	<i>Actinobacillus ureae</i> <i>Actinomyces bovis</i> <i>Actinomyces israelii</i> <i>Actinomyces meyeri</i> <i>Actinomyces naeslundii</i>	100	<i>Bacillus circulans</i> <i>Bacillus coagulans</i> <i>Bacillus firmus</i> <i>Bacillus lentus</i> <i>Bacillus licheniformis</i>	175	<i>Campylobacter hyointestinalis</i> <i>Campylobacter jejuni</i> subsp. <i>doylei</i> <i>Campylobacter jejuni</i> subsp. <i>jejuni</i> <i>Campylobacter lari</i>
35	<i>Actinomyces neuii</i> subsp. <i>anitratus</i> <i>Actinomyces neuii</i> subsp. <i>neuii</i> <i>Actinomyces odontolyticus</i> <i>Actinomyces pyogenes</i> <i>Actinomyces radingae</i>	105	<i>Bacillus megaterium</i> <i>Bacillus mycoides</i> <i>Bacillus pantothenicus</i> <i>Bacillus pumilus</i> <i>Bacillus</i> species	180	<i>Campylobacter lari</i> subsp. UPTC <i>Campylobacter mucosalis</i> <i>Campylobacter</i> species <i>Campylobacter sputorum</i> <i>Campylobacter sputorum</i> subsp. <i>bubulus</i>
40	<i>Actinomyces viscosus</i> <i>Aerococcus</i> species <i>Aerococcus viridans</i>	110	<i>Bacillus sphaericus</i> <i>Bacillus stearothermophilus</i> <i>Bacillus subtilis</i> <i>Bacillus thuringiensis</i> <i>Bacteroides caccae</i>	185	<i>Campylobacter sputorum</i> subsp. <i>fecalis</i> <i>Campylobacter sputorum</i> subsp. <i>sputorum</i> <i>Campylobacter upsaliensis</i> <i>Candida</i> (<i>Clavispora</i>) <i>lusitaniae</i> <i>Candida</i> (<i>Pichia</i>) <i>guilliermondii</i>
45	<i>Aeromonas caviae</i> <i>Aeromonas hydrophila</i> <i>Aeromonas hydrophila</i> group <i>Aeromonas jandaei</i> <i>Aeromonas salmonicida</i>	115	<i>Bacteroides merdae</i> <i>Bacteroides ovatus</i> <i>Bacteroides species</i> <i>Bacteroides splanchnicus</i> <i>Bacteroides stercoris</i>	190	<i>Candida</i> (<i>Torulopsis</i>) <i>glabrata</i> <i>Candida albicans</i> <i>Candida boidinii</i> <i>Candida catenulata</i> <i>Candida ciferrii</i>
50	<i>Aeromonas salmonicida</i> subsp. <i>achromogenes</i> <i>Aeromonas salmonicida</i> subsp. <i>masoucida</i> <i>Aeromonas salmonicida</i> subsp. <i>salmonicida</i>	120	<i>Bacteroides thalassiomicron</i> <i>Bacteroides uniformis</i> <i>Bacteroides ureolyticus</i> (<i>B. corrodens</i>) <i>Bacteroides vulgatus</i> <i>Bergeyella</i> (<i>Weeksella</i>) <i>zoohecum</i>	195	<i>Candida colliculosa</i> <i>Candida conglobata</i> <i>Candida curvata</i> (<i>Cryptococcus curvatus</i>) <i>Candida dattila</i>
55	<i>Aeromonas schubertii</i> <i>Aeromonas sobria</i> <i>Aeromonas</i> species <i>Aeromonas trota</i>	125	<i>Bifidobacterium adolescentis</i> <i>Bifidobacterium bifidum</i> <i>Bifidobacterium breve</i> <i>Bifidobacterium dentium</i> <i>Bifidobacterium infantis</i>	200	<i>Candida dubliniensis</i> <i>Candida famata</i> <i>Candida globosa</i> <i>Candida hellenica</i> <i>Candida holmii</i>
60	<i>Aeromonas veronii</i> <i>Aeromonas veronii biovar sobria</i> <i>Agrobacterium radiobacter</i> <i>Agrobacterium</i> species	130	<i>Bifidobacterium species</i> <i>Blastoschizomyces</i> (<i>Dipodascus</i>) <i>capitatus</i> <i>Bordetella avium</i> <i>Bordetella bronchiseptica</i>	205	<i>Candida inconspicua</i> <i>Candida intermedia</i> <i>Candida kefyr</i> <i>Candida krusei</i> <i>Candida lambica</i>
65	<i>Agrobacterium tumefaciens</i> <i>Alcaligenes denitrificans</i> <i>Alcaligenes faecalis</i> <i>Alcaligenes odorans</i> <i>Alcaligenes odorans</i> (<i>Alcaligenes faecalis</i>)	135	<i>Bordetella pertussis</i> <i>Bordetella</i> species <i>Borrelia</i> species <i>Branhamella</i> (<i>Moraxella</i>) <i>catarrhalis</i> <i>Branhamella</i> species	210	<i>Candida magnoliae</i> <i>Candida maris</i> <i>Candida melibiosica</i> <i>Candida membranaefaciens</i> <i>Candida norvegensis</i>
70	<i>Alcaligenes</i> species <i>Alcaligenes xylosoxidans</i> <i>Alcaligenes xylosoxidans</i> subsp. <i>denitrificans</i>	140	<i>Brevibacillus brevis</i> <i>Brevibacillus laterosporus</i> <i>Brevibacterium casei</i> <i>Brevibacterium epidermidis</i> <i>Brevibacterium linens</i>	215	<i>Candida norvegica</i> <i>Candida parapsilosis</i> <i>Candida paratropicalis</i> <i>Candida pelliculosa</i>

Table 15. Microorganisms identified by automated systems (continued).

5	<i>Candida pseudotropicalis</i>	80	<i>Clostridium hastiforme</i>	160	<i>Corynebacterium urealyticum</i> (group D2)
	<i>Candida pulcherrima</i>		<i>Clostridium histolyticum</i>		<i>Corynebacterium xerosis</i>
	<i>Candida raubitsii</i>		<i>Clostridium innocuum</i>		<i>Cryptococcus albidus</i>
	<i>Candida rugosa</i>		<i>Clostridium limosum</i>		<i>Cryptococcus aler</i>
	<i>Candida sake</i>		<i>Clostridium novyi</i>		<i>Cryptococcus cereanus</i>
	<i>Candida silvicola</i>	85	<i>Clostridium novyi A</i>		<i>Cryptococcus gastricus</i>
	<i>Candida species</i>		<i>Clostridium paraputrificum</i>		<i>Cryptococcus humicola</i>
	<i>Candida sphaenica</i>		<i>Clostridium perfringens</i>	165	<i>Cryptococcus lactativorus</i>
	<i>Candida stellatoidea</i>		<i>Clostridium putrificum</i>		<i>Cryptococcus laurentii</i>
10	<i>Candida tenuis</i>		<i>Clostridium ramosum</i>		<i>Cryptococcus luteolus</i>
	<i>Candida tropicalis</i>	90	<i>Clostridium septicum</i>		<i>Cryptococcus melibiosum</i>
	<i>Candida utilis</i>		<i>Clostridium sordellii</i>	170	<i>Cryptococcus neoformans</i>
	<i>Candida valida</i>		<i>Clostridium species</i>		<i>Cryptococcus species</i>
	<i>Candida vini</i>		<i>Clostridium sphenoides</i>		<i>Cryptococcus terreus</i>
15	<i>Candida viswanathii</i>		<i>Clostridium sporogenes</i>		<i>Cryptococcus uniguttulatus</i>
	<i>Candida zeylanoides</i>	95	<i>Clostridium subterminale</i>		<i>Debaryomyces hansenii</i>
	<i>Capnocytophaga gingivallis</i>		<i>Clostridium tertium</i>	175	<i>Debaryomyces marasma</i>
	<i>Capnocytophaga ochracea</i>		<i>Clostridium tetani</i>		<i>Debaryomyces polymorphus</i>
20	<i>Capnocytophaga species</i>		<i>Clostridium tyrobutyricum</i>		<i>Debaryomyces species</i>
	<i>Cardiobacterium hominis</i>	100	<i>Comamonas (Pseudomonas) acidovorans</i>		<i>Dermabacter hominis</i>
	<i>Cardiobacterium divergens</i>		<i>Comamonas (Pseudomonas) testosteroni</i>		<i>Dermacoccus (Micrococcus) nishinomiyaensis</i>
	<i>Cardiobacterium piscicola</i>		<i>Comamonas species</i>	180	<i>Dietzia species</i>
25	CDC group ED-2		<i>Corynebacterium accolens</i>		<i>Edwardsiella hoshinae</i>
	CDC group EF4 (<i>Pasteurella</i> sp.)		<i>Corynebacterium afermentans</i>		<i>Edwardsiella ictaluri</i>
	CDC group EF-4A	105	<i>Corynebacterium amycolatum</i>		<i>Edwardsiella species</i>
	CDC group EF-4B		<i>Corynebacterium aquaticum</i>		<i>Edwardsiella tarda</i>
	CDC group EQ-Z		<i>Corynebacterium argenteolactense</i>	185	<i>Eikenella corrodens</i>
	CDC group HB-5		<i>Corynebacterium auris</i>		<i>Empedobacter brevis</i> (<i>Flavobacterium breve</i>)
30	CDC group II K-2		<i>Corynebacterium bovis</i>		<i>Enterobacter aerogenes</i>
	CDC group IV C-2 (<i>Bordetella</i> -like)	110	<i>Corynebacterium coyleae</i>		<i>Enterobacter agglomerans</i>
	CDC group M5		<i>Corynebacterium cystitidis</i>	190	<i>Enterobacter amnigenus</i>
	CDC group M6		<i>Corynebacterium diphtheriae</i>		<i>Enterobacter amnigenus asburiae</i> (CDC enteric group 17)
35	<i>Cedecea davisae</i>		<i>Corynebacterium diphtheriae</i> biotype belfanti		<i>Enterobacter amnigenus biogroup 1</i>
	<i>Cedecea lapagei</i>	115	<i>Corynebacterium diphtheriae</i> biotype gravis		<i>Enterobacter amnigenus biogroup 2</i>
	<i>Cedecea neteri</i>		<i>Corynebacterium diphtheriae</i> biotype intermedius	195	<i>Enterobacter asburiae</i>
	<i>Cedecea species</i>		<i>Corynebacterium diphtheriae</i> biotype mitis		<i>Enterobacter cancerogenus</i>
	<i>Cellulomonas (Oerskovia) turbata</i>		<i>Corynebacterium diphtheriae</i> biotype mitis		<i>Enterobacter cloacae</i>
40	<i>Cellulomonas species</i>	120	<i>Corynebacterium flavescens</i>		<i>Enterobacter gergoviae</i>
	<i>Chlamydia species</i>		<i>Corynebacterium glucuronolyticum</i>	200	<i>Enterobacter hormaechei</i>
	<i>Chromobacterium violaceum</i>		<i>Corynebacterium glucuronolyticum-seminale</i>		<i>Enterobacter intermedius</i>
	<i>Chryseobacterium (Flavobacterium) indologenes</i>	125	<i>Corynebacterium group A</i>		<i>Enterobacter sakazakii</i>
45	<i>Chryseobacterium (Flavobacterium) meningosepticum</i>		<i>Corynebacterium group A-4</i>		<i>Enterobacter species</i>
	<i>Chryseobacterium gleum</i>		<i>Corynebacterium group A-5</i>	205	<i>Enterobacter taylorae</i>
	<i>Chryseomonas indologenes</i>		<i>Corynebacterium group ANF</i>		<i>Enterobacter taylorae</i> (CDC enteric group 19)
50	<i>Citeromyces matritensis</i>		<i>Corynebacterium group B</i>		<i>Enterococcus (Streptococcus) caecorum</i>
	<i>Citrobacter amalonaticus</i>	130	<i>Corynebacterium group B-3</i>		<i>Enterococcus (Streptococcus) faecalis</i> (Group D)
	<i>Citrobacter braakii</i>		<i>Corynebacterium group F</i>	210	<i>Enterococcus (Streptococcus) faecium</i> (Group D)
	<i>Citrobacter diversus</i>		<i>Corynebacterium group F-1</i>		<i>Enterococcus (Streptococcus) faecium</i> (Group D)
	<i>Citrobacter farmeri</i>		<i>Corynebacterium group F-2</i>		<i>Enterococcus (Streptococcus) saccharolyticus</i>
55	<i>Citrobacter freundii</i>		<i>Corynebacterium group G</i>		<i>Enterococcus avium</i> (Group D)
	<i>Citrobacter freundii</i> complex	135	<i>Corynebacterium group G-1</i>	215	<i>Enterococcus casseliflavus</i> (<i>Streptococcus faecium</i> subsp. casseliflavus)
	<i>Citrobacter koseri</i>		<i>Corynebacterium group G-2</i>		<i>Enterococcus durans</i> (<i>Streptococcus faecium</i> subsp. durans) (Group D)
	<i>Citrobacter sedlakii</i>		<i>Corynebacterium group I</i>		<i>Enterococcus gallinarum</i>
	<i>Citrobacter species</i>		<i>Corynebacterium group I-2</i>		<i>Enterococcus hirae</i>
60	<i>Citrobacter werkmanii</i>		<i>Corynebacterium jeikeium</i> (group JK)		<i>Enterococcus malodoratus</i>
	<i>Citrobacter youngae</i>	140	<i>Corynebacterium kutscheri</i> (<i>C. murium</i>)	220	<i>Enterococcus mundtii</i>
	<i>Clostridium acetobutylicum</i>		<i>Corynebacterium macginleyi</i>		<i>Enterococcus raffinosus</i>
	<i>Clostridium baratii</i>		<i>Corynebacterium minutissimum</i>	225	<i>Enterococcus species</i>
65	<i>Clostridium beijerinckii</i>		<i>Corynebacterium pilosum</i>		<i>Erwinia amylovora</i>
	<i>Clostridium bifementans</i>	145	<i>Corynebacterium propinquum</i>		<i>Erwinia carotovora</i>
	<i>Clostridium botulinum</i>		<i>Corynebacterium pseudodiphtheriticum</i>		<i>Erwinia carotovora</i> subsp. atroseptica
	<i>Clostridium botulinum</i> (NP) B&F		<i>Corynebacterium pseudotuberculosis</i>	230	<i>Erwinia carotovora</i> subsp. carotovora
	<i>Clostridium botulinum</i> (NP) E		<i>Corynebacterium pyogenes</i>		<i>Erwinia chrysanthemi</i>
	<i>Clostridium botulinum</i> (P) A&H		<i>Corynebacterium renale</i>		<i>Erwinia cyprinidii</i>
70	<i>Clostridium botulinum</i> (P) F	150	<i>Corynebacterium renale</i> group		<i>Erwinia malitiosa</i>
	<i>Clostridium botulinum</i> G1		<i>Corynebacterium seminale</i>		
	<i>Clostridium botulinum</i> G2		<i>Corynebacterium species</i>		
	<i>Clostridium butyricum</i>		<i>Corynebacterium striatum</i> (<i>C. flavidum</i>)		
	<i>Clostridium cadaveris</i>	155	<i>Corynebacterium ulcerans</i>		
75	<i>Clostridium chauvoei</i>				
	<i>Clostridium clostridioforme</i>				
	<i>Clostridium difficile</i>				
	<i>Clostridium fallax</i>				
	<i>Clostridium glycolicum</i>				

Table 15. Microorganisms identified by automated systems (continued).

Erwinia nigrifluens	80	VII	Haemophilus parainfluenzae biotype	160	Lactobacillus paracasei subsp. paracasei
Erwinia quercina		VIII	Haemophilus paraphrohaemolyticus		Lactobacillus pentosus
Erwinia raphontici			Haemophilus paraphrophilus		Lactobacillus plantarum
Erwinia rubifaciens			Haemophilus segnis		Lactobacillus salivarius
5 Erwinia salicis			Haemophilus somnus		Lactobacillus salivarius var. salicinius
Erwinia species			Haemophilus species		Lactobacillus species
Erysipelothrix rhusiopathiae	85		Hafnia alvei	165	Lactococcus diacetylactis
Erysipelothrix species			Hanseniaspora guilliermondii		Lactococcus garvieae
Escherichia blattae			Hanseniaspora uvarum		Lactococcus lactis subsp. cremoris
10 Escherichia coli			Hanseniaspora valbyensis		Lactococcus lactis subsp. diacetylactis
Escherichia coli A-D			Hansenula anomala		Lactococcus lactis subsp. hordniae
Escherichia coli O157:H7	90		Hansenula holstii	170	Lactococcus plantarum
Escherichia fergusonii			Hansenula polymorpha		Lactococcus raffinolactis
Escherichia hermannii			Helicobacter (Campylobacter) cinaedi		Leclercia adecarboxylata
Escherichia species			Helicobacter (Campylobacter) fennelliae		Legionella species
Escherichia vulneris	95		Helicobacter (Campylobacter) pylori	175	Leminorella species
Eubacterium aerofaciens			Issatchenkia orientalis		Leptospira species
Eubacterium alactolyticum			Kingella denitrificans		Leptotrichia buccalis
Eubacterium lentum			Kingella indologenes		Leuconostoc (Weissella) paramesenteroides
20 Eubacterium limosum			Kingella kingae	180	Leuconostoc carnosum
Eubacterium species	100		Kingella species		Leuconostoc citreum
Ewingella americana			Klebsiella ornithinolytica		Leuconostoc gelidum
Filobasidium neoformans			Klebsiella oxytoca		Leuconostoc lactis
Filobasidium floriforme			Klebsiella planticola		Leuconostoc mesenteroides
25 Filobasidium unguiculatum	105		Klebsiella pneumoniae subsp. ozaenae	185	Leuconostoc mesenteroides subsp. cremoris
Flavimonas oryzae habitans			Klebsiella pneumoniae subsp. pneumoniae		Leuconostoc mesenteroides subsp. dextranicum
Flavobacterium gleum			Klebsiella pneumoniae subsp. rhinoscleromatis	190	Leuconostoc species
Flavobacterium indologenes			Klebsiella species		Listeria grayi
Flavobacterium odoratum			Klebsiella terrigena		Listeria innocua
30 Flavobacterium species	110		Kloeckera apiculata		Listeria ivanovii
Francisella novicida			Kloeckera apis		Listeria monocytogenes
Francisella philomiragia			Kloeckera japonica	195	Listeria murrayi
Francisella species			Kloeckera species		Listeria seeligeri
Francisella tularensis			Kluyvera ascorbata		Listeria species
35 Fusobacterium mortiferum	115		Kluyvera cryocrescens		Listeria welshimeri
Fusobacterium necrogenes			Kluyvera species	200	Megasphaera elsdenii
Fusobacterium necrophorum			Kluyveromyces lactis		Methylobacterium mesophilicum
Fusobacterium nucleatum			Kluyveromyces marxianus		Metschnikowia pulcherrima
Fusobacterium species			Kluyveromyces thermotolerans		Microbacterium species
40 Fusobacterium varium			Kocuria (Micrococcus) kristinae		Micrococcus luteus
Gaffkya species			Kocuria (Micrococcus) rosea		Micrococcus lylae
Gardnerella vaginalis			Kocuria (Micrococcus) varians	205	Micrococcus species
Gemella haemolysans			Koserella trabulsii		Mobiluncus curtisii
Gemella morbillorum			Kytococcus (Micrococcus) sedentarius		Mobiluncus mulieris
45 Gemella species	125		Lactobacillus (Weissella) viridescens		Mobiluncus species
Geotrichum candidum			Lactobacillus A		Moellerella wisconsensis
Geotrichum fermentans			Lactobacillus acidophilus	210	Moraxella (Branhamella) catarrhalis
Geotrichum penicilliarum			Lactobacillus B		Moraxella atlantae
Geotrichum penicilliatum			Lactobacillus brevis		Moraxella bovis
50 Geotrichum species			Lactobacillus buchneri		Moraxella lacunata
Gordona species			Lactobacillus casei		Moraxella nonliquefaciens
Haemophilus aegyptius			Lactobacillus casei subsp. casei	215	Moraxella osloensis
Haemophilus aphrophilus			Lactobacillus casei subsp. lactosus		Moraxella phenylpyruvica
Haemophilus ducreyi			Lactobacillus casei subsp. rhamnosus		Moraxella species
55 Haemophilus haemoglobinophilus			Lactobacillus cateniformis		Morganella morganii
Haemophilus haemolyticus			Lactobacillus cellobiosus		Morganella morganii subsp. morganii
Haemophilus influenzae			Lactobacillus collinoides	220	Morganella morganii subsp. sibonii
Haemophilus influenzae biotype I			Lactobacillus coprophilus		Mycobacterium africanum
Haemophilus influenzae biotype II			Lactobacillus crispatus		Mycobacterium asiaticum
Haemophilus influenzae biotype III			Lactobacillus curvatus		Mycobacterium avium
Haemophilus influenzae biotype IV			Lactobacillus delbrueckii subsp. bulgaricus	225	Mycobacterium bovis
Haemophilus influenzae biotype V			Lactobacillus delbrueckii subsp. delbrueckii		Mycobacterium chelonae
Haemophilus influenzae biotype VI			Lactobacillus delbrueckii subsp. lactis		Mycobacterium fortuitum
Haemophilus influenzae biotype VII			Lactobacillus fermentum		Mycobacterium gordonae
Haemophilus influenzae biotype VIII			Lactobacillus fructivorans	230	Mycobacterium kansasii
Haemophilus paragallinarum			Lactobacillus helveticus		Mycobacterium malmoense
Haemophilus parahaemolyticus			Lactobacillus helveticus subsp. jugurti		Mycobacterium marinum
Haemophilus parainfluenzae			Lactobacillus jensenii		Mycobacterium phlei
Haemophilus parainfluenzae biotype I			Lactobacillus lindneri		Mycobacterium scrofulaceum
Haemophilus parainfluenzae biotype II			Lactobacillus minutus		Mycobacterium smegmatis
Haemophilus parainfluenzae biotype III					Mycobacterium species
Haemophilus parainfluenzae biotype IV					
75 Haemophilus parainfluenzae biotype V					
Haemophilus parainfluenzae biotype VI					
Haemophilus parainfluenzae biotype VII					

Table 15. Microorganisms identified by automated systems (continued).

5	<i>Mycobacterium tuberculosis</i>	80	<i>Pichia fermentans</i>	160	<i>Saccharomyces exiguus</i>
	<i>Mycobacterium ulcerans</i>		<i>Pichia membranaefaciens</i>		<i>Saccharomyces kluyveri</i>
	<i>Mycobacterium xenopi</i>		<i>Pichia norvegensis</i>		<i>Saccharomyces species</i>
	<i>Mycoplasma fermentans</i>		<i>Pichia ohmeri</i>		<i>Sakaguchia dacryoides</i>
	<i>Mycoplasma hominis</i>		<i>Pichia spartinae</i>		(<i>Rhodospiridium dacryoidum</i>)
	<i>Mycoplasma orale</i>		<i>Pichia species</i>		<i>Salmonella arizonae</i>
	<i>Mycoplasma pneumoniae</i>	85	<i>Plesiomonas shigelloides</i>		<i>Salmonella choleraesuis</i>
	<i>Mycoplasma species</i>		<i>Porphyromonas asaccharolytica</i>	165	<i>Salmonella enteritidis</i>
	<i>Myroides species</i>		<i>Porphyromonas endodontalis</i>		<i>Salmonella gallinarum</i>
10	<i>Neisseria cinerea</i>		<i>Porphyromonas gingivalis</i>		<i>Salmonella paratyphi A</i>
	<i>Neisseria elongata</i> subsp. <i>elongata</i>		<i>Porphyromonas levii</i>		<i>Salmonella paratyphi B</i>
	<i>Neisseria flava</i>	90	<i>Prevotella (Bacteroides) buccae</i>		<i>Salmonella pullorum</i>
	<i>Neisseria flavescens</i>		<i>Prevotella (Bacteroides) buccalis</i>	170	<i>Salmonella species</i>
	<i>Neisseria gonorrhoeae</i>		<i>Prevotella (Bacteroides) corporis</i>		<i>Salmonella typhi</i>
15	<i>Neisseria lactamica</i>		<i>Prevotella (Bacteroides) denticola</i>		<i>Salmonella typhimurium</i>
	<i>Neisseria meningitidis</i>		<i>Prevotella (Bacteroides) loeschii</i>		<i>Salmonella typhisuis</i>
	<i>Neisseria mucosa</i>	95	<i>Prevotella (Bacteroides) oralis</i>		<i>Salmonella/Arizona</i>
	<i>Neisseria perflava</i>		<i>Prevotella (Bacteroides) disiens</i>	175	<i>Serratia ficaria</i>
	<i>Neisseria polysaccharea</i>		<i>Prevotella (Bacteroides) oris</i>		<i>Serratia fonticola</i>
20	<i>Neisseria saprophytes</i>		<i>Prevotella bivia (Bacteroides bivius)</i>		<i>Serratia grimesii</i>
	<i>Neisseria sicca</i>	100	<i>Prevotella intermedia (Bacteroides intermedius)</i>		<i>Serratia liquefaciens</i>
	<i>Neisseria subflava</i>		<i>Prevotella melaninogenica (Bacteroides melaninogenicus)</i>	180	<i>Serratia marcescens</i>
	<i>Neisseria weaveri</i>		<i>Prevotella ruminicola</i>		<i>Serratia odorifera</i>
	<i>Neisseria weaveri</i> (CDC group M5)		<i>Propionibacterium acnes</i>		<i>Serratia odorifera</i> type 1
25	<i>Nocardia species</i>		<i>Propionibacterium avidum</i>		<i>Serratia odorifera</i> type 2
	<i>Ochrobactrum anthropi</i>	105	<i>Propionibacterium granulosum</i>		<i>Serratia phymuthica</i>
	<i>Oerskovia species</i>		<i>Propionibacterium propionicum</i>	185	<i>Serratia proteamaculans</i>
	<i>Oerskovia xanthineolytica</i>		<i>Propionibacterium propionicum</i>		<i>Serratia proteamaculans</i> subsp.
	<i>Oligella (Moraxella) urethralis</i>		<i>Propionibacterium species</i>		<i>proteamaculans</i>
30	<i>Oligella species</i>		<i>Proteus mirabilis</i>		<i>Serratia proteamaculans</i> subsp.
	<i>Oligella ureolytica</i>	110	<i>Proteus penneri</i>		<i>quinovora</i>
	<i>Paenibacillus alvei</i>		<i>Proteus species</i>	190	<i>Serratia rubidaea</i>
	<i>Paenibacillus macerans</i>		<i>Proteus vulgaris</i>		<i>Serratia species</i>
	<i>Paenibacillus polymyxa</i>		<i>Prototheca species</i>		<i>Shewanella (Pseudomonas, Alteromonas) putrefaciens</i>
35	<i>Pantoea agglomerans</i>		<i>Prototheca wickerhamii</i>		<i>Shigella boydii</i>
	<i>Pantoea ananas (Erwinia uredovora)</i>	115	<i>Prototheca zopfii</i>		<i>Shigella dysenteriae</i>
	<i>Pantoea dispersa</i>		<i>Providencia alcalifaciens</i>		<i>Shigella flexneri</i>
	<i>Pantoea species</i>		<i>Providencia heimbachae</i>	195	<i>Shigella sonnei</i>
	<i>Pantoea stewartii</i>		<i>Providencia rettgeri</i>		<i>Shigella species</i>
40	<i>Pasteurella (Haemophilus) avium</i>		<i>Providencia rustigianii</i>		<i>Sphingobacterium multivorum</i>
	<i>Pasteurella aerogenes</i>	120	<i>Providencia species</i>		<i>Sphingobacterium species</i>
	<i>Pasteurella gallinarum</i>		<i>Providencia stuartii</i>		<i>Sphingobacterium spiritivorum</i>
	<i>Pasteurella haemolytica</i>		<i>Providencia stuartii urea + Pseudomonas (Chryseomonas) luteola</i>	200	<i>Sphingobacterium thalpophilum</i>
	<i>Pasteurella haemolyticus</i>				<i>Sphingomonas (Pseudomonas) paucimobilis</i>
45	<i>Pasteurella multocida</i>				<i>Sporidiobolus salmonicolor</i>
	<i>Pasteurella multocida SF</i>	125	<i>Pseudomonas acidovorans</i>		<i>Sporobolomyces roseus</i>
	<i>Pasteurella multocida</i> subsp. <i>multocida</i>		<i>Pseudomonas aeruginosa</i>	205	<i>Sporobolomyces salmonicolor</i>
	<i>Pasteurella multocida</i> subsp. <i>septica</i>		<i>Pseudomonas alcaligenes</i>		<i>Sporobolomyces species</i>
50	<i>Pasteurella pneumotropica</i>		<i>Pseudomonas cepacia</i>		<i>Staphylococcus (Peptococcus) saccharolyticus</i>
	<i>Pasteurella species</i>	130	<i>Pseudomonas chlororaphis (P. aureofaciens)</i>		<i>Staphylococcus arlettae</i>
	<i>Pasteurella ureae</i>		<i>Pseudomonas fluorescens</i>	210	<i>Staphylococcus aureus</i>
	<i>Pediococcus acidilactici</i>		<i>Pseudomonas fluorescens</i> group		<i>Staphylococcus aureus (Coagulase-negative)</i>
	<i>Pediococcus damnosus</i>		<i>Pseudomonas mendocina</i>		<i>Staphylococcus auricularis</i>
55	<i>Pediococcus pentosaceus</i>		<i>Pseudomonas pseudoalcaligenes</i>		<i>Staphylococcus capitis</i>
	<i>Pediococcus species</i>	135	<i>Pseudomonas putida</i>		<i>Staphylococcus capitis</i> subsp. <i>capitis</i>
	<i>Peptococcus niger</i>		<i>Pseudomonas species</i>	215	<i>Staphylococcus capitis</i> subsp. <i>ureolyticus</i>
	<i>Peptococcus species</i>		<i>Pseudomonas stutzeri</i>		<i>Staphylococcus caprae</i>
60	<i>Peptostreptococcus anaerobius</i>		<i>Pseudomonas testosteroni</i>		<i>Staphylococcus camosus</i>
	<i>Peptostreptococcus asaccharolyticus</i>		<i>Pseudomonas vesicularis</i>		<i>Staphylococcus caseolyticus</i>
	<i>Peptostreptococcus indolicus</i>	140	<i>Pseudoramibacter (Eubacterium) alactolyticus</i>	220	<i>Staphylococcus chromogenes</i>
	<i>Peptostreptococcus magnus</i>		<i>Psychrobacter (Moraxella) phenylpyruvicus</i>		<i>Staphylococcus cohnii</i>
	<i>Peptostreptococcus micros</i>		<i>Rahnella aquatilis</i>		<i>Staphylococcus cohnii</i> subsp. <i>cohnii</i>
65	<i>Peptostreptococcus parvulus</i>		<i>Ralstonia (Pseudomonas, Burkholderia) pickettii</i>	225	<i>Staphylococcus cohnii</i> subsp. <i>urealyticum</i>
	<i>Peptostreptococcus prevotii</i>		<i>Rhodococcus (Corynebacterium) equi</i>		<i>Staphylococcus epidermidis</i>
	<i>Peptostreptococcus productus</i>		<i>Rhodococcus species</i>		<i>Staphylococcus equorum</i>
	<i>Peptostreptococcus species</i>	145	<i>Rhododermatitis toruloides</i>		<i>Staphylococcus gallinarum</i>
	<i>Peptostreptococcus tetradius</i>		<i>Rhodotorula glutinis</i>		<i>Staphylococcus haemolyticus</i>
	<i>Phaeococcomyces exophialae</i>	150	<i>Rhodotorula minuta</i>	230	<i>Staphylococcus hominis</i>
70	<i>Photobacterium damsela</i>		<i>Rhodotorula mucilaginosa (R. rubra)</i>		<i>Staphylococcus hominis</i> subsp. <i>hominis</i>
	<i>Pichia (Hansenula) anomala</i>		<i>Rhodotorula species</i>		<i>Staphylococcus hominis</i> subsp. <i>novobiosepticus</i>
	<i>Pichia (Hansenula) jadinii</i>		<i>Rickettsia species</i>		
	<i>Pichia (Hansenula) petersonii</i>	155	<i>Rothia dentocariosa</i>		
	<i>Pichia angusta (Hansenula polymorpha)</i>		<i>Saccharomyces cerevisiae</i>		
75	<i>Pichia carsonii (P. vini)</i>				
	<i>Pichia etchellsii</i>				
	<i>Pichia farinosa</i>				

Table 15. Microorganisms identified by automated systems (continued).

	<i>Staphylococcus hyicus</i>	60	<i>Streptococcus</i> Gamma (non)-hemolytic	120	<i>Tetragenococcus</i> (<i>Pediococcus</i>) <i>halophilus</i>
	<i>Staphylococcus intermedius</i>		<i>Streptococcus gordonii</i>		<i>Torulaspora delbrueckii</i>
5	<i>Staphylococcus kloosii</i>		<i>Streptococcus</i> Group B		(<i>Saccharomyces rosei</i>)
	<i>Staphylococcus lentus</i>	65	<i>Streptococcus</i> Group C		<i>Torulopsis candida</i>
	<i>Staphylococcus lugdunensis</i>		<i>Streptococcus</i> Group D	125	<i>Torulopsis haemulonii</i>
	<i>Staphylococcus saprophyticus</i>		<i>Streptococcus</i> Group E		<i>Torulopsis inconspicua</i>
	<i>Staphylococcus schleiferi</i>		<i>Streptococcus</i> Group F		<i>Treponema</i> species
10	<i>Staphylococcus sciuri</i>		<i>Streptococcus</i> Group G		<i>Trichosporon asahii</i>
	<i>Staphylococcus simulans</i>	70	<i>Streptococcus</i> Group L		<i>Trichosporon asteroides</i>
	<i>Staphylococcus species</i>		<i>Streptococcus</i> Group P		<i>Trichosporon beigeli</i>
	<i>Staphylococcus warneri</i>		<i>Streptococcus</i> Group U	130	<i>Trichosporon cutaneum</i>
	<i>Staphylococcus xylosum</i>		<i>Streptococcus intermedius</i>		<i>Trichosporon inkin</i>
15	<i>Stenotrophomonas</i> (<i>Xanthomonas</i>) <i>maltophilia</i>		<i>Streptococcus intermedius</i> (<i>Streptococcus milleri</i> II)		<i>Trichosporon mucoides</i>
	<i>Stephanosascus cliffernii</i>	75	<i>Streptococcus intermedius</i> (<i>Streptococcus milleri</i> II)		<i>Trichosporon ovoides</i>
	<i>Stomatococcus mucilaginosus</i>		<i>Streptococcus intermedius</i> (<i>Streptococcus milleri</i> II)	135	<i>Trichosporon pullulans</i>
	<i>Streptococcus acidominimus</i>		<i>Streptococcus mitis</i>		<i>Trichosporon species</i>
20	<i>Streptococcus agalactiae</i>		<i>Streptococcus mitis</i> (<i>Streptococcus mitis</i> group)		<i>Tunicella otitidis</i>
	<i>Streptococcus agalactiae</i> (Group B)	80	<i>Streptococcus mutans</i>		<i>Ureaplasma</i> species
	<i>Streptococcus agalactiae</i> hemolytic		<i>Streptococcus mutans</i> (<i>Streptococcus mutans</i> group)		<i>Ureaplasma urealyticum</i>
	<i>Streptococcus agalactiae</i> non-hemolytic		<i>Streptococcus mutans</i> (<i>Streptococcus mutans</i> group)	140	<i>Veillonella parvula</i> (<i>V. alcalescens</i>)
25	<i>Streptococcus alactolyticus</i>		<i>Streptococcus mutans</i> (<i>Streptococcus mutans</i> group)		<i>Veillonella species</i>
	<i>Streptococcus anginosus</i>	85	<i>Streptococcus mutans</i> (<i>Streptococcus mutans</i> group)		<i>Vibrio alginolyticus</i>
	<i>Streptococcus anginosus</i> (Group D, nonenterococci)		<i>Streptococcus oralis</i>		<i>Vibrio cholerae</i>
	<i>Streptococcus beta-hemolytic group A</i>		<i>Streptococcus parasanguis</i>	145	<i>Vibrio damsela</i>
30	<i>Streptococcus beta-hemolytic non-group A or B</i>		<i>Streptococcus pneumoniae</i>		<i>Vibrio fluvialis</i>
	<i>Streptococcus beta-hemolytic non-group A</i>	90	<i>Streptococcus pyogenes</i>		<i>Vibrio furnissii</i>
	<i>Streptococcus beta-hemolytic</i>		<i>Streptococcus pyogenes</i> (Group A)		<i>Vibrio harveyi</i>
	<i>Streptococcus bovis</i> (Group D, nonenterococci)		<i>Streptococcus salivarius</i>	150	<i>Vibrio holtsiae</i>
35	<i>Streptococcus bovis</i> I		<i>Streptococcus salivarius</i> (viridans)		<i>Vibrio metschnikovii</i>
	<i>Streptococcus bovis</i> II	95	<i>Streptococcus salivarius</i> (viridans)		<i>Vibrio mimicus</i>
	<i>Streptococcus canis</i>		<i>Streptococcus salivarius</i> subsp. <i>salivarius</i>		<i>Vibrio parahaemolyticus</i>
40	<i>Streptococcus constellatus</i>		<i>Streptococcus salivarius</i> subsp. <i>thermophilus</i>		<i>Vibrio species</i>
	<i>Streptococcus constellatus</i> (<i>Streptococcus milleri</i> I)	100	<i>Streptococcus sanguis</i>		<i>Vibrio species SF</i>
	<i>Streptococcus constellatus</i> (viridans)		<i>Streptococcus sanguis</i> I (viridans)		<i>Vibrio vulnificus</i>
	<i>Streptococcus constellatus</i> (viridans)		<i>Streptococcus sanguis</i> II (viridans)	155	<i>Weeksella</i> (<i>Bergeyella</i>) <i>virosa</i>
45	<i>Streptococcus downei</i>		<i>Streptococcus sanguis</i> II (viridans)		<i>Weeksella virosa</i>
	<i>Streptococcus dysgalactiae</i> subsp. <i>dysgalactiae</i>	105	<i>Streptococcus sobrinus</i>		<i>Williopsis</i> (<i>Hansenula</i>) <i>saturus</i>
	<i>Streptococcus dysgalactiae</i> subsp. <i>equisimilis</i>		<i>Streptococcus species</i>		<i>Xanthomonas campestris</i>
50	<i>Streptococcus equi</i> (Group C/Group G)		<i>Streptococcus suis</i> I	160	<i>Xanthomonas species</i>
	<i>Streptococcus equi</i> subsp. <i>equi</i>		<i>Streptococcus suis</i> II		<i>Yarrowia</i> (<i>Candida</i>) <i>lipolytica</i>
	<i>Streptococcus equi</i> subsp. <i>zooepidemicus</i>	110	<i>Streptococcus uberis</i>		<i>Yersinia aldovae</i>
55	<i>Streptococcus equinus</i>		<i>Streptococcus uberis</i> (viridans)		<i>Yersinia enterocolitica</i>
	<i>Streptococcus equinus</i> (Group D, nonenterococci)		<i>Streptococcus vestibularis</i>	165	<i>Yersinia enterocolitica</i> group
	<i>Streptococcus equisimilis</i>		<i>Streptococcus zooepidemicus</i>		<i>Yersinia frederiksenii</i>
	<i>Streptococcus equisimilis</i> (Group C/Group G <i>Streptococcus</i>)	115	<i>Streptococcus zooepidemicus</i> (Group C)		<i>Yersinia intermedia</i>
			<i>Streptomyces somaliensis</i>	170	<i>Yersinia intermedius</i>
			<i>Streptomyces species</i>		<i>Yersinia kristensenii</i>
			<i>Suttonella</i> (<i>Kingella</i>) <i>indologenes</i>	175	<i>Yersinia pestis</i>
			<i>Tatumella ptyseos</i>		<i>Yersinia pseudotuberculosis</i>
					<i>Yersinia pseudotuberculosis</i> SF
					<i>Yersinia ruckeri</i>
					<i>Yersinia species</i>
					<i>Yokenella regensburgi</i>
					<i>Yokenella regensburgi</i> (<i>Koserella trabulsi</i>)
					<i>Zygoascus hellenicus</i>
					<i>Zygosaccharomyces</i> species

Figure 1: *atpD* sequences databases and main subsets.

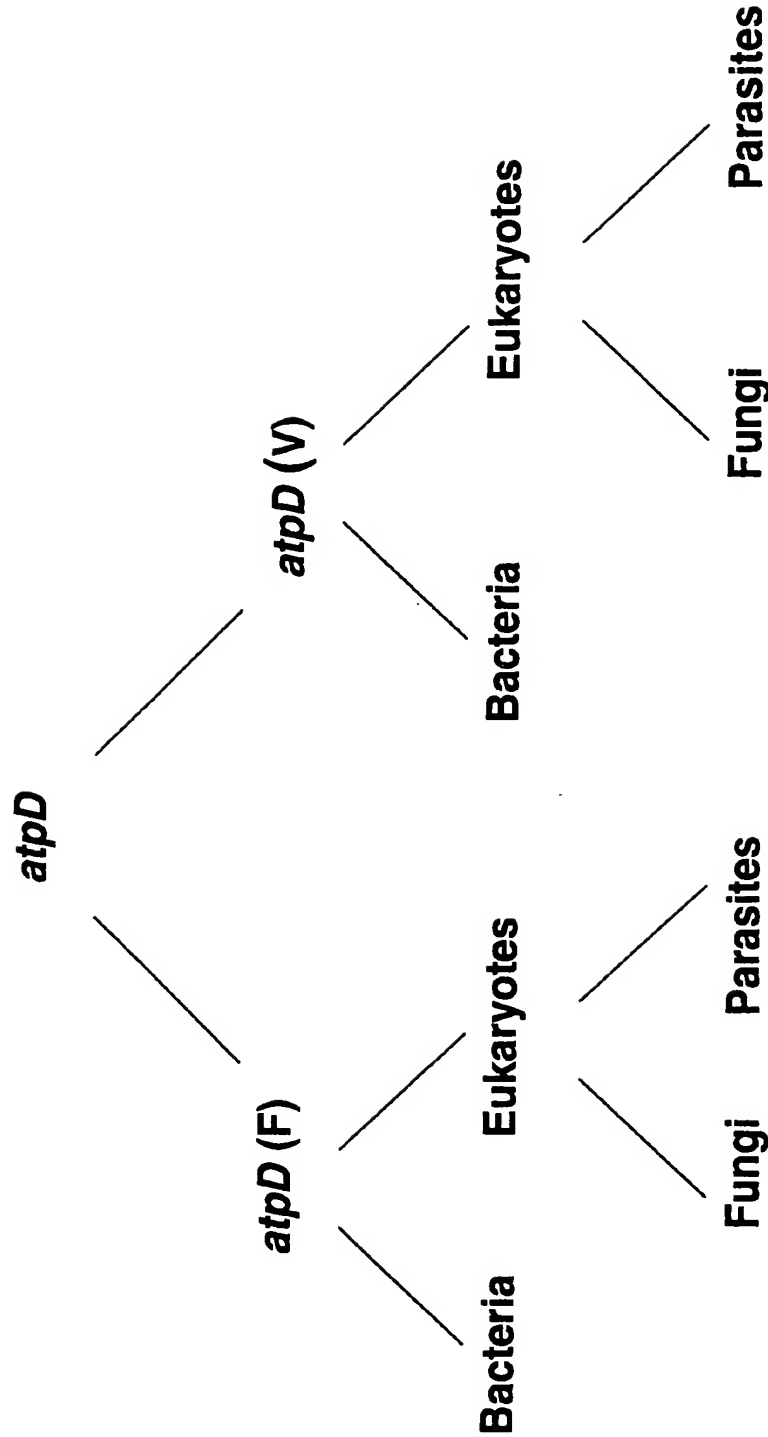


Figure 2: *tuf* sequences databases and main subsets.

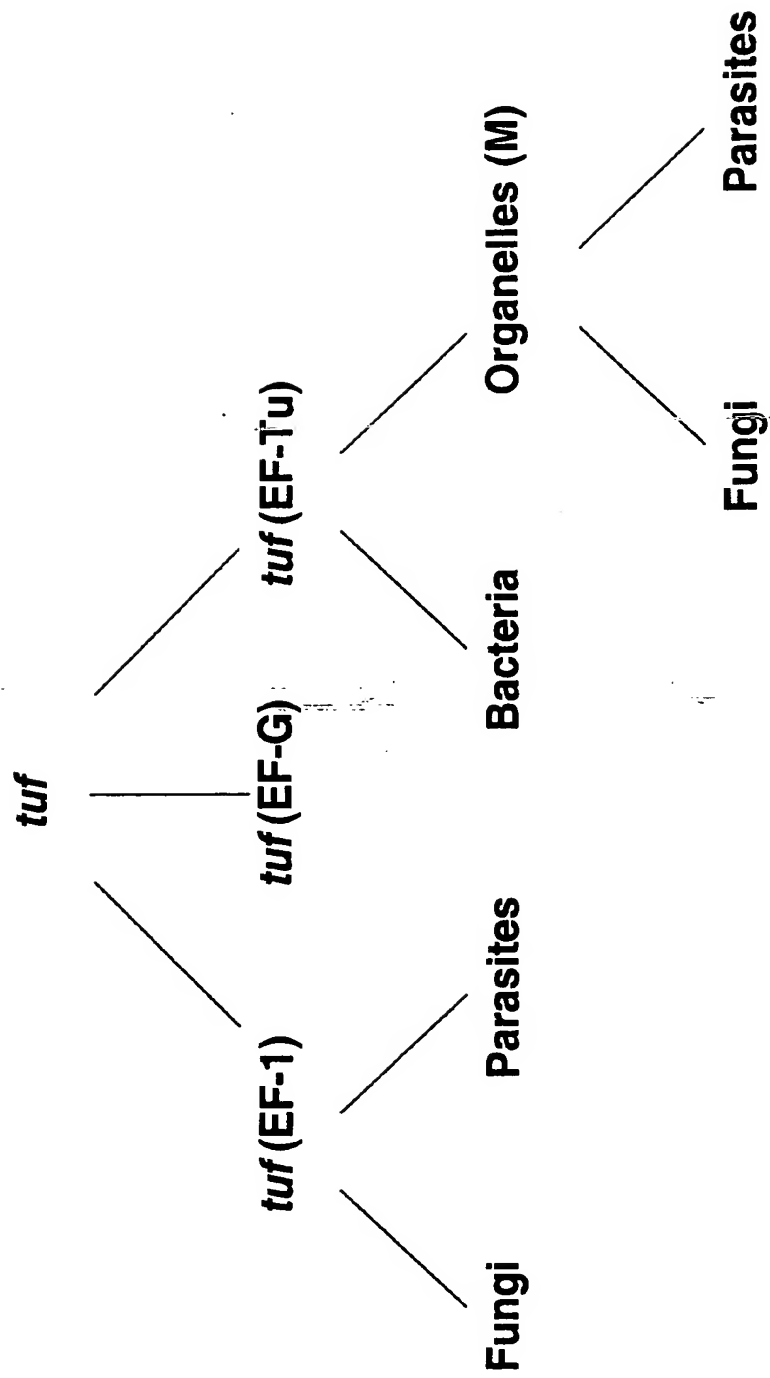
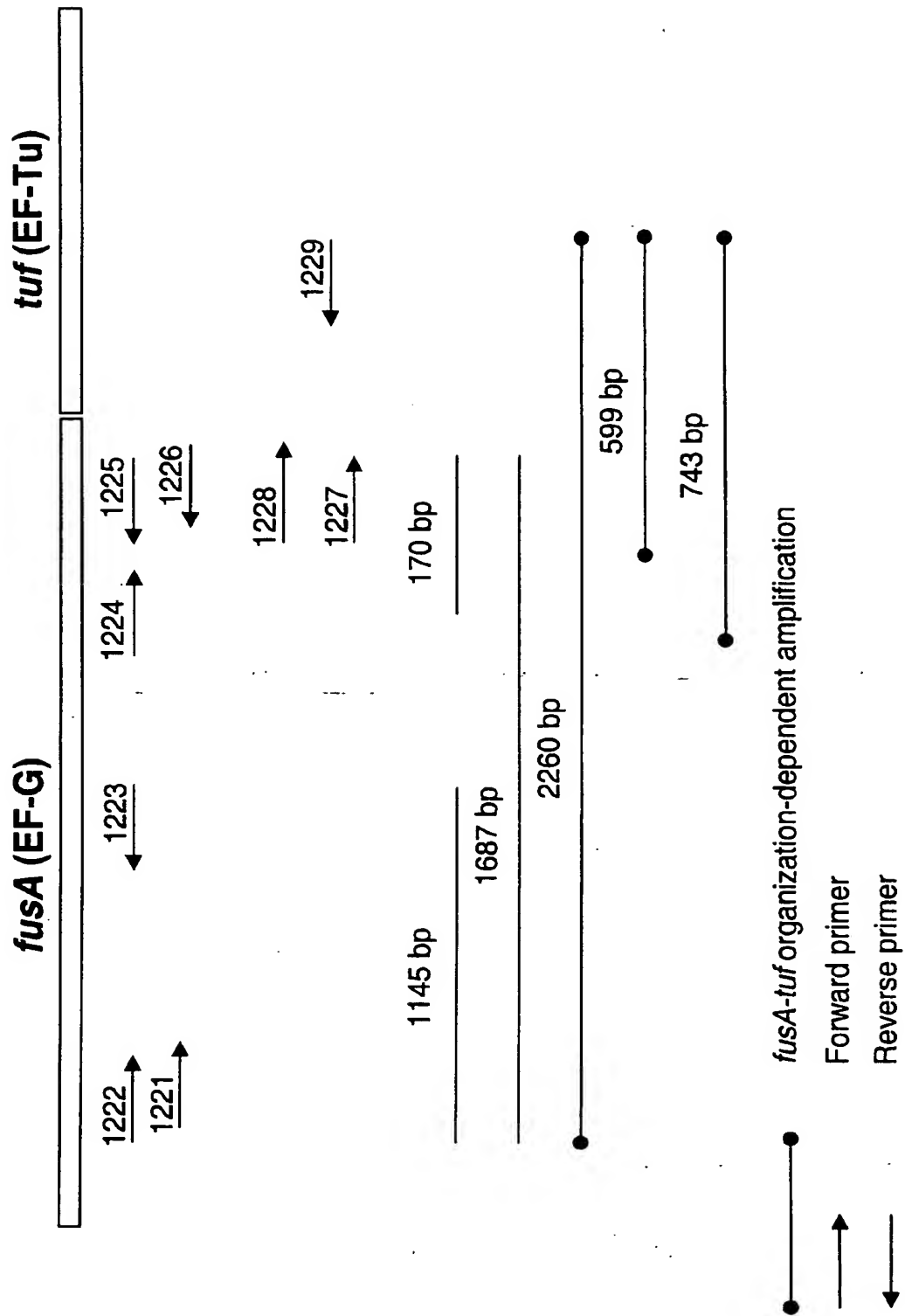


Figure 3: Schematic organization of universal amplification primers in the *str* operon.



Annex I: Specific and ubiquitous primers for nucleic acid amplification (tuf sequences).

5			Originating DNA fragment	
	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	Bacterial species: <i>Chlamydia pneumoniae</i>			
	630	5'-CGG AGC TAT CCT AGT CGT TTC A	20	2-23
	629 ^a	5'-AAG TTC CAT CTC AAC AAG GTC AAT A	20	146-170
15	Bacterial species: <i>Chlamydia trachomatis</i>			
	554	5'-GTT CCT TAC ATC GTT GTT TTT CTC	22	82-105
	555 ^a	5'-TCT CGA ACT TTC TCT ATG TAT GCA	22	249-272
20	Parasitical species: <i>Cryptosporidium parvum</i>			
	798	5'-TGG TTG TCC CAG CCG ATC GTT T	865	158-179
	804 ^a	5'-CCT GGG ACG GCC TCT GGC AT	865	664-683
25	799	5'-ACC TGT GAA TAC AAG CAA TCT	865	280-300
	805 ^a	5'-CTC TTG TCC ATC TTA GCA GT	865	895-914
	800	5'-GAT GAA ATC TTC AAC GAA GTT GAT	865	307-330
	806 ^a	5'-AGC ATC ACC AGA CTT GAT AAG	865	946-966
30	801	5'-ACA ACA CCG AGA AGA TCC CA	865	353-372
	803 ^a	5'-ACT TCA GTG-GTA ACA-CCA GC-	865	616-635
	802	5'-TTG CCA TTT CTG GTT TCG TT	865	377-396
35	807 ^a	5'-AAA GTG GCT TCA AAG GTT GC	865	981-1000
	Bacterial species: <i>Neisseria gonorrhoeae</i>			
	551	5'-GAA GAA AAA ATC TTC GAA CTG GCT A	126	256-280
40	552 ^a	5'-TAC ACG GCC GGT GAC TAC G	126	378-396
	Bacterial species: <i>Streptococcus agalactiae</i>			
	549	5'-GAA CGT GAT ACT GAC AAA CCT TTA	207-210 ^b	308-331 ^c
45	550 ^a	5'-GAA GAA GAA CAC CAA CGT TG	207-210 ^b	520-539 ^c
	Bacterial species: <i>Streptococcus pyogenes</i>			
	999	5'-TTG ACC TTG TTG ATG ACG AAG AG	1002	143-165
50	1000 ^a	5'-TTA GTG TGT GGG TTG ATT GAA CT	1002	622-644
	1001	5'-AAG AGT TGC TTG AAT TAG TTG AG	1002	161-183
	1000 ^a	5'-TTA GTG TGT GGG TTG ATT GAA CT	1002	622-644

^a These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

^b These sequences were aligned to derive the corresponding primer.

^c The nucleotide positions refer to the *S. agalactiae* tuf sequence fragment (SEQ ID NO. 209).

Annex I: Specific and ubiquitous primers for nucleic acid amplification (tuf sequences) (continued).

			Originating DNA fragment	
5	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	<u>Parasitital species:</u> <i>Trypanosoma brucei</i>			
	820	5'-GAA GGA GGT GTC TGC TTA CAC	864	513-533
	821 ^a	5'-GGC GCA AAC GTC ACC ACA TCA	864	789-809
15	820	5'-GAA GGA GGT GTC TGC TTA CAC	864	513-533
	822 ^a	5'-CGG CGG ATG TCC TTA ACA GAA	864	909-929
	<u>Parasitital species:</u> <i>Trypanosoma cruzi</i>			
20	794	5'-GAC GAC AAG TCG GTG AAC TT	840-842 ^b	281-300 ^c
	795 ^a	5'-ACT TGC ACG CGA TGT GGC AG	840-842 ^b	874-893 ^c
	<u>Bacterial genus:</u> <i>Bordetella sp.</i>			
25	825	5'-ATG AGC ARC GSA ACC ATC GTT CAG TG	863	1-26
	826	5'-TCG ATC GTG CCG ACC ATG TAG AAC GC	863	1342-1367
	<u>Fungal genus:</u> <i>Candida sp.</i>			
30	576	5'-AAC TTC RTC AAG AAG GTY GGT TAC AA	407-426, 428-432 ^b	332-357 ^d
	632 ^a	5'-CCC TTT GGT GGR TCS TKC TTG GA	407-426, 428-432 ^b	791-813 ^d
35	631	5'-CAG ACC AAC YGA IAA RCC ATT RAG AT	407-426, 428-432 ^b	523-548 ^d
	632 ^a	5'-CCC TTT GGT GGR TCS TKC TTG GA	407-426, 428-432 ^b	791-813 ^d
40	633	5'-CAG ACC AAC YGA IAA RCC ITT RAG AT	407-426, 428-432 ^b	523-548 ^d
	632 ^a	5'-CCC TTT GGT GGR TCS TKC TTG GA	407-426, 428-432 ^b	791-813 ^d

- 45
- ^a These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.
- ^b These sequences were aligned to derive the corresponding primer.
- 50 ^c The nucleotide positions refer to the *T. cruzi* tuf sequence fragment (SEQ ID NO. 842).
- ^d The nucleotide positions refer to the *C. albicans* tuf(EF-1) sequence fragment (SEQ ID NO. 408).

Annex I: Specific and ubiquitous primers for nucleic acid amplification (tuf sequences) (continued).

			Originating DNA fragment	
5	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	<u>Bacterial genus:</u> <i>Clostridium</i> sp.			
	796	5'-GGT CCA ATG CCW CAA ACW AGA	32,719-724,736 ^a	32-52 ^b
	797 ^c	5'-CAT TAA GAA TGG YTT ATC TGT SKC TCT	32,719-724,736 ^a	320-346 ^b
15	808	5'-GCI TTA IWR GCA TTA GAA RAY CCA	32,719-724,736 ^a	224-247 ^b
	809 ^c	5'-TCT TCC TGT WGC AAC TGT TCC TCT	32,719-724,736 ^a	337-360 ^b
20	810	5'-AGA GMW ACA GAT AAR SCA TTC TTA	32,719-724,736 ^a	320-343 ^b
	811 ^c	5'-TRA ART AGA ATT GTG GTC TRT ATC C	32,719-724,736 ^a	686-710 ^b
25	<u>Bacterial genus:</u> <i>Corynebacterium</i> sp.			
	545	5'-TAC ATC CTB GTY GCI CTI AAC AAG TG	34-44,662 ^a	89-114 ^d
	546 ^c	5'-CCR CGI CCG GTR ATG GTG AAG AT	34-44,662 ^a	350-372 ^d
30	<u>Parasitical genus:</u> <i>Entamoeba</i> sp.			
	703	5'-TAT GGA AAT TCG AAA CAT CT	512	38-57
	704 ^c	5'-AGT GCT CCA ATT AAT GTT GG	512	442-461
35	703	5'-TAT GGA AAT TCG AAA CAT CT	512	38-57
	705 ^c	5'-GTA CAG TTC CAA TAC CTG AA	512	534-553
	703	5'-TAT GGA AAT TCG AAA CAT CT	512	38-57
40	706 ^c	5'-TGA AAT CTT CAC ATC CAA CA	512	768-787
	793	5'-TTA TTG TTG CTG CTG GTA CT	512	149-168
	704 ^c	5'-AGT GCT CCA ATT AAT GTT GG	512	442-461
45				

^a These sequences were aligned to derive the corresponding primer.

^b The nucleotide positions refer to the *C. perfringens* tuf sequence fragment (SEQ ID NO. 32).

^c These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

^d The nucleotide positions refer to the *C. diphtheriae* tuf sequence fragment (SEQ ID NO. 662).

Annex I: Specific and ubiquitous primers for nucleic acid amplification (tuf sequences) (continued).

			Originating DNA fragment	
5	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	<u>Bacterial genus:</u> <i>Enterococcus</i> sp.			
	656	5'-AAT TAA TGG CTG CAG TTG AYG A	58-72 ^a	273-294 ^b
	657 ^c	5'-TTG TCC ACG TTC GAT RTC TTC A	58-72 ^a	556-577 ^b
15	656	5'-AAT TAA TGG CTG CAG TTG AYG A	58-72 ^a	273-294 ^b
	271 ^c	5'-TTG TCC ACG TTG GAT RTC TTC A	58-72 ^a	556-577 ^b
	1137	5'-AAT TAA TGG CTG CWG TTG AYG AA	58-72 ^a	273-295 ^b
20	1136 ^c	5'-ACT TGT CCA CGT TSG ATR TCT	58-72 ^a	559-579 ^b
	<u>Parasitical genus:</u> <i>Giardia</i> sp.			
	816	5'-GCT ACG ACG AGA TCA AGG GC	513	305-324
25	819 ^c	5'-TCG AGC TTC TGG AGG AAG AG	513	895-914
	817	5'-TGG AAG AAG GCC GAG GAG TT	513	355-374
	818 ^c	5'-AGC CGG GCT GGA TCT TCT TC	513	825-844
30	<u>Parasitical genus:</u> <i>Leishmania</i> sp.			
	701	5'-GTG TTC ACG ATC ATC GAT GCG	514-526 ^a	94-114 ^d
	702 ^c	5'-CTC TCG ATA TCC GCG AAG CG	514-526 ^a	913-932 ^d
35	<u>Bacterial genus:</u> <i>Staphylococcus</i> sp.			
	553	5'-GGC CGT GTT GAA CGT GGT CAA ATC A	176-203 ^a	313-337 ^e
	575 ^c	5'-TIA CCA TTT CAG TAC CTT CTG GTA A	176-203 ^a	653-677 ^e
	553	5'-GGC CGT GTT GAA CGT GGT CAA ATC A	176-203 ^a	313-337 ^e
40	707 ^c	5'-TWA CCA TTT CAG TAC CTT CTG GTA A	176-203 ^a	653-677 ^e
	<u>Bacterial genus:</u> <i>Streptococcus</i> sp.			
	547	5'-GTA CAG TTG CTT CAG GAC GTA TC	206-231 ^a	372-394 ^f
45	548 ^c	5'-ACG TTC GAT TTC ATC ACG TTG	206-231 ^a	548-568 ^f

^a These sequences were aligned to derive the corresponding primer.

50 ^b The nucleotide positions refer to the *E. durans* tuf sequence fragment (SEQ ID NO. 61).

^c These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

^d The nucleotide positions refer to the *L. tropica* tuf(EF-1) sequence fragment (SEQ ID NO. 526).

55 ^e The nucleotide positions refer to the *S. aureus* tuf sequence fragment (SEQ ID NO. 179).

^f The nucleotide positions refer to the *S. agalactiae* tuf sequence fragment (SEQ ID NO. 209).

Annex I: Specific and ubiquitous primers for nucleic acid amplification (tuf sequence s) (continued).

			Originating DNA fragment	
5	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	<u>Parasitical genus:</u> <i>Trypanosoma</i> sp.			
	823	5'-GAG CGG TAT GAY GAG ATT GT	529,840-842,864 ^a	493-512 ^b
	824 ^c	5'-GGC TTC TGC GGC ACC ATG CG	529,840-842,864 ^a	1171-1190 ^b
15	<u>Bacterial family:</u> <i>Mycobacteriaceae</i>			
	539	5'-CCI TAC ATC CTB GTY GCI CTI AAC AAG	122	85-111
20	540 ^c	5'-GGD GCI TCY TCR TCG WAI TCC TG	122	181-203
	<u>Bacterial group:</u> <i>Enterobacteriaceae</i> group			
	933	5'-CAT CAT CGT ITT CMT GAA CAA RTG	78,103,146, 168,238,698 ^a	390-413 ^d
25	934 ^c	5'-TCA CGY TTR RTA CCA CGC AGI AGA	78,103,146, 168,238,698 ^a	831-854 ^d
	<u>Parasitical family:</u> <i>Trypanosomatidae</i> family			
30	923	5'-GAC GCI GCC ATC CTG ATG ATC	511,514-526, 529,840-842, 864 ^a	166-188 ^e
	924 ^c	5'-ACC TCA GTC GTC ACG TTG GCG	511,514-526, 529,840-842, 864 ^a	648-668 ^e
35	925	5'-AAG CAG ATG GTT GTG TGC TG	511,514-526, 529,840-842, 864 ^a	274-293 ^e
40	926 ^c	5'-CAG CTG CTC GTG GTG CAT CTC GAT	511,514-526, 529,840-842, 864 ^a	676-699 ^e

^a These sequences were aligned to derive the corresponding primer.

^b The nucleotide positions refer to the *T. brucei* tuf (EF-1) sequence fragment (SEQ ID NO. 864).

^c These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

^d The nucleotide positions refer to the *E. coli* tuf sequence fragment (SEQ ID NO. 698).

^e The nucleotide positions refer to the *L. tropica* tuf sequence fragment (SEQ ID NO. 526).

Annex I: Specific and ubiquitous primers for nucleic acid amplification (tuf sequences) (continued).

			Originating DNA fragment	
5	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	<u>Parasitical family:</u> Trypanosomatidae family (continued)			
	927	5'-ACG CGG AGA AGG TGC GCT T	511,514-526, 529,840-842, 864 ^a	389-407 ^b
15	928 ^c	5'-GGT CGT TCT TCG AGT CAC CGC A	511,514-526, 529,840-842, 864 ^a	778-799 ^b
20	<u>Bacterial group:</u> Pseudomonads group			
	541	5'-GTK GAA ATG TTC CGC AAG CTG CT	153-155 ^a	476-498 ^d
	542 ^c	5'-CGG AAR TAG AAC TGS GGA CGG TAG	153-155 ^a	679-702 ^d
	541	5'-GTK GAA ATG TTC CGC AAG CTG CT	153-155 ^a	476-498 ^d
25	544 ^c	5'-AYG TTG TCG CCM GGC ATT MCC AT	153-155 ^a	749-771 ^d
	Universal primers			
30	636	5'-ACT GGY GTT GAI ATG TTC CGY AA	7,54,78, 100,103,159, 209,224,227 ^b	470-492 ^e
	637 ^a	5'-ACG TCA GTI GTA CGG AAR TAG AA	7,54,78, 100,103,159, 209,224,227 ^b	692-714 ^e
35	638	5'-CCA ATG CCA CAA ACI CGT GAR CAC AT	7,54,78, 100,103,159, 209,224,227 ^b	35-60 ^f
40	639 ^a	5'-TTT ACG GAA CAT TTC WAC ACC WGT IAC A	7,54,78, 100,103,159, 209,224,227 ^b	469-496 ^f

^a These sequences were aligned to derive the corresponding primer.

45 ^b The nucleotide positions refer to the *L. tropica* tuf (EF-1) sequence fragment (SEQ ID NO. 526).

^c These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

50 ^d The nucleotide positions refer to the *P. aeruginosa* tuf sequence fragment (SEQ ID NO. 153).

^e The nucleotide positions refer to the *E. coli* tuf sequence fragment (SEQ ID NO. 78).

^f The nucleotide positions refer to the *B. cereus* tuf sequence fragment (SEQ ID NO. 7).

Annex I: Specific and ubiquitous primers for nucleic acid amplification (tuf sequences) (continued).

5	SEQ ID NO.	Nucleotide sequence	Originating DNA fragment	
			SEQ ID NO.	Nucleotide position
10	643	5'-ACT GGI GTI GAR ATG TTC CGY AA	1,3,4,7,12, 13,16,49,54, 72,78,85,88, 91,94,98,103, 108,112,115, 116,120,121, 126,128,134, 136,146,154, 159,179,186, 205,209,212, 224,238 ^a	470-492 ^b
15				
20	544 ^c	5'-ACS TCI GTI GTI CKG AAR TAG AA	1,3,4,7,12, 13,16,49,54, 72,78,85,88, 91,94,98,103, 108,112,115, 116,120,121, 126,128,134, 136,146,154, 159,179,186, 205,209,212, 224,238 ^a	692-714 ^b
25				
30				

- 35
- ^a These sequences were aligned to derive the corresponding primer.
 - ^b The nucleotide positions refer to the *E. coli* tuf sequence fragment (SEQ ID NO. 78).
 - ^c These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

Annex I: Specific and ubiquitous primers for nucleic acid amplification (tuf sequences) (continued).

5	SEQ ID NO.	Nucleotide sequence	Originating DNA fragment	
			SEQ ID NO.	Nucleotide position
10	643	5'-ACT GGI GTI GAR ATG TTC CGY AA	1,3,4,7,12, 13,16,49,54, 72,78,85,88, 91,94,98,103, 108,112,115, 116,120,121, 126,128,134, 136,146,154, 159,179,186, 205,209,212, 224,238 ^a	470-492 ^b
15				
20	645 ^c	5'-ACG TCI GTI GTI CKG AAR TAR AA	1,3,4,7,12, 13,16,49,54, 72,78,85,88, 91,94,98,103, 108,112,115, 116,120,121, 126,128,134, 136,146,154, 159,179,186, 205,209,212, 224,238 ^a	692-714 ^b
25				
30				
	646	5'-ATC GAC AAG CCI TTC YTI ATG SC	2,13,82 122,145 ^a	317-339 ^d
35	647 ^c	5'-ACG TCC GTS GTR CGG AAG TAG AAC TG	2,13,82 122,145 ^a	686-711 ^d
	646	5'-ATC GAC AAG CCI TTC YTI ATG SC	2,13,82 122,145 ^a	317-339 ^d
40	648 ^c	5'-ACG TCS GTS GTR CGG AAG TAG AAC TG	2,13,82 122,145 ^a	686-711 ^d

45 ^a These sequences were aligned to derive the corresponding primer.

^b The nucleotide positions refer to the *E. coli* tuf sequence fragment (SEQ ID NO. 78).

^c These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

50 ^d The nucleotide positions refer to the *A. meyeri* tuf sequence fragment (SEQ ID NO. 2)

Annex I: Specific and ubiquitous primers for nucleic acid amplification (*tuf* sequences) (continued).

			Originating DNA fragment	
5	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	Universal primers (continued)			
	649	5'-GTC CTA TGC CTC ARA CWC GIG AGC AC	8,86,141,143 ^a	33-58 ^b
	650 ^c	5'-TTA CGG AAC ATY TCA ACA CCI GT	8,86,141,143 ^a	473-495 ^b
15	636	5'-ACT GGY GTT GAI ATG TTC CGY AA	8,86,141,143 ^a	473-495 ^b
	651 ^c	5'-TGA CGA CCA CCI TCY TCY TTY TTC A	8,86,141,143 ^a	639-663 ^b
	Sequencing primers			
20	556	5'-CGG CGC NAT CYT SGT TGT TGC	668 ^d	306-326
	557 ^c	5'-CCM AGG CAT RAC CAT CTC GGT G	668 ^d	1047-1068
	694	5'-CGG CGC IAT CYT SGT TGT TGC	668 ^d	306-326
	557 ^c	5'-CCM AGG CAT RAC CAT CTC GGT G	668 ^d	1047-1068
25	664	5'-AAY ATG ATI ACI GGI GCI GCI CAR ATG GA	619 ^d	604-632
	652 ^c	5'-CCW AYA GTI YKI CCI CCY TCY CTI ATA	619 ^d	1482-1508
	664	5'-AAY ATG ATI ACI GGI GCI GCI CAR ATG GA	619 ^d	604-632
30	561 ^c	5'-ACI GTI CGG CCR CCC TCA CGG AT	619 ^d	1483-1505
	543	5'-ATC TTA GTA GTT TCT GCT GCT GA	607	8-30
	660 ^c	5'-GTA GAA TTG AGG ACG GTA GTT AG	607	678-700
35	658	5'-GAT YTA GTC GAT GAT GAA GAA TT	621	116-138
	659 ^c	5'-GCT TTT TGI GTT TCW GGT TTR AT	621	443-465
	658	5'-GAT YTA GTC GAT GAT GAA GAA TT	621	116-138
40	661 ^c	5'-GTA GAA YTG TGG WCG ATA RTT RT	621	678-700
	558	5'-TCI TTY AAR TAY GCI TGG GT	665 ^d	157-176
	559 ^c	5'-CCG ACR GCR AYI GTY TGI CKC AT	665 ^d	1279-1301
	813	5'-AAT CYG TYG AAA TGC AYC ACG A	665 ^d	687-708
45	559 ^c	5'-CCG ACR GCR AYI GTY TGI CKC AT	665 ^d	1279-1301

^a These sequences were aligned to derive the corresponding primer.

^b The nucleotide positions refer to the *B. distasonis tuf* sequence fragment (SEQ ID NO. 8).

^c These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

^d Sequences from databases.

Annex I: Specific and ubiquitous primers for nucleic acid amplification (tuf sequences) (continued).

			Originating DNA fragment	
5	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	Sequencing primers (continued)			
	558	5'-TCI TTY AAR TAY GCI TGG GT	665 ^a	157-176
	815 ^b	5'-TGG TGC ATY TCK ACR GAC TT	665 ^a	686-705
15	560	5'-GAY TTC ATY AAR AAY ATG ATY AC	665 ^a	289-311
	559 ^b	5'-CCG ACR GCR AYI GTY TGI CKC AT	665 ^a	1279-1301
	653	5'-GAY TTC ATI AAR AAY ATG AT	665 ^a	289-308
	559 ^b	5'-CCG ACR GCR AYI GTY TGI CKC AT	665 ^a	1279-1301
20	558	5'-TCI TTY AAR TAY GCI TGG GT	665 ^a	157-176
	655 ^b	5'-CCR ATA CCI CMR ATY TTG TA	665 ^a	754-773
	654	5'-TAC AAR ATY KGI GGT ATY GG	665 ^a	754-773
25	559 ^b	5'-CCG ACR GCR AYI GTY TGI CKC AT	665 ^a	1279-1301
	696	5'-ATI GGI CAY RTI GAY CAY GGI AAR AC	698 ^a	52-77
	697 ^b	5'-CCI ACI GTI CKI CCR CCY TCR CG	698 ^a	1132-1154
30	911	5'-GAC GGM KKC ATG CCG CAR AC	853	22-41
	914 ^b	5'-GAA RAG CTG CGG RCG RTA GTG	853	700-720
	912	5'-GAC GGC GKC ATG CCG CAR AC	846	20-39
	914 ^b	5'-GAA RAG CTG CGG RCG RTA GTG	846	692-712
35	913	5'-GAC GGY SYC ATG CCK CAG AC	843	251-270
	915 ^b	5'-AAA CGC CTG AGG RCG GTA GTT	843	905-925
	916	5'-GCC GAG CTG GCC GGC TTC AG	846	422-441
40	561 ^b	5'-ACI GTI CGG CCR CCC TCA CGG AT	619 ^a	1483-1505
	664	5'-AAY ATG ATI ACI GGI GCI GCI CAR ATG GA	619 ^a	604-632
	917 ^b	5'-TCG TGC TAC CCG TYG CCG CCA T	846	593-614
45				

^a Sequences from databases.

^b These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

Annex I: Specific and ubiquitous primers for nucleic acid amplification (tuf sequence s) (continued).

			Originating DNA fragment	
5	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	Sequencing primers (continued)			
	1221	5'-GAY ACI CCI GGI CAY GTI GAY TT	1230 ^a	292-314
	1226 ^b	5'-GTI RMR TAI CCR AAC ATY TC	1230 ^a	2014-2033
15	1222	5'-ATY GAY ACI CCI GGI CAY GTI GAY TT	1230 ^a	289-314
	1223 ^b	5'-AYI TCI ARR TGI ARY TCR CCC ATI CC	1230 ^a	1408-1433
	1224	5'-CCI GYI HTI YTI GAR CCI ATI ATG	1230 ^a	1858-1881
	1225 ^b	5'-TAI CCR AAC ATY TCI SMI ARI GGI AC	1230 ^a	2002-2027
20	1227	5'-GTI CCI YTI KCI GAR ATG TTY GGI TA	1230 ^a	2002-2027
	1229 ^b	5'-TCC ATY TGI GCI GCI CCI GTI ATC AT	698 ^a	4-29
	1228	5'-GTI CCI YTI KCI GAR ATG TTY GGI TAY GC	1230 ^a	2002-2030
25	1229 ^b	5'-TCC ATY TGI GCI GCI CCI GTI ATC AT	698 ^a	4-29

^a Sequences from databases.

^b These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

Annex II: Specific and ubiquitous primers for nucleic acid amplification (atpD sequences).

			Originating DNA fragment	
5	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	<u>Bacterial species:</u> <i>Streptococcus agalactiae</i>			
	627	5'-ATT GTC TAT AAA AAT GGC GAT AAG TC	379-383 ^a	42-67 ^b
	625 ^c	5'-CGT TGA AGA CAC GAC CCA AAG TAT CC	379-383 ^a	206-231 ^b
15	628	5'-AAA ATG GCG ATA AGT CAC AAA AAG TA	379-383 ^a	52-77 ^b
	625 ^c	5'-CGT TGA AGA CAC GAC CCA AAG TAT CC	379-383 ^a	206-231 ^b
	627	5'-ATT GTC TAT AAA AAT GGC GAT AAG TC	379-383 ^a	42-67 ^b
	626 ^c	5'-TAC CAC CTT TTA AGT AAG GTG CTA AT	379-383 ^a	371-396 ^b
20	628	5'-AAA ATG GCG ATA AGT CAC AAA AAG TA	379-383 ^a	52-77 ^b
	626 ^c	5'-TAC CAC CTT TTA AGT AAG GTG CTA AT	379-383 ^a	371-396 ^b
25	<u>Bacterial genus:</u> <i>Candida</i> sp.			
	634	5'-AAC ACY GTC AGR RCI ATT GCY ATG GA	460-472, 474-478 ^a	101-126 ^d
	635 ^c	5'-AAA CCR GTI ARR GCR ACT CTI GCT CT	460-472, 474-478 ^a	617-642 ^d
30				

^a These sequences were aligned to derive the corresponding primer.

^b The nucleotide positions refer to the *S. agalactiae* atpD sequence fragment (SEQ ID NO. 380).

35 ^c These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

^d The nucleotide positions refer to the *C. albicans* atpD sequence fragment (SEQ ID NO. 460).

Ann x II: Specific and ubiquitous primers for nucleic acid amplification (atpD sequences) (continued).

		Originating DNA fragment	
SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
Universal primers			
562	5'-CAR ATG RAY GAR CCI CCI GGI GYI MGI ATG	243,244,262, 264,280,284, 291,297,309, 311,315,317, 324,329,332, 334-336,339, 342,343,351, 356,357,364- 366,370,375, 379,393 ^a	528-557 ^b
563 ^c	5'-GGY TGR TAI CCI ACI GCI GAI GGC AT	243,244,262, 264,280,284, 291,297,309, 311,315,317, 324,329,332, 334-336,339, 342,343,351, 356,357,364- 366,370,375, 379,393 ^a	687-712 ^b
564	5'-TAY GGI CAR ATG AAY GAR CCI CCI GGI AA	243,244,262, 264,280,284, 291,297,309, 311,315,317, 324,329,332, 334-336,339, 342,343,351, 356,357,364- 366,370,375, 379,393 ^a	522-550 ^b
565 ^c	5'-GGY TGR TAI CCI ACI GCI GAI GGD AT	243,244,262, 264,280,284, 291,297,309, 311,315,317, 324,329,332, 334-336,339, 342,343,351, 356,357,364- 366,370,375, 379,393 ^a	687-712 ^b

^a These sequences were aligned to derive the corresponding primer.

^b The nucleotide positions refer to the *K. pneumoniae* atpD sequence fragment (SEQ ID NO. 317).

^c These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

Annex II: Specific and ubiquitous primers for nucleic acid amplification (atpD sequences) (continued).

			Originating DNA fragment	
5	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
	Universal primers (continued)			
10	640	5'-TCC ATG GTI TWY GGI CAR ATG AA	248,284,315, 317,343,357, 366,370,379,393 ^a	513-535 ^b
15	641 ^c	5'-TGA TAA CCW ACI GCI GAI GGC ATA CG	248,284,315, 317,343,357, 366,370,379,393 ^a	684-709 ^b
20	642	5'-GGC GTI GGI GAR CGI ACI CGT GA	248,284,315, 317,343,357, 366,370,379,393 ^a	438-460 ^b
	641 ^c	5'-TGA TAA CCW ACI GCI GAI GGC ATA CG	248,284,315, 317,343,357, 366,370,379,393 ^a	684-709 ^b
25	Sequencing primers			
	566	5'-TTY GGI GGI GCI GGI GTI GGI AAR AC	669 ^d	445-470
	567 ^c	5'-TCR TCI GCI GGI ACR TAI AYI GCY TG	669 ^d	883-908
30	566	5'-TTY GGI GGI GCI GGI GTI GGI AAR AC	669 ^d	445-470
	814	5'-GCI GGC ACG TAC ACI GCC TG	666 ^d	901-920
	568	5'-RTI ATI GGI GCI GTI RTI GAY GT	669 ^d	25-47
35	567 ^c	5'-TCR TCI GCI GGI ACR TAI AYI GCY TG	669 ^d	883-908
	570	5'-RTI RYI GGI CCI GTI RTI GAY GT	672 ^d	31-53
	567 ^c	5'-TCR TCI GCI GGI ACR TAI AYI GCY TG	669 ^d	883-908
40	572	5'-RTI RTI GGI SCI GTI RTI GA	669 ^d	25-44
	567 ^c	5'-TCR TCI GCI GGI ACR TAI AYI GCY TG	669 ^d	883-908
	569	5'-RTI RTI GGI SCI GTI RTI GAT AT	671 ^d	31-53
	567 ^c	5'-TCR TCI GCI GGI ACR TAI AYI GCY TG	669 ^d	883-908
45	571	5'-RTI RTI GGI CCI GTI RTI GAT GT	670 ^d	31-53
	567 ^c	5'-TCR TCI GCI GGI ACR TAI AYI GCY TG	669 ^d	883-908

^a These sequences were aligned to derive the corresponding primer.

50 ^b The nucleotide positions refer to the *K. pneumoniae* atpD sequence fragment (SEQ ID NO. 317).

^c These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

^d Sequences from databases.

Ann x II: Specific and ubiquitous primers for nucleic acid amplification (atpD sequences) (continued).

			Originating DNA fragment	
5	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	Sequencing primers (continued)			
	700	5'-TIR TIG AYG TCG ART TCC CTC ARG	669 ^a	38-61
	567 ^b	5'-TCR TCI GCI GGI ACR TAI AYI GCY TG	669 ^a	883-908
15	568	5'-RTI ATI GGI GCI GTI RTI GAY GT	669 ^a	25-47
	573 ^b	5'-CCI CCI ACC ATR TAR AAI GC	666 ^a	1465-1484
	574	5'-ATI GCI ATG GAY GGI ACI GAR GG	666 ^a	283-305
	573 ^b	5'-CCI CCI ACC ATR TAR AAI GC	666 ^a	1465-1484
20	574	5'-ATI GCI ATG GAY GGI ACI GAR GG	666 ^a	283-305
	708 ^b	5'-TCR TCC ATI CCI ARI ATI GCI ATI AT	666 ^a	1258-1283
	681	5'-GGI SSI TTY GGI ISI GGI AAR AC	685	694-716
25	682 ^b	5'-GTI ACI GGY TCY TCR AAR TTI CCI CC	686	1177-1202
	681	5'-GGI SSI TTY GGI ISI GGI AAR AC	685	694-716
	683 ^b	5'-GTI ACI GGI TCI SWI AWR TCI CCI CC	685	1180-1205
30	681	5'-GGI SSI TTY GGI ISI GGI AAR AC	685	694-716
	699 ^b	5'-GTI ACI GGY TCY TYR ARR TTI CCI CC	686	1177-1202
	681	5'-GGI SSI TTY GGI ISI GGI AAR AC	685	694-716
	812 ^b	5'-GTI ACI GGI TCY TYR ARR TTI CCI CC	685	1180-1205
35	1213	5'-AAR GGI GGI ACI GCI GCI ATH CCI GG	714 ^a	697-722
	1212 ^b	5'-CCI CCI RGI GGI GAI ACI GCW CC	714 ^a	1189-1211
	1203	5'-GGI GAR MGI GGI AAY GAR ATG	709 ^a	724-744
40	1207 ^b	5'-CCI TCI TCW CCI GGC ATY TC	709 ^a	985-1004
	1204	5'-GCI AAY AAC ITC IWM YAT GCC	709 ^a	822-842
	1206 ^b	5'-CKI SRI GTI GAR TCI GCC A	709 ^a	926-944
45	1205	5'-AAY ACI TCI AWY ATG CCI GT	709 ^a	826-845
	1207 ^b	5'-CCI TCI TCW CCI GGC ATY TC	709 ^a	985-1004

^a Sequences from databases.

50 ^b These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

Annex III: Internal probes for nucleic acid hybridization and specific detection of *tuf* s quences.

5			Originating DNA fragment	
	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	<u>Bacterial species:</u> <i>Candida albicans</i>			
	577	5'-CAT GAT TGA ACC ATC CAC CA	407-411 ^a	406-425 ^b
15	<u>Bacterial species:</u> <i>Candida dubliniensis</i>			
	578	5'-CAT GAT TGA AGC TTC CAC CA	412,414-415 ^a	418-437 ^c
	<u>Bacterial species:</u> <i>Enterococcus faecalis</i>			
20	580	5'-GCT AAA CCA GCT ACA ATC ACT CCA C	62-63,607 ^a	584-608 ^d
	603	5'-GGT ATT AAA GAC GAA ACA TC	62-63,607 ^a	440-459 ^d
	1174	5'-GAA CGT GGT GAA GTT CGC	62-63,607 ^a	398-415 ^d
25	<u>Bacterial species:</u> <i>Enterococcus faecium</i>			
	602	5'-AAG TTG AAG TTG TTG GTA TT	64,608 ^a	426-445 ^e
	<u>Bacterial species:</u> <i>Enterococcus gallinarum</i>			
30	604	5'-GGT GAT GAA GTA GAA ATC GT	66,609 ^a	419-438 ^f
	<u>Bacterial species:</u> <i>Escherichia coli</i>			
35	579	5'-GAA GGC CGT GCT GGT GAG AA	78	503-522

^a These sequences were aligned to derive the corresponding primer.

^b The nucleotide positions refer to the *C. albicans tuf*(EF-1) sequence fragment (SEQ ID NO. 408).

40 ^c The nucleotide positions refer to the *C. dubliniensis tuf*(EF-1) sequence fragment (SEQ ID NO. 414).

^d The nucleotide positions refer to the *E. faecalis tuf* sequence fragment (SEQ ID NO. 607).

45 ^e The nucleotide positions refer to the *E. faecium tuf* sequence fragment (SEQ ID NO. 608).

^f The nucleotide positions refer to the *E. gallinarum tuf* sequence fragment (SEQ ID NO. 609).

Annex III: Internal probes for nucleic acid hybridization and specific detection of *tuf* sequences (continued).

			Originating DNA fragment	
5	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	<u>Bacterial species:</u> <i>Haemophilus influenzae</i>			
	581	5'-ACA TCG GTG CAT TAT TAC GTG G	610 ^a	551-572 ^b
15	<u>Bacterial species:</u> <i>Staphylococcus aureus</i>			
	584	5'-ACA TGA CAC ATC TAA AAC AA	176-180 ^c	369-388 ^d
	585	5'-ACC ACA TAC TGA ATT CAA AG	176-180 ^c	525-544 ^d
	586	5'-CAG AAG TAT ACG TAT TAT CA	176-180 ^c	545-564 ^d
	587	5'-CGT ATT ATC AAA AGA CGA AG	176-180 ^c	555-574 ^d
20	588	5'-TCT TCT CAA ACT ATC GTC CA	176-180 ^c	593-612 ^d
	<u>Bacterial species:</u> <i>Staphylococcus epidermidis</i>			
	589	5'-GCA CGA AAC TTC TAA AAC AA	185,611 ^c	445-464 ^e
25	590	5'-TAT ACG TAT TAT CTA AAG AT	185,611 ^c	627-646 ^e
	591	5'-TCC TGG TTC TAT TAC ACC AC	185,611 ^c	586-605 ^e
	592	5'-CAA AGC TGA AGT ATA CGT AT	185,611 ^c	616-635 ^e
	593	5'-TTC ACT AAC TAT CGC CCA CA	185,611 ^c	671-690 ^e
30	<u>Bacterial species:</u> <i>Staphylococcus haemolyticus</i>			
	594	5'-ATT GGT ATC CAT GAC ACT TC	186,188-190 ^c	437-456 ^f
	595	5'-TTA AAG CAG ACG TAT ACG TT	186,188-190 ^c	615-634 ^f
35	<u>Bacterial species:</u> <i>Staphylococcus hominis</i>			
	596	5'-GAA ATT ATT GGT ATC AAA GA	191,193-196 ^c	431-450 ^g
	597	5'-ATT GGT ATC AAA GAA ACT TC	191,193-196 ^c	437-456 ^g
40	598	5'-AAT TAC ACC TCA CAC AAA AT	191,193-196 ^c	595-614 ^g

^a Sequences from databases.

^b The nucleotide positions refer to the *H. influenzae* *tuf* sequence fragment (SEQ ID NO. 610).

^c These sequences were aligned to derive the corresponding probe.

^d The nucleotide positions refer to the *S. aureus* *tuf* sequence fragment (SEQ ID NO. 179).

^e The nucleotide positions refer to the *S. epidermidis* *tuf* sequence fragment (SEQ ID NO. 611).

^f The nucleotide positions refer to the *S. haemolyticus* *tuf* sequence fragment (SEQ ID NO. 186).

^g The nucleotide positions refer to the *S. hominis* *tuf* sequence fragment (SEQ ID NO. 191).

Annex III: Internal probes for nucleic acid hybridization and specific detection of *tuf* sequences (continued).

			Originating DNA fragment	
5	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	Bacterial species: <i>Staphylococcus saprophyticus</i>			
	599	5'-CGG TGA AGA AAT CGA AAT CA	198-200 ^a	406-425 ^b
	600	5'-ATG CAA GAA GAA TCA AGC AA	198-200 ^a	431-450 ^b
	601	5'-GTT TCA CGT GAT GAT GTA CA	198-200 ^a	536-555 ^b
15	695	5'-GTT TCA CGT GAT GAC GTA CA	198-200 ^a	563-582 ^b
	Bacterial species: <i>Streptococcus agalactiae</i>			
	582 ^c	5'-TTT CAA CTT CGT CGT TGA CAC GAA CAG T	207-210 ^a	404-431 ^d
20	583 ^c	5'-CAA CTG CTT TTT GGA TAT CTT CTT TAA TAC CAA CG	207-210 ^a	433-467 ^d
	1199	5'-GTA TTA AAG AAG ATA TCC AAA AAG C	207-210 ^a	438-462 ^d
	Bacterial species: <i>Streptococcus pneumoniae</i>			
25	1201	5'-TCA AAG AAG AAA CTA AAA AAG CTG T	971,977, 979,986 ^a	513-537 ^e
	Bacterial species: <i>Streptococcus pyogenes</i>			
30	1200	5'-TCA AAG AAG AAA CTA AAA AAG CTG T	1002	473-497
	Bacterial group: <i>Enterococcus casseliflavus-flavescens-gallinarum</i> group			
35	620	5'-ATT GGT GCA TTG CTA CGT	58,65,66 ^a	527-544 ^f
	1122	5'-TGG TGC ATT GCT ACG TGG	58,65,66 ^a	529-546 ^f
	Bacterial genus: <i>Staphylococcus</i> sp.			
40	605	5'-GAA ATG TTC CGT AAA TTA TT	176-203 ^a	403-422 ^g
	606	5'-ATT AGA CTA CGC TGA AGC TG	176-203 ^a	420-439 ^g
	1175	5'-GTT ACT GGT GTA GAA ATG TTC	176-203 ^a	391-411 ^g
	1176	5'-TAC TGG TGT AGA AAT GTT C	176-203 ^a	393-411 ^g
45				

^a These sequences were aligned to derive the corresponding primer.

^b The nucleotide positions refer to the *S. saprophyticus* *tuf* sequence fragment (SEQ ID NO. 198).

^c These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

^d The nucleotide positions refer to the *S. agalactiae* *tuf* sequence fragment (SEQ ID NO. 209).

^e The nucleotide positions refer to the *S. pneumoniae* *tuf* sequence fragment (SEQ ID NO. 986).

^f The nucleotide positions refer to the *E. flavescens* *tuf* sequence fragment (SEQ ID NO. 65).

^g The nucleotide positions refer to the *S. aureus* *tuf* sequence fragment (SEQ ID NO. 179).

Annex III: Internal probes for nucleic acid hybridization and specific detection of tuf sequences.

			Originating DNA fragment	
5	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	Bacterial genus: <i>Streptococcus</i> sp.			
	1202	5'-GTG TTG AAA TGT TCC GTA AAC A	206-231,971, 977,979,982-986 ^a	466-487 ^b
15	fungus species: <i>Candida albicans</i>			
	1156	5'-GTT GAA ATG CAT CAC GAA CAA TT	407-412,624 ^a	680-702 ^c
20	fungus species: <i>Candida albicans</i> and <i>tropicalis</i>			
	1160	5'-CGT TTC TGT TAA AGA AAT TAG AAG	407-412, 429,624 ^a	748-771 ^c
25	fungus species: <i>Candida dubliniensis</i>			
	1166	5'-ACG TTA AGA ATG TTT CTG TCA A	414-415 ^a	750-771 ^d
	1168	5'-GAA CAA TTG GTT GAA GGT GT	414-415 ^a	707-726 ^d
30	fungus species: <i>Candida glabrata</i>			
	1158	5'-AAG AGG TAA TGT CTG TGG T	417	781-799
	1159	5'-TGA AGG TTT GCC AGG TGA	417	718-735
35	fungus species: <i>Candida krusei</i>			
	1161	5'-TCC AGG TGA TAA CGT TGG	422	720-737
40	fungus species: <i>Candida lusitaniae</i> and <i>guilliermondii</i>			
	1162	5'-CAA GTC CGT GGA AAT GCA	418,424 ^a	682-699 ^e
45	fungus species: <i>Candida parapsilosis</i>			
	1157	5'-AAG AAC GTT TCA GTT AAG GAA AT	426	749-771
50	fungus species: <i>Candida zeylanoides</i>			
	1165	5'-GGT TTC AAC GTG AAG AAC	432	713-730
<hr/>				
a These sequences were aligned to derive the corresponding primer.				
b The nucleotide positions refer to the <i>S. pneumoniae</i> tuf sequence fragment (SEQ ID NO. 986).				
c The nucleotide positions refer to the <i>C. albicans</i> tuf(EF-1) sequence fragment (SEQ ID NO. 408).				
d The nucleotide positions refer to the <i>C. dubliniensis</i> tuf(EF-1) sequence fragment (SEQ ID NO. 414).				
e The nucleotide positions refer to the <i>C. lusitaniae</i> tuf(EF-1) sequence fragment (SEQ ID NO. 424).				

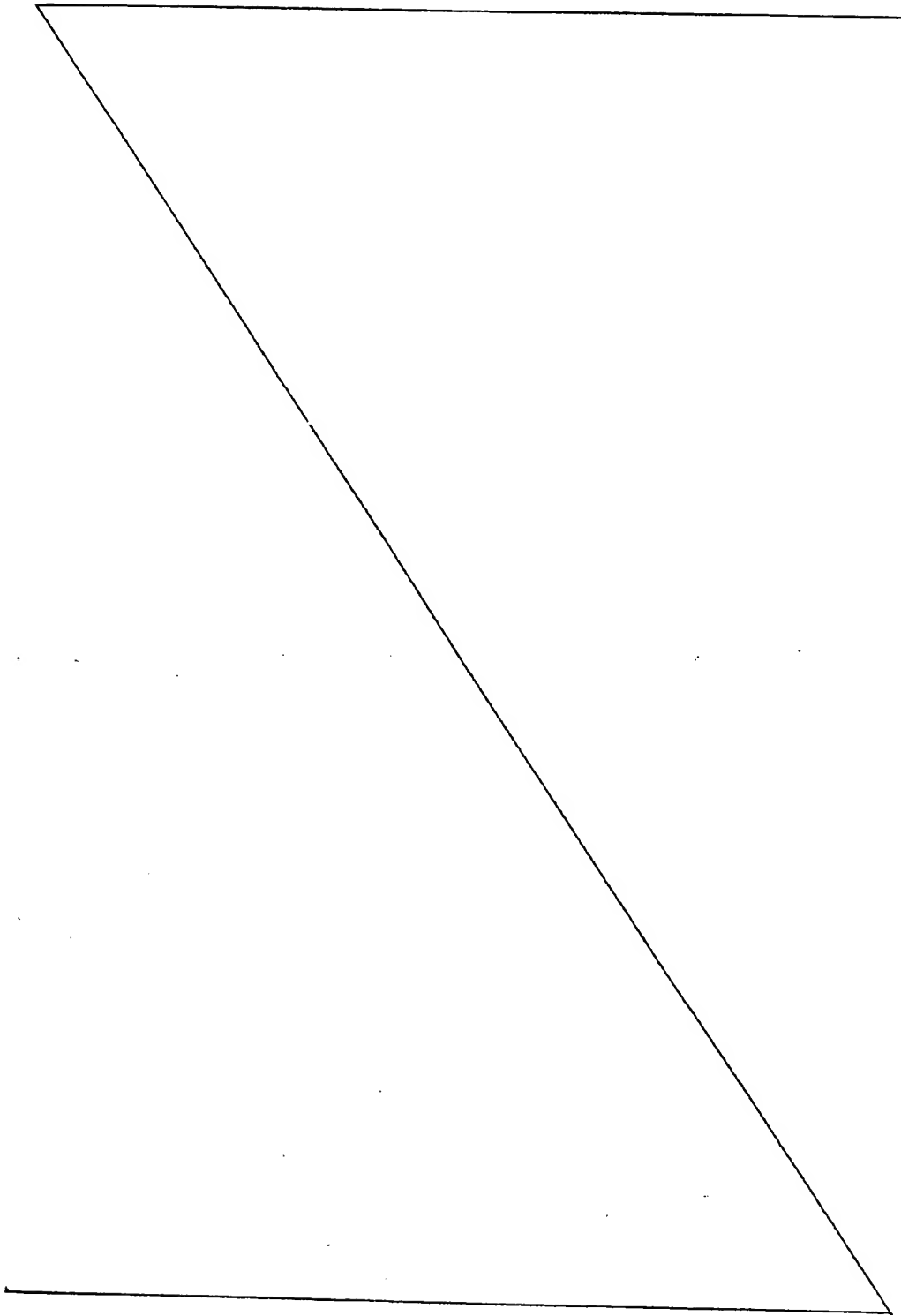
**Annex III: Internal probes for nucleic acid hybridization and
specific detection of tuf sequences (continued).**

		Originating DNA fragment	
5	SEQ ID NO.	Nucleotide sequence	SEQ ID NO. Nucleotide position
10	<u>fungus genus:</u> <i>Candida sp.</i>		
	1163	5'-GTT GGT TTC AAC GTT AAG AAC	407-412,414- 728-748 ^b 415,417,418, 422,429 ^a
15	1164	5'-GGT TTC AAC GTC AAG AAC	413,416,420, 740-757 ^c 421,424,425, 426,428,431 ^a
20	1167	5'-GTT GGT TTC AAC GT	406-426, 428- 728-741 ^b 432, 624 ^a

^a These sequences were aligned to derive the corresponding primer.

^b The nucleotide positions refer to the *C. albicans* tuf(EF-1) sequence fragment (SEQ ID NO. 408).

^c The nucleotide positions refer to the *C. lusitanae* tuf(EF-1) sequence fragment (SEQ ID NO. 424).



Annex IV: Strategy for the selection of amplification/sequencing primers from atpD sequences.

5

		23	49	443	472	881	910	SEQ ID	NO.:	Accession #:
	<i>B. cepacia</i>	AGTTCAT	CGCGCCCGTT	ATGACCTGG...TGTTCC	CGGTGGCTGG	CGGTGGCTGG	CGGTGGCTGG	910	-	X76877
	<i>B. pertussis</i>	AGTTCAT	CGCGCCCGTT	ATGACCTGG...TGTTCC	CGGTGGCTGG	CGGTGGCTGG	CGGTGGCTGG	910	-	X76877
	<i>P. aeruginosa</i>	AAATCAT	CGCGCCCGTT	ATGACCTGG...TGTTCC	CGGTGGCTGG	CGGTGGCTGG	CGGTGGCTGG	910	-	Genome project
10	<i>E. coli</i>	AGTTCAT	CGCGCCCGTT	ATGACCTGG...TGTTCC	CGGTGGCTGG	CGGTGGCTGG	CGGTGGCTGG	910	-	Genome project
	<i>N. gonorrhoeae</i>	AAATCAT	CGGTGGCTGG	ATGACCTGG...TGTTCC	CGGTGGCTGG	CGGTGGCTGG	CGGTGGCTGG	910	-	J01594
	<i>M. thermoacetica</i>	AGTTCAT	CGGTGGCTGG	ATGACCTGG...TGTTCC	CGGTGGCTGG	CGGTGGCTGG	CGGTGGCTGG	910	-	Genome project
	<i>S. aurantiaca</i>	AGTTCAT	CGGTGGCTGG	ATGACCTGG...TGTTCC	CGGTGGCTGG	CGGTGGCTGG	CGGTGGCTGG	910	-	U64318
15	<i>M. tuberculosis</i>	GGGTTC	CGGTGGCTGG	ATGACCTGG...TGTTCC	CGGTGGCTGG	CGGTGGCTGG	CGGTGGCTGG	910	-	X76879
	<i>B. fragilis</i>	AGTTCAT	CGGTGGCTGG	ATGACCTGG...TGTTCC	CGGTGGCTGG	CGGTGGCTGG	CGGTGGCTGG	910	-	273419
	<i>C. lytica</i>	AGTTCAT	CGGTGGCTGG	ATGACCTGG...TGTTCC	CGGTGGCTGG	CGGTGGCTGG	CGGTGGCTGG	910	-	M22247
	<i>A. woodii</i>	AGTTCAT	CGGTGGCTGG	ATGACCTGG...TGTTCC	CGGTGGCTGG	CGGTGGCTGG	CGGTGGCTGG	910	-	M22535
	<i>C. acetobutylicum</i>	AGTTCAT	CGGTGGCTGG	ATGACCTGG...TGTTCC	CGGTGGCTGG	CGGTGGCTGG	CGGTGGCTGG	910	-	U10505
20	<i>M. pneumoniae</i>	AGTTCAT	CGGTGGCTGG	ATGACCTGG...TGTTCC	CGGTGGCTGG	CGGTGGCTGG	CGGTGGCTGG	910	-	AF101055
	<i>H. pylori</i>	AGTTCAT	CGGTGGCTGG	ATGACCTGG...TGTTCC	CGGTGGCTGG	CGGTGGCTGG	CGGTGGCTGG	910	-	U43738
									-	AF004014

Selected sequences
for universal primers

RTIAT IGGICIGTI RTIATGT
RTIY IGGICIGTI RTIATGT
RTIY IGGICIGTI RTIATGT
RTIY IGGICIGTI RTIATGT
RTIY IGGICIGTI RTIATGT

25

Selected sequence
for universal primer*

TTTG GGGGCGTG GTGGGCTGG

30

CA RCICITIT AYTICICIGTG IGATGA

567

568
570
572
569
571
566

The sequence numbering refers to the *Escherichia coli atpD* gene fragment (SEQ ID NO. 669). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches are indicated by lower-case letters. Dots indicate gaps in the sequences displayed.

35

"R" "Y" "M" "K" "W" and "S" designate nucleotide positions which are degenerated. "R" stands for A or G; "Y" stands for C or T; "M" stands for A or C; "K" stands for G or T; "W" stands for A or T; "S" stands for C or G. "I" stands for inosine which is a nucleotide analog that can bind to any of the four nucleotides A, C, G or T.

40

* This sequence is the reverse-complement of the selected primer.

Annex V: Strategy for the selection of universal amplification/sequencing primers from atpD (V-type) sequences.

5

	691	719	1177	1208	SEQ ID NO.:
<i>E. hirae</i>	CC AGTCCCGTTT GGTGCAGGGA AGACAGT...TCTGTGGAG ATATCTCTGA ACCAGTGA				685
<i>H. salinarum</i>	CC GGGCCCGTTC GGTCCCGGGA AGACGGT...CCCGCGGGG ACTTGTCCGA GCCGTCACC				687
<i>T. thermophilus</i>	CC TGGCCCTTC GGCAGCGGA AGACCGT...CCGCGCGCG AGATGTCCGA GCCCTGACC				693
Human	CC TGGGCGCTTC GGTGTGGCA AGACTGT...CCCGGTGGAG ACTTCTCAGA TCCCTGACG				688
<i>T. congolense</i>	CC TGGCGCGTTT GGTTCGGGA AGACGGT...CCTGGAGGTG ACTTCTCAGA CCAATGACG				692
<i>P. falciparum</i>	CC TGGTGCATTT GGTGTGGGA AAATGTG...CCAGGTGGT ATTCTCTGA CCTGTAACT				689
<i>C. pneumoniae</i>	CC AGGACCTTTT GGTGCAGGGA AAACAGT...GCAGGAGGA ACTTGAAGA ACCAGTCACT				686
15 Selected sequences for universal primers	GGTSSITTY GGIISIGGIA ARAC				681
20 Selected sequences for universal primers ^a					
			GGIGGIA AYTTYGARGA RCCIGTIAC		682
			GGIGGIG AYWTIVSIGA ICCIGTIAC		683

25 The sequence numbering refers to the *Enterococcus hirae* atpD gene fragment (SEQ ID NO. 685). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches for SEQ ID NOS. 681 and 682 are indicated by lower-case letters. Mismatches for SEQ ID NO. 683 are indicated by underlined nucleotides. Dots indicate gaps in the sequences displayed.

30 "R" "Y" "M" "K" "W" and "S" designate nucleotide positions which are degenerated. "R" stands for A or G; "Y" stands for C or T; "M" stands for A or C; "K" stands for G or T; "W" stands for A or T; "S" stands for C or G. "I" stands for inosine which is a nucleotide analog that can bind to any of the four nucleotides A, C, G or T.

^a These sequences are the reverse-complement of the selected primers.

Annex VI: Strategy for the selection of universal amplification/sequencing primers from tuf (M) sequences (organelle origin).

5	601	635	1479	1511	SEQ ID NO.:	Accession #:
	C. neoformans ^a	AAGAA CATGATCACC GGTaCCTCCC AGgtGACTG...CGCgtTCGGA	GACatCGGAC AGACcGTTGc	CGT	-	U81803
	S. cerevisiae ^a	AAGAA CATGATTACT GGTaCTtCTC AGgtGACTG...CGCTgtTCAGA	GACatGaGAC AAActGTtCGc	TGT	665	X00779
	O. volvulus ^a	AAGAA TATGATCACA GGTaCTtCTC AGgtGACTG...TGCTgtTCGct	GATatGaGAC AAACaGTTGc	GGT	-	M64333
	Human ^a	AAAAA CATGATTACA GGGaCAtCTC AGgtGACTG...TGCTgtTCGt	GATatGaGAC AGACaGTTGc	TGT	-	X03558
	G. max B1 ^b	AAGAA CATGATCACC GCGGCTGCC AGATGGACGG...TGCTATTAGA	GAAGGAGGCA AAActGTTGG	AGC	-	Y15107
10	G. max B2 ^b	AAAAA CATGATCACC GCGGCTGCC AGATGGACGG...TGCTATTAGA	GAAGGAGGCA AAActGTTGG	AGC	-	Y15108
	E. coli ^c	AAAAA CATGATCACC GGTGCTGCTC AGATGGACGG...CGCaATCCgt	GAAGGCGGCC GTACcGTTGG	CGC	78	-
	S. aureofaciens ^c	AAGAA CATGATCACC GGTGCGGCC AGATGGACGG...CGCaATCCgt	GAGGTGGTC GTACcGTTGG	CGC	-	AF007125
	E. tenella ^b	AAAAA TATGATTACA GGAGCAGCAC AAATGGATGG...TGCTATTAGA	GAAGCAGGAA AAActATAGG	AGC	-	AI755521
	T. gondii ^b	AAGAA TATGATTACT GGAGCGGCAC AAATGGATGG...TGCTATTAGA	GAAGGAGGTC GTACTATAGG	AGC	-	Y11431
15	S. cerevisiae ^b	AAGAA TATGATTACC GGTGCTGCTC AAATGGATGG...CAATATCAGA	GAGGCTGGAA GAActGTTGG	TAC	619	K00428
	A. thaliana ^b	AAAAA TATGATTACT GGAGCTGCGC AAATGGATGG...TGCTtTAAGG	GAAGGAGGTA GAACaGTTGG	AGC	-	X89227
20	Selected sequence for universal primer	AA YATGATTACI GGIGCTGCIC ARATGGA			664	
	Selected sequences for universal primers		TATTAGR GARGGIGGIM RIACTRTWGG ATCCGT GAGGGYGGCC GITCIGT		652 561	

25 The sequence numbering refers to the *Saccharomyces cerevisiae* tuf (M) gene (SEQ ID NO. 619). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches for SEQ ID NOS. 652 and 664 are indicated by lower-case letters. Mismatches for SEQ ID NO. 561 are indicated by underlined nucleotides. Dots indicate gaps in the sequences displayed.

30 "R" "Y" "M" "K" "W" and "S" designate nucleotide positions which are degenerated. "R" stands for A or G; "Y" stands for C or T; "M" stands for A or C; "K" stands for G or T; "W" stands for A or T; "S" stands for C or G. "I" stands for inosine which is a nucleotide analog that can bind to any of the four nucleotides A, C, G or T.

^a This sequence refers to tuf(EP-1) gene.

^b This sequence refers to tuf (M) or organelle gene.

^c This sequence refers to tuf gene from bacteria.

^d These sequences are the reverse-complement of the selected primers.

Annex VII: Strategy for the selection of eukaryotic sequencing primers from tuf (EF-1) sequences.

[illegible]

30 The sequence numbering refers to the *Saccharomyces cerevisiae* *tuf* (EF-1) gene fragment (SEQ ID NO. 665). Nucleotides in capitals are identical to the selected sequences SEQ ID NOS. 558, 560 or 653, or match those sequences. Mismatches for SEQ ID no. 558 and 560 are indicated by lower-case letters. Mismatches for SEQ ID NO. 653 are indicated by underlined nucleotides. Dots indicate gaps in the sequences displayed.

"R" "Y" "M" "K" "W" and "S" designate nucleotide positions which are degenerated. "R" stands for A or G; "Y" stands for C or T; "M" stands for A or C; "K" stands for G or T; "W" stands for A or T; "S" stands for C or G. "I" stands for inosine which is a nucleotide analog that can bind to any of the four nucleotides A, C, G or T.

Annex VII: Strategy for the selection of eukaryotic sequencing primers from tuf (EF-1) sequences (continued).

Accession #:	SEQ ID NO.:	1304	776	1276	751
S. cerevisiae	665	TGT	ATTCGTTAC...GACATG	GATCGGTGGT	...GTTTACAA
B. hominis	-	TGT	ATTCGTTAC...GATATG	GATTGGCGGT	...GTGTACAA
C. albicans	-	TGT	ATTCGTTAC...GATATG	GATCGGTGGT	...GTTTACAA
C. neoformans	-	TGT	ATTCGTTAC...GACATG	GATCGGTGGT	...GTCTACAA
E. histolytica	-	TGT	ATTCGTTAC...GATATG	GATTTCAGGT	...GTTTACAA
G. lamblia	-	AGT	ATTCGTTAC...GATATG	GATTCGGGG	...GTCTACAA
H. capsulatum	-	AGT	ATTCGTTAC...GATATG	GATTCGGGG	...GTCTACAA
Human	-	AGT	ATTCGTTAC...GATATG	GATTCGGGG	...GTCTACAA
L. braziliensis	-	TGT	ATTCGTTAC...GATATG	GATTCGGGG	...GTCTACAA
O. volvulus	-	TGT	ATTCGTTAC...GATATG	GATTCGGGG	...GTCTACAA
P. berghiei	-	TGT	ATTCGTTAC...GATATG	GATTCGGGG	...GTCTACAA
P. knowlesi	-	TGT	ATTCGTTAC...GATATG	GATTCGGGG	...GTCTACAA
S. pombe	-	TGT	ATTCGTTAC...GATATG	GATTCGGGG	...GTCTACAA
T. cruzi	-	TGT	ATTCGTTAC...GATATG	GATTCGGGG	...GTCTACAA
Y. lipolytica	-	TGT	ATTCGTTAC...GATATG	GATTCGGGG	...GTCTACAA
Selected sequence for amplification primer	654				TACAA RATYKGIGGT ATYGG
Selected sequences for amplification primers ^a	655				TACAA RATYKGIGGT ATYGG
	559				ATG MGICARACIR TYGCTGTCCG

The sequence numbering refers to the *Saccharomyces cerevisiae* *tuf* (EF-1) gene fragment (SEQ ID NO. 665). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches are indicated by lower-case letters. "-" indicate incomplete sequence data. Dots indicate gaps in the sequences displayed.

"R" "Y" "M" "K" "W" and "S" designate nucleotide positions which are degenerated. "R" stands for A or G; "Y" stands for C or T; "M" stands for A or C; "K" stands for G or T; "W" stands for A or T; "S" stands for C or G. "I" stands for inosine which is a nucleotide analog that can bind to any of the four nucleotides A, C, G or T.

^a This sequences are the reverse-complement of the selected primers.

Annex VIII: Strategy for the selection of *Streptococcus agalactiae*-specific amplification primers from *tuf* sequences.

				SEQ ID NO.:	Accession #:
5	<i>S. agalactiae</i>	305	CCAGAA CGTGATACCTG ACAACCTTT ACTT...GGAC AACGTTGGTG TTCTTCTTCG TG	542	
	<i>S. agalactiae</i>		CCAGAA CGTGATACCTG ACAACCTTT ACTT...GGAC AACGTTGGTG TTCTTCTTCG TG	207	
	<i>S. agalactiae</i>		CCAGAA CGTGATACCTG ACAACCTTT ACTT...GGAC AACGTTGGTG TTCTTCTTCG TG	208	
	<i>S. agalactiae</i>		CCAGAA CGTGATACCTG ACAACCTTT ACTT...GGAC AACGTTGGTG TTCTTCTTCG TG	209	
10	<i>S. anginosus</i>		CCAGAA CGTGATACCTG ACAACCTTT ACTT...GGAC AACGTTGGTG TTCTTCTTCG TG	210	
	<i>S. anginosus</i>		CCAGAA CGTGATACCTG ACAACCTTT ACTT...GGAC AACGTTGGTG TTCTTCTTCG TG	211	
	<i>S. bovis</i>		CCAGAA CGTGATACCTG ACAACCTTT ACTT...GGAC AACGTTGGTG TTCTTCTTCG TG	221	
	<i>S. gordonii</i>		CCAGAA CGTGATACCTG ACAACCTTT ACTT...GGAC AACGTTGGTG TTCTTCTTCG TG	212	
	<i>S. mutans</i>		CCAGAA CGTGATACCTG ACAACCTTT ACTT...GGAC AACGTTGGTG TTCTTCTTCG TG	223	
	<i>S. pneumoniae</i>		CCAGAA CGTGATACCTG ACAACCTTT ACTT...GGAC AACGTTGGTG TTCTTCTTCG TG	224	
15	<i>S. sanguinis</i>		CCAGAA CGTGATACCTG ACAACCTTT ACTT...GGAC AACGTTGGTG TTCTTCTTCG TG	145 ^a	
	<i>S. sobrinus</i>		CCAGAA CGTGATACCTG ACAACCTTT ACTT...GGAC AACGTTGGTG TTCTTCTTCG TG	227	
	<i>B. cepacia</i>		CCAGAA CGTGATACCTG ACAACCTTT ACTT...GGAC AACGTTGGTG TTCTTCTTCG TG	228	
	<i>B. fragilis</i>		CCAGAA CGTGATACCTG ACAACCTTT ACTT...GGAC AACGTTGGTG TTCTTCTTCG TG	16	P33165
	<i>B. subtilis</i>		CCAGAA CGTGATACCTG ACAACCTTT ACTT...GGAC AACGTTGGTG TTCTTCTTCG TG	-	299104
20	<i>C. diptheriae</i>		CCAGAA CGTGATACCTG ACAACCTTT ACTT...GGAC AACGTTGGTG TTCTTCTTCG TG	662	
	<i>C. trachomatis</i>		CCAGAA CGTGATACCTG ACAACCTTT ACTT...GGAC AACGTTGGTG TTCTTCTTCG TG	22	
	<i>E. coli</i>		CCAGAA CGTGATACCTG ACAACCTTT ACTT...GGAC AACGTTGGTG TTCTTCTTCG TG	78	
	<i>G. vaginalis</i>		CCAGAA CGTGATACCTG ACAACCTTT ACTT...GGAC AACGTTGGTG TTCTTCTTCG TG	135 ^a	
25	<i>S. aureus</i>		CCAGAA CGTGATACCTG ACAACCTTT ACTT...GGAC AACGTTGGTG TTCTTCTTCG TG	179	
	Selected sequence for species-specific primer		GAA CGTGATACCTG ACAACCTTT A	549	
30	Selected sequence for species-specific primer ^b		C AACGTTGGTG TTCTTCTTC	550	

The sequence numbering refers to the *Streptococcus agalactiae* *tuf* gene fragment (SEQ ID NO. 209). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches are indicated by lower-case letters. Dots indicate gaps in the sequences displayed.

"R" "Y" "M" "K" "W" and "S" designate nucleotide positions which are degenerated. "R" stands for A or G; "Y" stands for C or T; "M" stands for A or C; "K" stands for G or T; "W" stands for A or T; "S" stands for C or G. "I" stands for inosine which is a nucleotide analog that can bind to any of the four nucleotides A, C, G or T.

^a The SEQ ID NO. refers to previous patent application WO98/20157.
^b This sequence is the reverse-complement of the selected primer.

Annex IX: Strategy for the selection of *Streptococcus agalactiae*-specific hybridization probes from *tuf* sequences.

[illegible]

Selected sequences for
species-specific hybri-
dization probes^b

ACTGT TCCTGTCTAAC GACGAACTTG AAA

CGTTGG TATTAAAGAA GATATCCAAA AAGCAGTTTG

582
583

The sequence numbering refers to the *Streptococcus agalactiae* *tuf* gene fragment (SEQ ID NO. 209). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches are indicated by lower-case letters. Dots indicate gaps in the sequences displayed.

The SEQ ID NO. refers to previous patent application W098/20157.
These sequences are the reverse-complement of the selected probes.

Annex X: Strategy for the selection of *Streptococcus agalactiae*-specific amplification primers from *atpD* sequences.

5	<i>S. agalactiae</i>	39	TT GATTGCTAT	80	203	234	368	399	SEQ ID NO.:
	<i>S. agalactiae</i>	TT GATTGCTAT	AAAATGGCG ATAGTCACA	AAAATAGTA	TAAGGATA	CTTGGGTCG	TGCTTCAC	ATTAGCACT TACTTAAAG	380
	<i>S. agalactiae</i>	TT GATTGCTAT	AAAATGGCG ATAGTCACA	AAAATAGTA	TAAGGATA	CTTGGGTCG	TGCTTCAC	ATTAGCACT TACTTAAAG	379
10	<i>S. agalactiae</i>	TT GATTGCTAT	AAAATGGCG ATAGTCACA	AAAATAGTA	TAAGGATA	CTTGGGTCG	TGCTTCAC	ATTAGCACT TACTTAAAG	381
	<i>S. agalactiae</i>	TT GATTGCTAT	AAAATGGCG ATAGTCACA	AAAATAGTA	TAAGGATA	CTTGGGTCG	TGCTTCAC	ATTAGCACT TACTTAAAG	382
	<i>S. bovis</i>	TT GATTGCTAT	AAAATGGCG ATAGTCACA	AAAATAGTA	TAAGGATA	CTTGGGTCG	TGCTTCAC	ATTAGCACT TACTTAAAG	383
	<i>S. salivarius</i>	TT GATTGCTAT	AAAATGGCG ATAGTCACA	AAAATAGTA	TAAGGATA	CTTGGGTCG	TGCTTCAC	ATTAGCACT TACTTAAAG	384
	<i>S. pneumoniae</i>	CT TGTGCTTAC	AAAATGGCG ATAGTCACA	AAAATAGTA	TAAGGATA	CTTGGGTCG	TGCTTCAC	ATTAGCACT TACTTAAAG	385
15	<i>S. pyogenes</i>	TT GATTGCTAT	AAAATGGCG ATAGTCACA	AAAATAGTA	TAAGGATA	CTTGGGTCG	TGCTTCAC	ATTAGCACT TACTTAAAG	387
	<i>S. anginosus</i>	CT TGTGCTTAC	AAAATGGCG ATAGTCACA	AAAATAGTA	TAAGGATA	CTTGGGTCG	TGCTTCAC	ATTAGCACT TACTTAAAG	388
	<i>S. sanguinis</i>	CT TGTGCTTAC	AAAATGGCG ATAGTCACA	AAAATAGTA	TAAGGATA	CTTGGGTCG	TGCTTCAC	ATTAGCACT TACTTAAAG	389
	<i>S. mutans</i>	TT GATTGCTAT	AAAATGGCG ATAGTCACA	AAAATAGTA	TAAGGATA	CTTGGGTCG	TGCTTCAC	ATTAGCACT TACTTAAAG	390
	<i>S. anthracis</i>	TT GATTGCTAT	AAAATGGCG ATAGTCACA	AAAATAGTA	TAAGGATA	CTTGGGTCG	TGCTTCAC	ATTAGCACT TACTTAAAG	391
20	<i>B. cereus</i>	GT AAAACAGAG	AAAATGGCG ATAGTCACA	AAAATAGTA	TAAGGATA	CTTGGGTCG	TGCTTCAC	ATTAGCACT TACTTAAAG	392
	<i>E. faecium</i>	GT AAAACAGAG	AAAATGGCG ATAGTCACA	AAAATAGTA	TAAGGATA	CTTGGGTCG	TGCTTCAC	ATTAGCACT TACTTAAAG	393
	<i>E. faecium</i>	GT AAAACAGAG	AAAATGGCG ATAGTCACA	AAAATAGTA	TAAGGATA	CTTGGGTCG	TGCTTCAC	ATTAGCACT TACTTAAAG	394
	<i>E. coli</i>	TT GATTGCTAT	AAAATGGCG ATAGTCACA	AAAATAGTA	TAAGGATA	CTTGGGTCG	TGCTTCAC	ATTAGCACT TACTTAAAG	395
25	<i>L. monocytogenes</i>	Ta cgaatctct	AAAATGGCG ATAGTCACA	AAAATAGTA	TAAGGATA	CTTGGGTCG	TGCTTCAC	ATTAGCACT TACTTAAAG	396
	<i>S. aureus</i>	Ta cgaatctct	AAAATGGCG ATAGTCACA	AAAATAGTA	TAAGGATA	CTTGGGTCG	TGCTTCAC	ATTAGCACT TACTTAAAG	397
	<i>S. epidermidis</i>	GT TATGATGTC	AAAATGGCG ATAGTCACA	AAAATAGTA	TAAGGATA	CTTGGGTCG	TGCTTCAC	ATTAGCACT TACTTAAAG	398
		ca CATGAGGTC	AAAATGGCG ATAGTCACA	AAAATAGTA	TAAGGATA	CTTGGGTCG	TGCTTCAC	ATTAGCACT TACTTAAAG	399
30	Selected sequences for species-specific primer	ATTCCTAT	AAAATGGCG ATAGTCACA	AAAATAGTA	TAAGGATA	CTTGGGTCG	TGCTTCAC	ATTAGCACT TACTTAAAG	627
		AAAATGGCG	ATAGTCACA	AAAATAGTA	TAAGGATA	CTTGGGTCG	TGCTTCAC	ATTAGCACT TACTTAAAG	628
35	Selected sequences for species-specific primers ^a	GGATA	CTTGGGTCG	TGCTTCAC	G			ATTAGCACT TACTTAAAG	625
								ATTAGCACT TACTTAAAG	626

The sequence numbering refers to the *Streptococcus agalactiae* *tuf* gene fragment (SEQ ID NO. 380). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches are indicated by lower-case letters. Dots indicate gaps in the sequences displayed.

^{a,d,e,f} These sequences were obtained from Genbank and have accession #: a=AB009314, d=AF001955, e=U31170, and f=V00311.

^g These sequences were obtained from genome sequencing projects.

^h These sequences are the reverse-complement of the selected primers.

Annex XI: Strategy for the selection of *Candida albicans*/*dubliniensis*-specific amplification primers, *Candida albicans*-specific hybridization probe and *Candida dubliniensis*-specific hybridization probe from tuf sequences.

5

337	C. albicans	CGTC	AGGAGGCTTG	GTTCACACCC	AAAGCTG...	CAACATGA	TTGAGCCATC	CACCAACT...	C	AAATCCGGTA	AGTTACTGG	TAAAGACCTTG	T	491	SEQ ID NO.:	Accession #:
	C. albicans	CGTC	AGGAGGCTTG	GTTCACACCC	AAAGCTG...	CAACATGA	TTGAGCCATC	CACCAACT...	C	AAATCCGGTA	AGTTACTGG	TAAAGACCTTG	T	624		
	C. albicans	CGTC	AGGAGGCTTG	GTTCACACCC	AAAGCTG...	CAACATGA	TTGAGCCATC	CACCAACT...	C	AAATCCGGTA	AGTTACTGG	TAAAGACCTTG	T	409		
	C. albicans	CGTC	AGGAGGCTTG	GTTCACACCC	AAAGCTG...	CAACATGA	TTGAGCCATC	CACCAACT...	C	AAATCCGGTA	AGTTACTGG	TAAAGACCTTG	T	410		
	C. albicans	CGTC	AGGAGGCTTG	GTTCACACCC	AAAGCTG...	CAACATGA	TTGAGCCATC	CACCAACT...	C	AAATCCGGTA	AGTTACTGG	TAAAGACCTTG	T	407		
	C. dubliniensis	CGTC	AGGAGGCTTG	GTTCACACCC	AAAGCTG...	CAACATGA	TTGAGCCATC	CACCAACT...	C	AAATCCGGTA	AGTTACTGG	TAAAGACCTTG	T	408		
	C. dubliniensis	CGTC	AGGAGGCTTG	GTTCACACCC	AAAGCTG...	CAACATGA	TTGAGCCATC	CACCAACT...	C	AAATCCGGTA	AGTTACTGG	TAAAGACCTTG	T	412		
	C. dubliniensis	CGTC	AGGAGGCTTG	GTTCACACCC	AAAGCTG...	CAACATGA	TTGAGCCATC	CACCAACT...	C	AAATCCGGTA	AGTTACTGG	TAAAGACCTTG	T	414		
	C. glabrata	CATC	AGGAGGCTTG	GTTCACACCC	AAAGCTG...	CAACATGA	TTGAGCCATC	CACCAACT...	C	AAATCCGGTA	AGTTACTGG	TAAAGACCTTG	T	415		
	C. guilliermondii	CGTC	AGGAGGCTTG	GTTCACACCC	AAAGCTG...	CAACATGA	TTGAGCCATC	CACCAACT...	C	AAATCCGGTA	AGTTACTGG	TAAAGACCTTG	T	417		
	C. kefyr	CATC	AGGAGGCTTG	GTTCACACCC	AAAGCTG...	CAACATGA	TTGAGCCATC	CACCAACT...	C	AAATCCGGTA	AGTTACTGG	TAAAGACCTTG	T	418		
	C. krusei	CATC	AGGAGGCTTG	GTTCACACCC	AAAGCTG...	CAACATGA	TTGAGCCATC	CACCAACT...	C	AAATCCGGTA	AGTTACTGG	TAAAGACCTTG	T	421		
	C. lusitanae	CGTC	AGGAGGCTTG	GTTCACACCC	AAAGCTG...	CAACATGA	TTGAGCCATC	CACCAACT...	C	AAATCCGGTA	AGTTACTGG	TAAAGACCTTG	T	422		
	C. neoformans	CATC	AGGAGGCTTG	GTTCACACCC	AAAGCTG...	CAACATGA	TTGAGCCATC	CACCAACT...	C	AAATCCGGTA	AGTTACTGG	TAAAGACCTTG	T	424		
	C. parapsilosis	CGTC	AGGAGGCTTG	GTTCACACCC	AAAGCTG...	CAACATGA	TTGAGCCATC	CACCAACT...	C	AAATCCGGTA	AGTTACTGG	TAAAGACCTTG	T	423		
	C. tropicalis	CGTC	AGGAGGCTTG	GTTCACACCC	AAAGCTG...	CAACATGA	TTGAGCCATC	CACCAACT...	C	AAATCCGGTA	AGTTACTGG	TAAAGACCTTG	T	426		
	A. fumigatus	CATC	AGGAGGCTTG	GTTCACACCC	AAAGCTG...	CAACATGA	TTGAGCCATC	CACCAACT...	C	AAATCCGGTA	AGTTACTGG	TAAAGACCTTG	T	429		
	Human	CATC	AGGAGGCTTG	GTTCACACCC	AAAGCTG...	CAACATGA	TTGAGCCATC	CACCAACT...	C	AAATCCGGTA	AGTTACTGG	TAAAGACCTTG	T	404		
	P. anomala	TATC	AGGAGGCTTG	GTTCACACCC	AAAGCTG...	CAACATGA	TTGAGCCATC	CACCAACT...	C	AAATCCGGTA	AGTTACTGG	TAAAGACCTTG	T		X03558	
	S. cerevisiae	TATC	AGGAGGCTTG	GTTCACACCC	AAAGCTG...	CAACATGA	TTGAGCCATC	CACCAACT...	C	AAATCCGGTA	AGTTACTGG	TAAAGACCTTG	T	447		
	S. pombe	CATC	AGGAGGCTTG	GTTCACACCC	AAAGCTG...	CAACATGA	TTGAGCCATC	CACCAACT...	C	AAATCCGGTA	AGTTACTGG	TAAAGACCTTG	T	622		
																U42189

Selected sequence

for species-specific

amplification primer^c C AGGAGGCTTG GTTCACACCC AAAGA

Selected sequence

for species-specific

amplification primer^{a,b}

Selected sequences

for species-specific

hybridization probes

CATGA TTGAGCCATC CACCA
CATGA TTGAGCTTC CACCA

577
578

ATCCGGTA AGTTACTGG TAAAGACCT

40

The sequence numbering refers to the *Candida albicans* tuf gene fragment (SEQ ID NO. 408). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches for SEQ ID NO. 577 are indicated by lower-case letters. Mismatches for SEQ ID NO. 578 are indicated by underlined nucleotides. Dots indicate gaps in the sequences displayed.

^a "R" "Y" "N" "K" "W" and "S" designate nucleotide positions which are degenerated. "R" stands for A or G; "Y" stands for C or T; "N" stands for A or C; "K" stands for G or T; "W" stands for C or G. "I" stands for inosine which is a nucleotide analog that can bind to any of the four nucleotides A, C, G or T.

^b *C. albicans* primers have been described in a previous patent (application W098/20157, SEQ ID Nos. 11-12)

^c This sequence is the reverse-complement of the selected primer.

153

Annex XII: Strategy for the selection of *Staphylococcus*-specific amplification primers from *tuf* sequences.

5	<i>S. aureus</i>	310	340	652	682	SEQ ID NO.:	Accession #:
	<i>S. aureus</i>	A CAGGCCCTGT TGAACGTGT CAAATCAAG...CACTTACCA	GAAGGTACTG	AAATGGTAAT	GC	179	-
	<i>S. aureus</i>	A CAGGCCCTGT TGAACGTGT CAAATCAAG...CACTTACCA	GAAGGTACTG	AAATGGTAAT	GC	176	-
	<i>S. aureus</i>	A CAGGCCCTGT TGAACGTGT CAAATCAAG...CACTTACCA	GAAGGTACTG	AAATGGTAAT	GC	177	-
	<i>S. aureus</i>	A CAGGCCCTGT TGAACGTGT CAAATCAAG...CACTTACCA	GAAGGTACTG	AAATGGTAAT	GC	180	-
	<i>S. aureus</i>	A CAGGCCCTGT TGAACGTGT CAAATCAAG...CACTTACCA	GAAGGTACTG	AAATGGTAAT	GC	181	-
	<i>S. capitis capitis</i>	A CAGGCCCTGT TGAACGTGT CAAATCAAG...CACTTACCA	GAAGGTACTG	AAATGGTAAT	GC	182	-
	<i>M. caseolyticus</i>	A CTGACCTGT TGAACGTGT CAAATCAAG...CACTTACCA	GAAGGTACTG	AAATGGTAAT	GC	183	-
	<i>S. cohnii</i>	A CAGGCCCTGT TGAACGTGT CAAATCAAG...CACTTACCA	GAAGGTACTG	AAATGGTAAT	GC	184	-
	<i>S. epidermidis</i>	A CAGGCCCTGT TGAACGTGT CAAATCAAG...CACTTACCA	GAAGGTACTG	AAATGGTAAT	GC	185	-
	<i>S. epidermidis</i>	A CAGGCCCTGT TGAACGTGT CAAATCAAG...CACTTACCA	GAAGGTACTG	AAATGGTAAT	GC	141*	-
	<i>S. haemolyticus</i>	A CAGGCCCTGT TGAACGTGT CAAATCAAG...CACTTACCA	GAAGGTACTG	AAATGGTAAT	GC	186	-
	<i>S. haemolyticus</i>	A CAGGCCCTGT TGAACGTGT CAAATCAAG...CACTTACCA	GAAGGTACTG	AAATGGTAAT	GC	188	-
	<i>S. haemolyticus</i>	A CAGGCCCTGT TGAACGTGT CAAATCAAG...CACTTACCA	GAAGGTACTG	AAATGGTAAT	GC	189	-
	<i>S. hominis</i>	A CAGGCCCTGT TGAACGTGT CAAATCAAG...CACTTACCA	GAAGGTACTG	AAATGGTAAT	GC	191	-
	<i>S. hominis</i>	A CAGGCCCTGT TGAACGTGT CAAATCAAG...CACTTACCA	GAAGGTACTG	AAATGGTAAT	GC	193	-
	<i>S. hominis</i>	A CAGGCCCTGT TGAACGTGT CAAATCAAG...CACTTACCA	GAAGGTACTG	AAATGGTAAT	GC	194	-
	<i>S. hominis</i>	A CAGGCCCTGT TGAACGTGT CAAATCAAG...CACTTACCA	GAAGGTACTG	AAATGGTAAT	GC	195	-
	<i>S. hominis</i>	A CAGGCCCTGT TGAACGTGT CAAATCAAG...CACTTACCA	GAAGGTACTG	AAATGGTAAT	GC	196	-
	<i>S. lugdunensis</i>	A CAGGCCCTGT TGAACGTGT CAAATCAAG...CACTTACCA	GAAGGTACTG	AAATGGTAAT	GC	197	-
	<i>S. saprophyticus</i>	A CAGGCCCTGT TGAACGTGT CAAATCAAG...CACTTACCA	GAAGGTACTG	AAATGGTAAT	GC	198	-
	<i>S. saprophyticus</i>	A CAGGCCCTGT TGAACGTGT CAAATCAAG...CACTTACCA	GAAGGTACTG	AAATGGTAAT	GC	199	-
	<i>S. saprophyticus</i>	A CAGGCCCTGT TGAACGTGT CAAATCAAG...CACTTACCA	GAAGGTACTG	AAATGGTAAT	GC	200	-
	<i>S. sciuri sciuri</i>	A CAGGCCCTGT TGAACGTGT CAAATCAAG...CACTTACCA	GAAGGTACTG	AAATGGTAAT	GC	201	-
	<i>S. warneri</i>	A CAGGCCCTGT TGAACGTGT CAAATCAAG...CACTTACCA	GAAGGTACTG	AAATGGTAAT	GC	187	-
	<i>S. warneri</i>	A CAGGCCCTGT TGAACGTGT CAAATCAAG...CACTTACCA	GAAGGTACTG	AAATGGTAAT	GC	192	-
	<i>S. warneri</i>	A CAGGCCCTGT TGAACGTGT CAAATCAAG...CACTTACCA	GAAGGTACTG	AAATGGTAAT	GC	202	-
	<i>B. subtilis</i>	A CTGACCTGT TGAACGTGT CAAATCAAG...CACTTACCA	GAAGGTACTG	AAATGGTAAT	GC	78	229104
	<i>B. coli</i>	A CAGGCCCTGT TGAACGTGT CAAATCAAG...CACTTACCA	GAAGGTACTG	AAATGGTAAT	GC	138*	-
	<i>L. monocytogenes</i>	A CTGACCTGT TGAACGTGT CAAATCAAG...CACTTACCA	GAAGGTACTG	AAATGGTAAT	GC	138*	-
35	Selected sequence for genus-specific primer	GAGCCTGT TGAACGTGT CAAATCA				553	
40	Selected sequences for genus-specific primers ^b	TTACCA GAAGGTACTG AAATGGTAA TTACCA GAAGGTACTG AAATGGTAA				575 707	

The sequence numbering refers to the *Staphylococcus aureus tuf* gene fragment (SEQ ID NO. 179). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches are indicated by lower-case letters. "-" indicate incomplete sequence data. Dots indicate gaps in the sequences displayed.

"R" "Y" "W" "K" "W" and "S" designate nucleotide positions which are degenerated. "R" stands for A or G; "Y" stands for C or T; "W" stands for A or C; "K" stands for G or T; "W" stands for A or T; "S" stands for C or G. "I" stands for inosine which is a nucleotide analog that can bind to any of the four nucleotides A, C, G or T.

^a The SEQ ID NO. refers to previous patent application W098/20157.
^b These sequences are the reverse-complement of the selected primers.

Annex XIII: Strategy for the selection of the *Staphylococcus* genus-specific hybridization probe from *tuf* sequences.

5

	400	425	SEQ ID NO.:	Accession #:
	G TTGAAATGTT CCGTAAATTA TTAGA		179	-
10 <i>S. aureus</i>	G TTGAAATGTT CCGTAAATTA TTAGA		176	-
<i>S. aureus</i>	G TTGAAATGTT CCGTAAATTA TTAGA		177	-
<i>S. aureus</i>	G TTGAAATGTT CCGTAAATTA TTAGA		178	-
<i>S. aureus aureus</i>	G TTGAAATGTT CCGTAAATTA TTAGA		180	-
<i>S. auricularis</i>	G TAGAAATGTT CCGTAAATTA TTAGA		181	-
15 <i>S. capitis capitis</i>	G TAGAAATGTT CCGTAAATTA TTAGA		182	-
<i>M. caseolyticus</i>	G TAGAAATGTT CCGTAAATTA TTAGA		183	-
<i>S. cohnii</i>	G TAGAAATGTT CCGTAAATTA TTAGA		184	-
<i>S. epidermidis</i>	G TAGAAATGTT CCGTAAATTA TTAGA		185	-
<i>S. haemolyticus</i>	G TAGAAATGTT CCGTAAATTA TTAGA		186	-
20 <i>S. haemolyticus</i>	G TAGAAATGTT CCGTAAATTA TTAGA		189	-
<i>S. haemolyticus</i>	G TAGAAATGTT CCGTAAATTA TTAGA		190	-
<i>S. haemolyticus</i>	G TAGAAATGTT CCGTAAATTA TTAGA		188	-
<i>S. hominis</i>	G TAGAAATGTT CCGTAAATTA TTAGA		196	-
<i>S. hominis</i>	G TAGAAATGTT CCGTAAATTA TTAGA		194	-
25 <i>S. hominis hominis</i>	G TAGAAATGTT CCGTAAATTA TTAGA		191	-
<i>S. hominis</i>	G TAGAAATGTT CCGTAAATTA TTAGA		193	-
<i>S. hominis</i>	G TAGAAATGTT CCGTAAATTA TTAGA		195	-
<i>S. lugdunensis</i>	G TAGAAATGTT CCGTAAATTA TTAGA		197	-
<i>S. saprophyticus</i>	G TAGAAATGTT CCGTAAATTA TTAGA		198	-
30 <i>S. saprophyticus</i>	G TAGAAATGTT CCGTAAATTA TTAGA		200	-
<i>S. saprophyticus</i>	G TAGAAATGTT CCGTAAATTA TTAGA		199	-
<i>S. sciuri sciuri</i>	G TTGAAATGTT CCGTAAATTA TTAGA		201	-
<i>S. warneri</i>	G TAGAAATGTT CCGTAAgTTA TTAGA		187	-
<i>S. warneri</i>	G TAGAAATGTT CCGTAAgTTA TTAGA		192	-
35 <i>S. warneri</i>	G TAGAAATGTT CCGTAAgTTA TTAGA		202	-
<i>S. warneri</i>	G TAGAAATGTT CCGTAAgTTA TTAGA		203	-
<i>B. subtilis</i>	G TTGAAATGTT CCGTAAgTt cTTGA		-	Z99104
<i>E. coli</i>	G TTGAAATGTT CCGcAAAcTg cTGGA		78	-
40 <i>L. monocytogenes</i>	G TAGAAATGTT CCGTAAATTA cTAGA		138 ^a	-

Selected sequence for
genus-specific hybridi-
zation probe

GAAATGTT CCGTAAATTA TT

605

45

The sequence numbering refers to the *Staphylococcus aureus* *tuf* gene fragment (SEQ ID NO. 179). Nucleotides in capitals are identical to the selected sequence or match that sequence. Mismatches are indicated by lower-case letters.

50 ^a The SEQ ID NO. refers to previous patent application WO98/20157.

Annex XIV: Strat gy for th s l ction of *Staphylococcus saprophyticus*-sp cific and of *Staphylococcus haemolyticus*-specific hybridization prob s from *tuf* sequences.

5

		339			383	SEQ ID NO.:
10	<i>S. aureus</i>	AG TtGGTGAAGA	AgTtGAAATC	ATcGGTtTaC	ATGACACaTC	TAA 179
	<i>S. aureus</i>	AG TtGGTGAAGA	AgTtGAAATC	ATcGGTtTaC	ATGACACaTC	TAA 176
	<i>S. aureus</i>	AG TtGGTGAAGA	AgTtGAAATC	ATcGGTtTaC	ATGACACaTC	TAA 177
	<i>S. aureus</i>	AG TtGGTGAAGA	AgTtGAAATC	ATcGGTtTaC	ATGACACaTC	TAA 178
15	<i>S. aureus aureus</i>	AG TtGGTGAAGA	AgTtGAAATC	ATcGGTtTaC	ATGACACaTC	TAA 180
	<i>S. auricularis</i>	AG TCGGTGAAGA	AgTtGAAATC	ATcGGTATga	AaGACAggTTC	AAA 181
	<i>S. capitis capitis</i>	AG TtGGTGAAGA	AgTtGAAATC	ATcGGTATCC	AcGAaACTTC	TAA 182
	<i>M. caseolyticus</i>	AG TtGGTGAAGA	AgTtGAAATC	ATTGGTtTaa	cTGAagaacC	AAA 183
	<i>S. cohnii</i>	AG TCGGTGAAGA	AgTtGAAATC	ATcGGTATgC	AaGAagaTTC	CAA 184
20	<i>S. epidermidis</i>	AG TtGGTGAAGA	AgTtGAAATC	ATcGGTATgC	AcGAaACTTC	TAA 185
	<i>S. haemolyticus</i>	AG TtGGTGAAGA	AgTtGAAATC	ATTGGTATCC	ATGACACTTC	TAA 186
	<i>S. haemolyticus</i>	AG TtGGTGAAGA	AgTtGAAATC	ATTGGTATCC	ATGACACTTC	TAA 189
	<i>S. haemolyticus</i>	AG TtGGTGAAGA	AgTtGAAATC	ATTGGTATCC	ATGACACTTC	TAA 190
	<i>S. haemolyticus</i>	AG TtGGTGAAGA	AgTtGAAATt	ATTGGTATCa	AaGAaACTTC	TAA 188
25	<i>S. hominis</i>	AG TtGGTGAAGA	AgTtGAAATt	ATTGGTATCa	AaGAaACTTC	TAA 194
	<i>S. hominis hominis</i>	AG TtGGTGAAGA	AgTtGAAATt	ATTGGTATCa	AaGAaACTTC	TAA 191
	<i>S. hominis</i>	AG TtGGTGAAGA	AgTtGAAATt	ATTGGTATCa	AaGAaACTTC	TAA 193
	<i>S. hominis</i>	AG TtGGTGAAGA	AgTtGAAATt	ATTGGTATCa	AaGAaACTTC	TAA 195
	<i>S. hominis</i>	AG TtGGTGAAGA	AgTtGAAATt	ATTGGTATCa	AaGAtACTTC	TAA 196
30	<i>S. lugdunensis</i>	AG TCGGTGAAGA	AgTtGAAATt	ATTGGTATCC	AcGAtACTaC	TAA 197
	<i>S. saprophyticus</i>	AG TCGGTGAAGA	AATCGAAATC	ATcGGTATgC	AaGAagaATC	CAA 198
	<i>S. saprophyticus</i>	AG TCGGTGAAGA	AATCGAAATC	ATcGGTATgC	AaGAagaATC	CAA 200
	<i>S. saprophyticus</i>	AG TCGGTGAAGA	AATCGAAATC	ATcGGTATgC	AaGAagaATC	CAA 199
	<i>S. sciuri sciuri</i>	TG TtGGTGAAGA	AgTtGAAATC	ATcGGTtTaa	cTGAagaATC	TAA 201
35	<i>S. warneri</i>	AG TtGGTGAAGA	AgTtGAAATC	ATcGGTtTaC	ATGACACTTC	TAA 187
	<i>S. warneri</i>	AG TtGGTGAAGA	AgTtGAAATC	ATcGGTtTaC	ATGACACTTC	TAA 192
	<i>S. warneri</i>	AG TtGGTGAAGA	AgTtGAAATC	ATcGGTtTaC	ATGACACTTC	TAA 202
	<i>S. warneri</i>	AG TtGGTGAAGA	AgTtGAAATC	ATcGGTtTaC	ATGACACTTC	TAA 203
	<i>B. subtilis</i>	AG TCGGTGAAGA	AgTtGAAATC	ATcGGTcTtC	AaGAagaagag	AAA - ^a
40	<i>E. coli</i>	AG TtGGTGAAGA	AgTtGAAATC	gTTGGTATCa	AaGAgACTca	GAA 78
	<i>L. monocytogenes</i>	AG TtGGTGAAGA	AgTaGAAGTt	ATcGGTATCg	AaGAagaag	AAA 138 ^b
	Selected sequences for species-specific hybridization probes	CGGTGAAGA	AATCGAAATC	A		599
45				ATTGGTATCC	ATGACACTTC	594

50

The sequence numbering refers to the *Staphylococcus aureus tuf* gene fragment (SEQ ID NO. 179). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches are indicated by lower-case letters.

^a This sequence was obtained from Genbank accession #Z99104.

^b The SEQ ID NO. refers to previous patent application WO98/20157.

Annex XV: Strat gy for th s l ction of *Staphylococcus aureus*-specific and of *Staphylococcus epidermidis*-sp cific hybridization prob s from *tuf* sequences.

5

		521	547	592	617	SEQ ID NO.:
10	<i>S. aureus</i>	TACACCACA TACTGAATTC AAAGCAG...TTCTTCTCa	AAAGCAG...TTCTTCTCa	AACTATCGtC	CACAATT	179
	<i>S. aureus</i>	TACACCACA TACTGAATTC AAAGCAG...TTCTTCTc-	AAAGCAG...TTCTTCTc-	AACTATCGtC	CACAATT	178
	<i>S. aureus</i>	TACACCACA TACTGAATTC AAAGCAG...TTCTTCTCa	AAAGCAG...TTCTTCTCa	AACTATCGtC	CACAATT	176
	<i>S. aureus</i>	TACACCACA TACTGAATTC AAAGCAG...TTCTTCTCa	AAAGCAG...TTCTTCTCa	AACTATCGtC	CACAATT	177
	<i>S. aureus aureus</i>	TACACCACA TACTGAATTC AAAGCAG...TTCTTCTCa	AAAGCAG...TTCTTCTCa	AACTATCGtC	CACAATT	180
15	<i>S. auricularis</i>	TACACCACA cACTaAATTC ActGCAG...TTCTTCTCT	AAAGCAG...TTCTTCTCT	AACTAcCGtC	CACAATT	181
	<i>S. capitis capitis</i>	CACACCACA cACTaAATTC AAAGCGG...TTCTTCAGt	AAAGCGG...TTCTTCAGt	AACTAcCGCC	CACAATT	182
	<i>M. caseolyticus</i>	TACtCCACA TACTaAATTC AAAGCTG...TTCTTCACT	AAAGCTG...TTCTTCACT	AACTAcCGCC	CtCAGTT	183
	<i>S. cohnii</i>	TACACCACA cACaaAATTC AAAGCGG...TTCTTCAGt	AAAGCGG...TTCTTCAGt	AACTATCGCC	CACAATT	184
	<i>S. epidermidis</i>	TACACCACA cACaaAATTC AAAGCTG...TTCTTCACT	AAAGCTG...TTCTTCACT	AACTATCGCC	CACAATT	185
20	<i>S. haemolyticus</i>	CACACctCA cACaaAATTC AAAGCAG...TTCTTCACa	AAAGCAG...TTCTTCACa	AACTATCGtC	CACAATT	186
	<i>S. haemolyticus</i>	CACACctCA cACaaAATTC AAAGCAG...TTCTTCACa	AAAGCAG...TTCTTCACa	AACTATCGtC	CACAATT	189
	<i>S. haemolyticus</i>	CACACctCA cACaaAATTC AAAGCAG...TTCTTCACa	AAAGCAG...TTCTTCACa	AACTATCGtC	CACAATT	190
	<i>S. haemolyticus</i>	TACACctCA cACaaAATTC AAAGCAG...TTCTTCACT	AAAGCAG...TTCTTCACT	AACTATCGtC	CACAATT	188
	<i>S. hominis</i>	CACACctCA cACaaAATTC AAAGCAG...TTCTTCACT	AAAGCAG...TTCTTCACT	AACTATCGtC	CACAATT	195
25	<i>S. hominis</i>	TACACctCA cACaaAATTC AAAGCAG...TTCTTCACT	AAAGCAG...TTCTTCACT	AACTATCGtC	CACAATT	196
	<i>S. hominis hominis</i>	TACACctCA cACaaAATTC AAAGCAG...TTCTTCTCT	AAAGCAG...TTCTTCTCT	AACTATCGtC	CACAATT	191
	<i>S. hominis</i>	TACACctCA cACaaAATTC AAAGCAG...TTCTTCTCT	AAAGCAG...TTCTTCTCT	AACTATCGtC	CACAATT	193
	<i>S. hominis</i>	TACACctCA cACaaAATTC AAAGCAG...TTCTTCTCT	AAAGCAG...TTCTTCTCT	AACTATCGtC	CACAATT	194
	<i>S. lugdunensis</i>	TACACctCA cACTaAATTC AAAGCTG...TTCTTCTCa	AAAGCTG...TTCTTCTCa	AACTAcCGCC	CACAATT	197
30	<i>S. saprophyticus</i>	TACACCACA TACaaAATTC AAAGCGG...TTCTTCACT	AAAGCGG...TTCTTCACT	AACTAcCGCC	CACAATT	198
	<i>S. saprophyticus</i>	TACACCACA TACaaAATTC AAAGCGG...TTCTTCACT	AAAGCGG...TTCTTCACT	AACTAcCGCC	CACAATT	199
	<i>S. saprophyticus</i>	TACACCACA TACaaAATTC AAAGCGG...TTCTTCACT	AAAGCGG...TTCTTCACT	AACTAcCGCC	CACAATT	200
	<i>S. sciuri sciuri</i>	CACACctCA cACTaAATTC AAAGCTG...TTCTTCACa	AAAGCTG...TTCTTCACa	AACTAcCGCC	CACAATT	201
	<i>S. warneri</i>	TACACCACA TACaaAATTC AAAGCGG...TTCTTCTCT	AAAGCGG...TTCTTCTCT	AACTAcCGCC	CACAATT	192
35	<i>S. warneri</i>	TACACCACA TACaaAATTC AAAGCGG...TTCTTCAGt	AAAGCGG...TTCTTCAGt	AACTAcCGCC	CACAATT	187
	<i>S. warneri</i>	TACACCACA TACaaAATTC AAAGCGG...TTCTTCAGt	AAAGCGG...TTCTTCAGt	AACTAcCGCC	CACAATT	202
	<i>S. warneri</i>	TACACCACA TACaaAATTC AAAGCGG...TTCTTCAGt	AAAGCGG...TTCTTCAGt	AACTAcCGCC	CACAATT	203
	<i>B. subtilis</i>	CACtCCACA cAgcaAATTC AAAGCTG...TTCTTCTCT	AAAGCTG...TTCTTCTCT	AACTAcCGtC	CtCAGTT	- ^a
	<i>E. coli</i>	CAAgCCGCA cACcaAgTTC gAAtCTG...TTCTTCAaa	gAAtCTG...TTCTTCAaa	ggCTAcCGtC	CgCAGTT	78
40	<i>L. monocytogenes</i>	TACtCCACA cACTaAATTC AAAGCTG...TTCTTCAaa	AAAGCTG...TTCTTCAaa	AACTAcCGCC	CACAATT	138 ^b

Selected sequences
for species-specific
hybridization
probes

45	ACCACA TACTGAATTC AAAG	585
	TTCACCT AACTATCGCC CACA	593

The sequence numbering refers to the *Staphylococcus aureus tuf* gene fragment (SEQ ID NO. 179). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches are indicated by lower-case letters. "-" indicate incomplete sequence data. Dots indicate gaps in the sequences displayed.

50

^a This sequence was obtained from Genbank accession #Z99104.

^b The SEQ ID NO. refers to previous patent application WO98/20157.

Annex XVI: Strategy for the selection of the *Staphylococcus hominis*-specific hybridization probe from *tuf* sequences.

5

	358	383	SEQ ID NO.:
<i>S. aureus</i>	ATC ATcGGTtTac AtGACACaTC TAA		179
10 <i>S. aureus</i>	ATC ATcGGTtTac AtGACACaTC TAA		176
<i>S. aureus</i>	ATC ATcGGTtTac AtGACACaTC TAA		177
<i>S. aureus</i>	ATC ATcGGTtTac AtGACACaTC TAA		178
<i>S. aureus aureus</i>	ATC ATcGGTtTac AtGACACaTC TAA		180
<i>S. auricularis</i>	ATC ATcGGTATgA AAGAcggTTC AAA		181
15 <i>S. capitis capitis</i>	ATC ATcGGTATCc AcGAAACTTC TAA		182
<i>M. caseolyticus</i>	ATC ATTGGTtTaA ctGAAGAacC AAA		183
<i>S. cohnii</i>	ATC ATcGGTATgc AAGAAGaTTC CAA		184
<i>S. epidermidis</i>	ATC ATcGGTATgc AcGAAACTTC TAA		185
<i>S. haemolyticus</i>	ATC ATTGGTATCc AtGACACTTC TAA		186
20 <i>S. haemolyticus</i>	ATC ATTGGTATCc AtGACACTTC TAA		189
<i>S. haemolyticus</i>	ATC ATTGGTATCc AtGACACTTC TAA		190
<i>S. haemolyticus</i>	ATT ATTGGTATCA AAGAACTTC TAA		188
<i>S. hominis</i>	ATT ATTGGTATCA AAGAtACTTC TAA		196
<i>S. hominis</i>	ATT ATTGGTATCA AAGAACTTC TAA		194
25 <i>S. hominis hominis</i>	ATT ATTGGTATCA AAGAACTTC TAA		191
<i>S. hominis</i>	ATT ATTGGTATCA AAGAACTTC TAA		193
<i>S. hominis</i>	ATT ATTGGTATCA AAGAACTTC TAA		195
<i>S. lugdunensis</i>	ATT ATTGGTATCc AcGAtACTaC TAA		197
<i>S. saprophyticus</i>	ATC ATcGGTATgc AAGAAGaaTC CAA		198
30 <i>S. saprophyticus</i>	ATC ATcGGTATgc AAGAAGaaTC CAA		200
<i>S. saprophyticus</i>	ATC ATcGGTATgc AAGAAGaaTC CAA		199
<i>S. sciuri sciuri</i>	ATC ATcGGTtTaA ctGAAGaaTC TAA		201
<i>S. warneri</i>	ATC ATcGGTtTac AtGACACTTC TAA		187
<i>S. warneri</i>	ATC ATcGGTtTac AtGACACTTC TAA		192
35 <i>S. warneri</i>	ATC ATcGGTtTac AtGACACTTC TAA		202
<i>S. warneri</i>	ATC ATcGGTtTac AtGACACTTC TAA		203
<i>B. subtilis</i>	ATC ATcGGTcTtc AAGAAGagag AAA		- ^a
<i>E. coli</i>	ATC gTTGGTATCA AAGAgACTca GAA		78
<i>L. monocytogenes</i>	GTT ATcGGTATCg AAGAAGaaag AAA		138 ^b

40 Selected sequence for
species-specific
hybridization probe **ATTGGTATCA AAGAACTTC** 597

45

The sequence numbering refers to the *Staphylococcus aureus tuf* gene fragment (SEQ ID NO. 179). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches are indicated by lower-case letters. Dots indicate gaps in the sequences displayed.

50

^a This sequence was obtained from Genbank accession #299104.

^b The SEQ ID NO. refers to previous patent application WO98/20157.

Annex XVII: Strategy for the selection of the *Enterococcus* genus-specific amplification primers from tuf sequences.

		270	298	556	582	SEQ ID NO.:	Accession #:
5	<i>E. avium</i>	TAGAATTAAAT GGCCTGCTGTT	GACGAATAT...TGAA	GATATCCAAAC	GTGGACAAGT ATT	131 ^a	-
	<i>E. casseliflavus</i>	TGGAATTAAAT GGTGCGAGTT	GACGAATAC...TGAA	GACATCCAAAC	GTGGACAAGT ATT	58	-
	<i>E. cecorum</i>	TAGAATTAAAT GGCCTGCGAGTT	GACGAATAC...TGAA	GATATCCAAAC	GTGGACAAGT ATT	59	-
	<i>E. dispar</i>	TAGAATTAAAT GGCCTGCGAGTT	GACGAATAT...TGAA	GATATCCAAAC	GTGGACAAGT ATT	60	-
10	<i>E. durans</i>	TGGAATTAAAT GGCCTGCGAGTT	GACGAATAT...TGAA	GATATCCAAAC	GTGGACAAGT TTT	61	-
	<i>E. flavescens</i>	TGGAATTAAAT GGCCTGCGAGTT	GACGAATAC...TGAA	GATATCCAAAC	GTGGACAAGT ATT	65	-
	<i>E. faecium</i>	TGGAATTAAAT GGCCTGCGAGTT	GACGAATAC...TGAA	GATATCCAAAC	GTGGACAAGT TTT	608	-
	<i>E. faecalis</i>	TAGAATTAAAT GGCCTGCGAGTT	GACGAATAT...TGAA	GATATCCAAAC	GTGGACAAGT ATT	607	-
	<i>E. gallinarum</i>	TGGAATTAAAT GGCCTGCGAGTT	GACGAATAC...TGAA	GATATCCAAAC	GTGGACAAGT ATT	609	-
	<i>E. hirae</i>	TGGAATTAAAT GGCCTGCGAGTT	GACGAATAT...TGAA	GATATCCAAAC	GTGGACAAGT TTT	67	-
15	<i>E. mundtii</i>	TGGAATTAAAT GGCCTGCGAGTT	GACGAATAT...TGAA	GATATCCAAAC	GTGGACAAGT TTT	68	-
	<i>E. pseudoavium</i>	TAGAATTAAAT GGCCTGCTGTT	GACGAATAC...TGAA	GATATCCAAAC	GTGGACAAGT ATT	69	-
	<i>E. raffinosus</i>	TAGAATTAAAT GGCCTGCTGTT	GATGAATAC...TGAA	GATATCCAAAC	GTGGACAAGT ATT	70	-
	<i>E. saccharolyticus</i>	TCGAATTAAAT GGCCTGCGAGTT	GACGAATAT...TGAA	GATATCCAAAC	GTGGACAAGT ATT	71	-
	<i>E. solitarius</i>	TGGAATTAAAT GGCCTGCGAGTT	GATGACTAC...TGAT	GATATCCAAAC	GTGGACAAGT ATT	72	-
20	<i>E. coli</i>	TGGAATTAAAT GGCCTGCTGTT	GATGACTAC...TGAT	GATATCCAAAC	GTGGACAAGT ATT	78	-
	<i>B. cepacia</i>	TGGAATTAAAT GGCCTGCTGTT	GATGACTAC...TGAT	GATATCCAAAC	GTGGACAAGT ATT	16	M22247
	<i>B. fragilis</i>	TGGAATTAAAT GGCCTGCTGTT	GATGACTAC...TGAT	GATATCCAAAC	GTGGACAAGT ATT	299104	-
	<i>B. subtilis</i>	TGGAATTAAAT GGCCTGCTGTT	GATGACTAC...TGAT	GATATCCAAAC	GTGGACAAGT ATT	-	-
25	<i>C. diphtheriae</i>	TGGAATTAAAT GGCCTGCTGTT	GATGACTAC...TGAT	GATATCCAAAC	GTGGACAAGT ATT	662	-
	<i>C. trachomatis</i>	TGGAATTAAAT GGCCTGCTGTT	GATGACTAC...TGAT	GATATCCAAAC	GTGGACAAGT ATT	22	-
	<i>G. vaginalis</i>	TGGAATTAAAT GGCCTGCTGTT	GATGACTAC...TGAT	GATATCCAAAC	GTGGACAAGT ATT	135 ^a	-
	<i>S. aureus</i>	TGGAATTAAAT GGCCTGCTGTT	GATGACTAC...TGAT	GATATCCAAAC	GTGGACAAGT ATT	179	-
	<i>S. pneumoniae</i>	TGGAATTAAAT GGCCTGCTGTT	GATGACTAC...TGAT	GATATCCAAAC	GTGGACAAGT ATT	145 ^a	-
	<i>A. adiacens</i>	TGGAATTAAAT GGCCTGCTGTT	GATGACTAC...TGAT	GATATCCAAAC	GTGGACAAGT ATT	118 ^a	-
30	<i>G. haemolysans</i>	TGGAATTAAAT GGCCTGCTGTT	GATGACTAC...TGAT	GATATCCAAAC	GTGGACAAGT TTT	87	-
	<i>G. morbillorum</i>	TGGAATTAAAT GGCCTGCTGTT	GATGACTAC...TGAT	GATATCCAAAC	GTGGACAAGT TTT	88	-
35	Selected sequence for amplification primer	AAATTAAT GGCCTGCTGTT	GATGAA			1137	
	Selected sequence for amplification primer ^b			A GATATCCAAAC	GTGGACAAGT	1136	

The sequence numbering refers to the *Enterococcus* *durans* tuf gene fragment (SEQ ID NO. 61). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches are indicated by lower-case letters. Dots indicate gaps in the sequences displayed. "y", "w" and "s" designate nucleotide positions which are degenerated. "y" stands for C or T; "w" stands for A or T; "s" stands for C or G. "I" stands for inosine which is a nucleotide analog that can bind to any of the four nucleotides A, C, G or T.

^a The SEQ ID NO. refers to previous patent application W098/20157.
^b This sequence is the reverse-complement of the selected primer.

Annex XVIII: Strategy for the selection of the *Enterococcus faecalis*-specific hybridization probe, of the *Enterococcus faecium*-specific hybridization probe and of the *Enterococcus casseliflavus*-*flavescens*-*gallinarum* group-specific hybridization probe from *tuf* sequences.

	395	448...526	549	SEQ ID NO.:	Accession #:
<i>E. avium</i>	GTGGA ACCTGGACAA GTTCGGTTG GTGACGAAAGT TGAATCGTA GGTATCGCT...CATC GGTGCTTTGT TACGTGGTGT			131 ^a	-
<i>E. casseliflavus</i>	GTGGA ACCTGGACAA GTTCGGTTG GTGACGAAAGT TGAATCGTA GGTATCGCT...CATC GGTGCTTTGT TACGTGGTGT			58	-
<i>E. cecorum</i>	GTGGA ACCTGGACAA GTTCGGTTG GTGACGAAAGT TGAATCGTA GGTATCGCT...CATC GGTGCTTTGT TACGTGGTGT			59	-
<i>E. dispar</i>	GTGGA ACCTGGACAA GTTCGGTTG GTGACGAAAGT TGAATCGTA GGTATCGCT...CATC GGTGCTTTGT TACGTGGTGT			60	-
<i>E. durans</i>	GTGGA ACCTGGACAA GTTCGGTTG GTGACGAAAGT TGAATCGTA GGTATCGCT...CATC GGTGCTTTGT TACGTGGTGT			61	-
<i>E. faecalis</i>	GTGGA ACCTGGACAA GTTCGGTTG GTGACGAAAGT TGAATCGTA GGTATCGCT...CATC GGTGCTTTGT TACGTGGTGT			62	-
<i>E. faecium</i>	GTGGA ACCTGGACAA GTTCGGTTG GTGACGAAAGT TGAATCGTA GGTATCGCT...CATC GGTGCTTTGT TACGTGGTGT			608	-
<i>E. flavescens</i>	GTGGA ACCTGGACAA GTTCGGTTG GTGACGAAAGT TGAATCGTA GGTATCGCT...CATC GGTGCTTTGT TACGTGGTGT			65	-
<i>E. gallinarum</i>	GTGGA ACCTGGACAA GTTCGGTTG GTGACGAAAGT TGAATCGTA GGTATCGCT...CATC GGTGCTTTGT TACGTGGTGT			609	-
<i>E. hirae</i>	GTGGA ACCTGGACAA GTTCGGTTG GTGACGAAAGT TGAATCGTA GGTATCGCT...CATC GGTGCTTTGT TACGTGGTGT			67	-
<i>E. mundtii</i>	GTGGA ACCTGGACAA GTTCGGTTG GTGACGAAAGT TGAATCGTA GGTATCGCT...CATC GGTGCTTTGT TACGTGGTGT			68	-
<i>E. pseudodavium</i>	GTGGA ACCTGGACAA GTTCGGTTG GTGACGAAAGT TGAATCGTA GGTATCGCT...CATC GGTGCTTTGT TACGTGGTGT			69	-
<i>E. raffinosus</i>	GTGGA ACCTGGACAA GTTCGGTTG GTGACGAAAGT TGAATCGTA GGTATCGCT...CATC GGTGCTTTGT TACGTGGTGT			70	-
<i>E. saccharolyticus</i>	GTGGA ACCTGGACAA GTTCGGTTG GTGACGAAAGT TGAATCGTA GGTATCGCT...CATC GGTGCTTTGT TACGTGGTGT			71	-
<i>E. solitarius</i>	GTGGA ACCTGGACAA GTTCGGTTG GTGACGAAAGT TGAATCGTA GGTATCGCT...CATC GGTGCTTTGT TACGTGGTGT			72	-
<i>C. diphtheriae</i>	GTGGA ACCTGGACAA GTTCGGTTG GTGACGAAAGT TGAATCGTA GGTATCGCT...CATC GGTGCTTTGT TACGTGGTGT			662	-
<i>G. vaginalis</i>	GTGGA ACCTGGACAA GTTCGGTTG GTGACGAAAGT TGAATCGTA GGTATCGCT...CATC GGTGCTTTGT TACGTGGTGT			135 ^a	-
<i>B. cepacia</i>	GTGGA ACCTGGACAA GTTCGGTTG GTGACGAAAGT TGAATCGTA GGTATCGCT...CATC GGTGCTTTGT TACGTGGTGT			16	-
<i>S. aureus</i>	GTGGA ACCTGGACAA GTTCGGTTG GTGACGAAAGT TGAATCGTA GGTATCGCT...CATC GGTGCTTTGT TACGTGGTGT			179	-
<i>B. subtilis</i>	GTGGA ACCTGGACAA GTTCGGTTG GTGACGAAAGT TGAATCGTA GGTATCGCT...CATC GGTGCTTTGT TACGTGGTGT			299104	-
<i>S. pneumoniae</i>	GTGGA ACCTGGACAA GTTCGGTTG GTGACGAAAGT TGAATCGTA GGTATCGCT...CATC GGTGCTTTGT TACGTGGTGT			145 ^a	-
<i>E. coli</i>	GTGGA ACCTGGACAA GTTCGGTTG GTGACGAAAGT TGAATCGTA GGTATCGCT...CATC GGTGCTTTGT TACGTGGTGT			78	-
<i>B. fragilis</i>	GTGGA ACCTGGACAA GTTCGGTTG GTGACGAAAGT TGAATCGTA GGTATCGCT...CATC GGTGCTTTGT TACGTGGTGT			M22247	-
<i>C. trachomatis</i>	GTGGA ACCTGGACAA GTTCGGTTG GTGACGAAAGT TGAATCGTA GGTATCGCT...CATC GGTGCTTTGT TACGTGGTGT			22	-
Selected sequences for species-specific or group-specific hybridization probes	GA ACCTGGACAA GTTCGG	AAAT TGAATCGTTT GGTATT	T GATCCATTGC TACGTGG	1174	
				602	
				1122	

The sequence numbering refers to the *Enterococcus faecium* *tuf* gene fragments (SEQ ID NO. 608). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches are indicated by lower-case letters. Dots indicate gaps in the sequences displayed.

^a The SEQ ID NO. refers to previous patent application W098/20157.

Ann x XIX: Strategy for the selection of primers for the identification of plat lets contaminants from tuf sequences.

		467	495	689	717	SEQ ID NO.:	Accession #:
5	<i>B. cereus</i>	GTA ACTGGGTGAG AGATGTTCCG TAAACT...C AGTTCTACTT	CCGTACAACT	GACGTAAC	7	-	-
	<i>B. subtilis</i>	GTT ACAGGTGTTG AATGTTCCG TAAGCT...C AGTTCTACTT	CCGTACAACT	GACGTAAC	-	299104	-
	<i>E. cloacae</i>	TGT ACTGGCGTTG AATGTTCCG CAAACT...C AGTTCTACTT	CCGTACAACT	GACGTGAC	54	-	-
	<i>E. coli</i>	TGT ACTGGCGTTG AATGTTCCG CAAACT...C AGTTCTACTT	CCGTACAACT	GACGTGAC	78	-	-
10	<i>K. oxytoca</i>	TGT ACTGGCGTTG AATGTTCCG CAAACT...C AGTTCTACTT	CCGTACAACT	GACGTGAC	100	-	-
	<i>K. pneumoniae</i>	TGT ACTGGCGTTG AATGTTCCG CAAACT...C AGTTCTACTT	CCGTACAACT	GACGTGAC	103	-	-
	<i>P. aeruginosa</i>	TGC ACGGCGTTG AATGTTCCG CAAACT...C AGTTCTACTT	CCGTACAACT	GACGTGAC	153	-	-
	<i>S. agalactiae</i>	GTT ACTGGGTGAG AATGTTCCG TAAACA...C AATTCTACTT	CCGTACAACT	GACGTAAC	209	-	-
	<i>S. aureus</i>	GTT ACAGGTGTTG AATGTTCCG TAAACT...C AATTCTACTT	CCGTACAACT	GACGTAAC	140 ^a	-	-
15	<i>S. choleraesuis</i>	TGT ACTGGCGTTG AATGTTCCG CAAACT...C AGTTCTACTT	CCGTACAACT	GACGTGAC	159	-	-
	<i>S. epidermidis</i>	GTT ACTGGGTGAG AATGTTCCG TAAACT...C AATTCTACTT	CCGTACAACT	GACGTAAC	611	-	-
	<i>S. marcescens</i>	TGT ACTGGCGTTG AATGTTCCG CAAACT...C AGTTCTACTT	CCGTACAACT	GACGTGAC	168	-	-
	<i>S. mutans</i>	GTT ACTGGGTGAG AATGTTCCG TAAACA...C AATTCTACTT	CCGTACAACT	GACGTAAC	224	-	-
	<i>S. pyogenes</i>	GTT ACTGGGTGAG AATGTTCCG TAAACA...C AATTCTACTT	CCGTACAACT	GACGTAAC	-	U40453	-
20	<i>S. salivarius</i>	GTT ACTGGGTGAG AATGTTCCG TAAACA...C AGTTCTACTT	CCGTACAACT	GACGTAAC	146 ^a	-	-
	<i>S. sanguinis</i>	GTT ACTGGGTGAG AATGTTCCG TAAACA...C AGTTCTACTT	CCGTACAACT	GACGTTAC	227	-	-
	<i>Y. enterocolitica</i>	TGT ACTGGCGTTG AATGTTCCG CAAACT...C AGTTCTACTT	CCGTACAACT	GATGTAAC	235	-	-

25 Selected sequence for amplification primer

ACTGGGTGAG AATGTTCCG TAA

636

Selected sequence for amplification primer^b

TTCTATTT CCGTACAACT GACGT

637

30 The sequence numbering refers to the *E. coli* tuf gene fragment (SEQ ID NO. 78). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches are indicated by lower-case letters. Dots indicate gaps in the sequences displayed.

35 "R" "Y" "M" "K" "W" and "S" designate nucleotide positions which are degenerated. "R" stands for A or G; "Y" stands for C or T; "M" stands for A or C; "K" stands for G or T; "W" stands for A or T; "S" stands for C or G. "I" stands for inosine which is a nucleotide analog that can bind to any of the four nucleotides A, C, G or T.

^a The SEQ ID NO. refers to previous patent application W098/20157.

^b This sequence is the reverse-complement of the selected primer.

Annex XX: Strategy for the selection of the universal amplification primers from *atpD* sequences.

		616	657	781	812	SEQ ID NO.:	Accession #:
5	<i>C. glutamicum</i>	GTGTTCCGTC AGATGGATGA GCCACACAGG GTCCGTATG CGC...CGTATG CTTCTCCGCG			TCGGTTATCCA GCCAAC	-	X76875
	<i>M. tuberculosis</i>	GTATTCGGAC AGATGGACGA GCCGCGGGCC ACCGTATG CGT...CGGATG CCGTCGGCCG			TCGGATATCCA GCCAAC	-	Z73419
	<i>E. faecalis</i>	GTGTTCCGAC AAATGAACGA ACCACACAGT GCTCGGATG CGG...CGTATG CTTCTCCGCG			TTGGTTATCCA ACCAAC	291	-
	<i>S. agalactiae</i>	GTCTTGGTC AAATGAATGA ACCACACAGT GCACGTATG CGT...CGTATG CTTCTCCGCG			TTGGTTATCCA ACCAAC	380	-
10	<i>B. subtilis</i>	GTATTCGGAC AAATGAACGA GCCGCGGGCC GCACGTATG CGT...CGTATG CTTCTCCGCG			TTGGTTATCCA GCCGAC	-	Z28592
	<i>L. monocytogenes</i>	GTATTCGGTC AAATGAACGA GCCACACAGT GCACGTATG CGT...CGTATG CTTCTCCGCG			TAGTTATCCA ACCAAC	324	-
	<i>S. aureus</i>	GTATTCGGCC AAATGAATGA GCCACCTGGT GCACGTATG CGT...CGTATG CTTCTCCGCG			TAGTTATCCA ACCAAC	366	-
	<i>A. baumannii</i>	GTCTACGGTC AGATGAACGA GCCACACAGT AACCGTCTA CGC...CGTATG CCACTCCGCG			TAGTTATCCA ACCTAC	243	-
	<i>N. gonorrhoeae</i>	GTGTATGGCC AAATGAACGA ACCTCCAGGC AACCGTCTG CGC...CGTATG CTTCTCCGCG			TCGGTTATCCA ACCGAC	-	Genome project
15	<i>C. freundii</i>	GTATATGGCC AGATGAACGA GCCGCTTGA AACCGTCTG CGT...CGTATG CCACTCCGCG			TAGCTTATCCA GCCGAC	264	-
	<i>E. cloacae</i>	GTATATGGCC AGATGAACGA GCCACACAGG AACCGTCTG CGC...CGTATG CTTCTCCGCG			TAGTTATCCA GCCTAC	284	-
	<i>E. coli</i>	GTGTATGGCC AGATGAACGA GCCGCTTGA AACCGTCTG CGC...CGTATG CTTCTCCGCG			TAGTTATCCA GCCGAC	669	V00267
	<i>S. typhimurium</i>	GTGTATGGCC AGATGAACGA GCCGCTTGA AACCGTCTG CGC...CGTATG CTTCTCCGCG			TAGTTATCCA GCCGAC	351	-
	<i>K. pneumoniae</i>	GTGTATGGCC AGATGAACGA GCCGCTTGA AACCGTCTG CGC...CGTATG CTTCTCCGCG			TAGTTATCCA GCCGAC	317	-
	<i>S. marcescens</i>	GTGTATGGCC AGATGAACGA GCCGCTTGA AACCGTCTG CGC...CGTATG CTTCTCCGCG			TAGTTATCCA GCCAAC	357	-
20	<i>Y. enterocolitica</i>	GTATATGGCC AAATGAATGA GCCACACAGT AACCGTCTG CGC...CGTATG CCACTCCGCG			TAGTTATCCA GCCAAC	393	-
	<i>B. cepacia</i>	GTGTATGGCC AGATGAACGA GCCGCTTGA AACCGTCTG CGC...CGTATG CTTCTCCGCG			TAGTTATCCA GCCGAC	-	X76877
	<i>H. influenzae</i>	GTGTATGGTC AAATGAACGA GCCGCTTGA AACCGTCTG CGC...CGTATG CCACTCCGCG			TAGTTATCCA GCCGAC	-	U32730
	<i>M. pneumoniae</i>	GTGTATGGTC AAATGAACGA GCCGCTTGA AACCGTCTG CGC...CGTATG CCACTCCGCG			TAGTTATCCA GCCAAC	-	U43738
	<i>H. pylori</i>	TGCTATGGCC AAATGAATGA GCCACACAGT GCACGTATG CGC...CGTATG CTTCTCCGCG			TGGGTATCCA GCCAAC	670	V00267
25	<i>B. fragilis</i>	GTGTTCGGAC AGATGAACGA ACCTCCCTGA GCACGTATG TCA...CGTATG CTTCTCCGCG			TAGTTATCCA ACCTAC	-	M22247
	Selected sequences for universal primers	C ARATGATGA RCICICIGGI GYINGIATG TAYGGIC ARATGAATGA RCICICIGGI AA					562 564
30	Selected sequences for universal primers ^a	ATG CCITCIGCIG TIGGITATCA RCC ATG CCITCIGCIG TIGGITATCA RCC					565 563

35 The sequence numbering refers to the *Escherichia coli atpD* gene fragment (SEQ ID NO. 669). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches for SEQ ID Nos. 562 and 565 are indicated by lower-case letters. Mismatches for SEQ ID Nos. 564 and 563 are indicated by underlined nucleotides. Dots indicate gaps in the sequences displayed.

40 "R" "Y" "M" "K" "W" and "S" letters designate nucleotide positions which are degenerated. "R" stands for A or G; "Y" stands for C or T; "M" stands for A or C; "K" stands for G or T; "W" stands for A or T; "S" stands for C or G. "I" stands for inosine which is a nucleotide analog that can bind to any of the four nucleotides A, C, G or T.
^a These sequences are the reverse-complement of the selected primers.

Annex XXI: Specific and ubiquitous primers for nucleic acid amplification (*recA* sequences).

5			Originating DNA fragment	
	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	Universal primers (<i>recA</i>)			
	919	5'-GGI CCI GAR TCI TMI GGI AAR AC	918 ^a	437-459
15	920 ^b	5'-TCI CCV ATI TCI CCI TCI AIY TC	918 ^a	701-723
	921	5'-TIY RTI GAY GCI GAR CAI GC	918 ^a	515-534
	922 ^b	5'-TAR AAY TTI ARI GCI YKI CCI CC	918 ^a	872-894
20	Universal primers (<i>rad51</i>)			
	935	5'-GGI AAR WSI CAR YTI TGY CAY AC	939 ^a	568-590
	936 ^b	5'-TCI SIY TCI GGI ARR CAI GG	939 ^a	1126-1145
25	Universal primers (<i>dmc1</i>)			
	937	5'-ATI ACI GAR GYI TTY GGI GAR TT	940 ^a	1038-1060
	938 ^b	5'-CYI GTI GYI SWI GCR TGI GC	940 ^a	1554-1573

^a Sequences from databases.

^b These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

Annex XXII: Specific and ubiquitous primers for nucleic acid amplification (*speA* sequences).

5			Originating DNA fragment	
	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	<u>Bacterial species: <i>Streptococcus pyogenes</i></u>			
	994	5'-TGG ACT AAC AAT CTC GCA AGA GG	993 ^a	60-82
15	995 ^b	5'-ACA TTC TCG TGA GTA ACA GGG T	993 ^a	173-194
	996	5'-ACA AAT CAT GAA GGG AAT CAT TTA G	993 ^a	400-424
	997 ^b	5'-CTA ATT CTT GAG CAG TTA CCA TT	993 ^a	504-526
20	998	5'-GGA GGG GTA ACA AAT CAT GAA GG	993 ^a	391-413
	997 ^b	5'-CTA ATT CTT GAG CAG TTA CCA TT	993 ^a	504-526

^a Sequence from databases.

25 ^b These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

Annex XXIII: First strategy for the selection of *Streptococcus pyogenes*-specific amplification primers from *speA* sequences.

Accession #	57	85	170	197	SEQ ID NO.:
speA X61573	CCTT	GGGCTAACAA	CCTCACAAGA	AGTAT...GTGACCTT.GT	CGTTCATCAG AATGTGAA
speA AF029051	----	GGGCTAACAA	CCTCACAAGA	AGTAT...GTGACCTT.GT	CGTTCATCAG AATGTGAA
speA X61571	TCCT	GGACTAACAA	TCTCGCAAGA	GGTAT...GTGACCTT.GT	TACTCAGAG AATGTGAA
speA X61570	TCCT	GGACTAACAA	TCTCGCAAGA	GGTAT...GTGACCTT.GT	TACTCAGAG AATGTGAA
speA X61568	TCCT	GGACTAACAA	TCTCGCAAGA	GGTAT...GTGACCTT.GT	TACTCAGAG AATGTGAA
speA X61569	TCCT	GGACTAACAA	TCTCGCAAGA	GGTAT...GTGACCTT.GT	TACTCAGAG AATGTGAA
speA X61572	TCCT	GGACTAACAA	TCTCGCAAGA	GGTAT...GTGACCTT.GT	TACTCAGAG AATGTGAA
speA X61560	TCCT	GGACTAACAA	TCTCGCAAGA	GGTAT...GTGACCTT.GT	TACTCAGAG AATGTGAA
speA U40453	TCCT	GGACTAACAA	TCTCGCAAGA	GGTAT...GTGACCTT.GT	TACTCAGAG AATGTGAA
speA X61554	TCCT	GGACTAACAA	TCTCGCAAGA	GGTAT...GTGACCTT.GT	TACTCAGAG AATGTGAA
speA X61557	TCCT	GGACTAACAA	TCTCGCAAGA	GGTAT...GTGACCTT.GT	TACTCAGAG AATGTGAA
speA X61559	TCCT	GGACTAACAA	TCTCGCAAGA	GGTAT...GTGACCTT.GT	TACTCAGAG AATGTGAA
speA X61558	TCCT	GGACTAACAA	TCTCGCAAGA	GGTAT...GTGACCTT.GT	TACTCAGAG AATGTGAA
speA X61556	TCCT	GGACTAACAA	TCTCGCAAGA	GGTAT...GTGACCTT.GT	TACTCAGAG AATGTGAA
speA X61555	TCCT	GGACTAACAA	TCTCGCAAGA	GGTAT...GTGACCTT.GT	TACTCAGAG AATGTGAA
speA X61560	TCCT	GGACTAACAA	TCTCGCAAGA	GGTAT...GTGACCTT.GT	TACTCAGAG AATGTGAA
speA X61561	TCCT	GGACTAACAA	TCTCGCAAGA	GGTAT...GTGACCTT.GT	TACTCAGAG AATGTGAA
speA X61566	TCCT	GGACTAACAA	TCTCGCAAGA	GGTAT...GTGACCTT.GT	TACTCAGAG AATGTGAA
speA X61567	TCCT	GGACTAACAA	TCTCGCAAGA	GGTAT...GTGACCTT.GT	TACTCAGAG AATGTGAA
speA X61562	TCCT	GGACTAACAA	TCTCGCAAGA	GGTAT...GTGACCTT.GT	TACTCAGAG AATGTGAA
speA X61563	TCCT	GGACTAACAA	TCTCGCAAGA	GGTAT...GTGACCTT.GT	TACTCAGAG AATGTGAA
speA X61564	TCCT	GGACTAACAA	TCTCGCAAGA	GGTAT...GTGACCTT.GT	TACTCAGAG AATGTGAA
speA X61565	TCCT	GGACTAACAA	TCTCGCAAGA	GGTAT...GTGACCTT.GT	TACTCAGAG AATGTGAA
speA AF055698	----	GGACTAACAA	TCTCGCAAGA	GGTAT...GTGACCTT.GT	TACTCAGAG AATGTGAA
speA X03929 ^a	TCCT	GGACTAACAA	TCTCGCAAGA	AGGTA...GTGACCTTGGT	TACTCAGAG AATGTGAA
Selected sequence for species-specific primer	T GGACTAACAA TCTCGCAAGA GG				
Selected sequence for species-specific primer ^b	ACCTT.GT TACTCAGAG AATGT				

The sequence numbering refers to the *Streptococcus pyogenes speA* gene fragment (SEQ ID NO. 993). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches are indicated by lower-case letters. "-" indicate incomplete sequence data. Dots indicate gaps in the sequences displayed.

^a The extra G nucleotide introducing a gap in the sequence is probably a sequencing error.
^b This sequence is the reverse-complement of the selected primer.

Annex XXIV: Second strategy for the selection of *Streptococcus pyogenes*-specific amplification primers from *speA* sequences.

Accession #	388	427	501	529	SEQ ID NO.:
5	speA X61573	TA TGGAGGGGTA ACAATCATG	TTTAGAAA...	AAATATGGT AACGCTCAA	529
	speA AF029051	TA TGGAGGGGTA ACAATCATG	TTTAGAAA...	AAATATGGT AACGCTCAA	-
	speA X61571	TA CGGAGGGGTA ACAATCATG	TTTAGAAA...	AAATATGGT AACGCTCAA	-
	speA X61570	TA CGGAGGGGTA ACAATCATG	TTTAGAAA...	AAATATGGT AACGCTCAA	-
	speA X61568	TA CGGAGGGGTA ACAATCATG	TTTAGAAA...	AAATATGGT AACGCTCAA	-
10	speA X61569	TA CGGAGGGGTA ACAATCATG	TTTAGAAA...	AAATATGGT AACGCTCAA	-
	speA X61572	TA CGGAGGGGTA ACAATCATG	TTTAGAAA...	AAATATGGT AACGCTCAA	-
	speA X61560	TA CGGAGGGGTA ACAATCATG	TTTAGAAA...	AAATATGGT AACGCTCAA	-
	speA U40453	TA CGGAGGGGTA ACAATCATG	TTTAGAAA...	AAATATGGT AACGCTCAA	-
	speA X61554	TA CGGAGGGGTA ACAATCATG	TTTAGAAA...	AAATATGGT AACGCTCAA	993
	speA X61557	TA CGGAGGGGTA ACAATCATG	TTTAGAAA...	AAATATGGT AACGCTCAA	-
15	speA X61559	TA CGGAGGGGTA ACAATCATG	TTTAGAAA...	AAATATGGT AACGCTCAA	-
	speA X61558	TA CGGAGGGGTA ACAATCATG	TTTAGAAA...	AAATATGGT AACGCTCAA	-
	speA X61556	TA CGGAGGGGTA ACAATCATG	TTTAGAAA...	AAATATGGT AACGCTCAA	-
	speA X61555	TA CGGAGGGGTA ACAATCATG	TTTAGAAA...	AAATATGGT AACGCTCAA	-
20	speA X61560	TA CGGAGGGGTA ACAATCATG	TTTAGAAA...	AAATATGGT AACGCTCAA	-
	speA X61561	TA CGGAGGGGTA ACAATCATG	TTTAGAAA...	AAATATGGT AACGCTCAA	-
	speA X61566	TA CGGAGGGGTA ACAATCATG	TTTAGAAA...	AAATATGGT AACGCTCAA	-
	speA X61567	TA CGGAGGGGTA ACAATCATG	TTTAGAAA...	AAATATGGT AACGCTCAA	-
25	speA X61562	TA CGGAGGGGTA ACAATCATG	TTTAGAAA...	AAATATGGT AACGCTCAA	-
	speA X61563	TA CGGAGGGGTA ACAATCATG	TTTAGAAA...	AAATATGGT AACGCTCAA	-
	speA X61564	TA CGGAGGGGTA ACAATCATG	TTTAGAAA...	AAATATGGT AACGCTCAA	-
	speA X61565	TA CGGAGGGGTA ACAATCATG	TTTAGAAA...	AAATATGGT AACGCTCAA	-
30	speA AF055698	TA CGGAGGGGTA ACAATCATG	TTTAGAAA...	AAATATGGT AACGCTCAA	-
	speA X03929	TA CGGAGGGGTA ACAATCATG	TTTAGAAA...	AAATATGGT AACGCTCAA	-
	Selected sequences for species-specific primers	CGGAGGGGTA ACAATCATG	TTTAG	AAATGGT AACGCTCAA	998
	Selected sequence for species-specific primer ^a	CGGAGGGGTA ACAATCATG	TTTAG	AAATGGT AACGCTCAA	996
35				AAATGGT AACGCTCAA	997

The sequence numbering refers to the *Streptococcus pyogenes speA* gene fragment (SEQ ID NO. 993). Dots indicate gaps in the sequences displayed.

^a This sequence is the reverse-complement of the selected primer.

Annex XXV: Strategy for the selection of *Streptococcus pyogenes*-specific amplification primers from *tuf* sequences.

		140	186	619	647	SEQ ID NO.:				
5	<i>S. anginosus</i>	A AGTTGACTTg	GTTCACGATg	AAGMaTTGCT	TGAATTgGTT	GAaATG...CC AGTTTCAATt	catccacaca	CTAAATt	211	
	<i>S. bovis</i>	A AGTTGACCTT	GTTCATGACg	AAGMaTTGCT	TGAATTgGTT	GAaATG...CC AGTTTCAATt	catccacaca	CTAAATt	212	
	<i>S. dysgalactiae</i>	A AATTGACCTT	GTTCACGATg	AAGMaTTGCT	TGAATTgGTT	GAaATG...CC AGTTTCAATt	catccacaca	CTAAATt	217	
	<i>S. pyogenes</i>	A AGTTGACCTT	GTTCATGACg	AAGMaTTGCT	TGAATTgGTT	GAaATG...CC AGTTTCAATt	catccacaca	CTAAATt	1002	
	<i>S. agalactiae</i>	A AGTTGACCTT	GTTCATGATg	AAGMaTTGCT	TGAATTgGTT	GAaATG...CC AGTTTCAATt	catccacaca	CTAAATt	144 ^a	
10	<i>S. oralis</i>	A AATTGACTTg	GTTCACGATg	AAGMaTTGCT	TGAATTgGTT	GAaATG...CC AGTTTCAATt	catccacaca	CTAAATt	985	
	<i>S. pneumoniae</i>	A AGTTGACTTg	GTTCACGATg	AAGMaTTGCT	TGAATTgGTT	GAaATG...CC AGTTTCAATt	catccacaca	CTAAATt	145 ^a	
	<i>S. cristatus</i>	A GATCGACTTg	GTTCATGACg	AAGMaTTGCT	TGAATTgGTT	GAaATG...CC AGTTTCAATt	catccacaca	CTAAATt	215	
	<i>S. mitis</i>	A GATCGACTTg	GTTCATGACg	AAGMaTTGCT	TGAATTgGTT	GAaATG...CC AGTTTCAATt	catccacaca	CTAAATt	982	
	<i>S. gordonii</i>	A AGTTGACTTg	GTTCACGATg	AAGMaTTGCT	TGAATTgGTT	GAaATG...CC AGTTTCAATt	catccacaca	CTAAATt	200	
15	<i>S. sanguinis</i>	A AGTTGACTTg	GTTCACGATg	AAGMaTTGCT	TGAATTgGTT	GAaATG...CC AGTTTCAATt	catccacaca	CTAAATt	227	
	<i>S. parvaquiniis</i>	A AGTTGACTTg	GTTCATGATg	AAGMaTTGCT	TGAATTgGTT	GAaATG...CC AGTTTCAATt	catccacaca	CTAAATt	225	
	<i>S. salivarius</i>	A AGTTGACTTg	GTTCACGATg	AAGMaTTGCT	TGAATTgGTT	GAaATG...CC TgTTTCAATt	catccacaca	CTAAATt	146 ^a	
	<i>S. vestibularis</i>	A AGTTGACTTg	GTTCACGATg	AAGMaTTGCT	TGAATTgGTT	GAaATG...CC TgTTTCAATt	catccacaca	CTAAATt	231	
	<i>S. suis</i>	A AGTTGACTTg	GTTCACGATg	AAGMaTTGCT	TGAATTgGTT	GAaATG...CC AGTTTCTATt	catccacaca	CTAAATt	229	
20	<i>S. mutans</i>	A AGTTGACTTg	GTTCACGATg	AAGMaTTGCT	TGAATTgGTT	GAaATG...CC AGTTTCAATt	catccacaca	CTAAATt	224	
	<i>S. rattii</i>	A GGTGACTTg	GTTCATGATg	AAGMaTTGCT	TGAATTgGTT	GAaATG...CC AGTTTCAATt	catccacaca	CTAAATt	226	
	<i>S. macacae</i>	A AGTTGACTTg	GTTCATGATg	AAGMaTTGCT	TGAATTgGTT	GAaATG...CC AGATCAATt	catccacaca	CTAAATt	222	
	<i>S. cricetus</i>	A GGTGACTTg	GTTCACGATg	AAGMaTTGCT	TGAATTgGTT	GAaATG...CC TgTTTCAATt	catccacaca	CTAAATt	214	
	<i>E. faecalis</i>	A AATGATAATg	GTTCATGACg	AAGMaTTATt	AGAAATAGTA	GAaATG...CC AGTaCAATt	actccacaca	CAAAATt	607	
25	<i>S. aureus</i>	A AGTTGACATg	GTTCACGATg	AAGMaTTATt	AGAAATAGTA	GAaATG...CC TgTTTCAATt	acaaccacaca	CTGAATt	176	
	<i>B. cereus</i>	A ATGCGACATg	GTATGACATg	AAGMaTTATt	AGAAATAGTA	GAaATG...AG CgTTTCTgTa	aaagctcag	CTAAATt	7	
	<i>E. coli</i>	A ATGCGACATg	GTTCATGACg	AAGAGCTGCT	gGAACCTgGTT	GAaATG...CC GgGCaCaATt	aaagccgcaca	CcAAGTT	78	
	Selected sequences for species-specific primers									
	30		TTGACCTT	GTTCATGACg	AAGAG	AAGAGTTGCT	TGAATTAGTT	GAG		999
									1001	
Selected sequence for species-specific primer ^b									1000	
								AGTTTCAATt	catccacaca	CTAA

35 The sequence numbering refers to the *Streptococcus pyogenes tuf* gene fragment (SEQ ID NO. 1002). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches are indicated by lower-case letters. Dots indicate gaps in the sequences displayed.

^a The SEQ ID NO. refers to previous patent application WO98/20157.

^b This sequence is the reverse-complement of the selected primer.

Annex XXVI: Strategy for the selection of shiga toxin-producing, *Escherichia coli*-specific amplification primers and hybridization probe from *stx*₁ sequenc s.

Accession #	230	263	343	375	391	421	SEQ ID NO.:
5	<i>stx</i> ₁ M19473a	TTGATGTC AGAGGATAG ATCCAGAGGA AGGGCG...TATCG	CTTTGCTGAT TTTTCACATG	TTACCTTT...GTTACAT	TGTCGTGGA	CAGTAGCTAT ACCA	421
	<i>stx</i> ₁ M16625	TTGATGTC AGAGGATAG ATCCAGAGGA AGGGCG...TATCG	CTTTGCTGAT TTTTCACATG	TTACCTTT...GTTACAT	TGTCGTGGA	CAGTAGCTAT ACCA	-
	<i>stx</i> ₁ M17358	TTGATGTC AGAGGATAG ATCCAGAGGA AGGGCG...TATCG	CTTTGCTGAT TTTTCACATG	TTACCTTT...GTTACAT	TGTCGTGGA	CAGTAGCTAT ACCA	-
	<i>stx</i> ₁ Z36900	TTGATGTC AGAGGATAG ATCCAGAGGA AGGGCG...TATCG	CTTTGCTGAT TTTTCACATG	TTACCTTT...GTTACAT	TGTCGTGGA	CAGTAGCTAT ACCA	-
	<i>stx</i> ₁ L04539	TTGATGTC AGAGGATAG ATCCAGAGGA AGGGCG...TATCG	CTTTGCTGAT TTTTCACATG	TTACCTTT...GTTACAT	TGTCGTGGA	CAGTAGCTAT ACCA	-
10	<i>stx</i> ₁ M19437	TTGATGTC AGAGGATAG ATCCAGAGGA AGGGCG...TATCG	CTTTGCTGAT TTTTCACATG	TTACCTTT...GTTACAT	TGTCGTGGA	CAGTAGCTAT ACCA	-
	<i>stx</i> ₁ M24352	TTGATGTC AGAGGATAG ATCCAGAGGA AGGGCG...TATCG	CTTTGCTGAT TTTTCACATG	TTACCTTT...GTTACAT	TGTCGTGGA	CAGTAGCTAT ACCA	-
	<i>stx</i> ₁ X07903	TTGATGTC AGAGGATAG ATCCAGAGGA AGGGCG...TATCG	CTTTGCTGAT TTTTCACATG	TTACCTTT...GTTACAT	TGTCGTGGA	CAGTAGCTAT ACCA	-
	<i>stx</i> ₁ Z36899	TTGATGTC AGAGGATAG ATCCAGAGGA AGGGCG...TATCG	CTTTGCTGAT TTTTCACATG	TTACCTTT...GTTACAT	TGTCGTGGA	CAGTAGCTAT ACCA	-
	<i>stx</i> ₁ Z36901	TTGATGTC AGAGGATAG ATCCAGAGGA AGGGCG...TATCG	CTTTGCTGAT TTTTCACATG	TTACCTTT...GTTACAT	TGTCGTGGA	CAGTAGCTAT ACCA	-
15	<i>stx</i> ₁ X61283	TTGATGTC AGAGGATAG ATCCAGAGGA AGGGCG...TATCG	CTTTGCTGAT TTTTCACATG	TTACCTTT...GTTACAT	TGTCGTGGA	CAGTAGCTAT ACCA	-
	<i>stx</i> ₂ L11079	TGGATATA CAGGGGCTTG ATGCTATCA GGGCG...TACCG	CTTTGCTGAT TTTTCACATG	TTACCTTT...GTTACAT	TGTCGTGGA	CAGTAGCTAT ACCA	1076
	<i>stx</i> ₂ M21534	TAGGATA CAGGGGCTTG ATGCTATCA GGGCG...TACCG	CTTTGCTGAT TTTTCACATG	TTACCTTT...GTTACAT	TGTCGTGGA	CAGTAGCTAT ACCA	-
	<i>stx</i> ₂ M36727	TAGGATA CAGGGGCTTG ATGCTATCA GGGCG...TACCG	CTTTGCTGAT TTTTCACATG	TTACCTTT...GTTACAT	TGTCGTGGA	CAGTAGCTAT ACCA	-
20	<i>stx</i> ₂ X81415	TAGGATA CAGGGGCTTG ATGCTATCA GGGCG...TACCG	CTTTGCTGAT TTTTCACATG	TTACCTTT...GTTACAT	TGTCGTGGA	CAGTAGCTAT ACCA	-
	<i>stx</i> ₂ X81416	TAGGATA CAGGGGCTTG ATGCTATCA GGGCG...TACCG	CTTTGCTGAT TTTTCACATG	TTACCTTT...GTTACAT	TGTCGTGGA	CAGTAGCTAT ACCA	-
	<i>stx</i> ₂ X81417	TAGGATA CAGGGGCTTG ATGCTATCA GGGCG...TACCG	CTTTGCTGAT TTTTCACATG	TTACCTTT...GTTACAT	TGTCGTGGA	CAGTAGCTAT ACCA	-
	<i>stx</i> ₂ X81418	TAGGATA CAGGGGCTTG ATGCTATCA GGGCG...TACCG	CTTTGCTGAT TTTTCACATG	TTACCTTT...GTTACAT	TGTCGTGGA	CAGTAGCTAT ACCA	-
25	<i>stx</i> ₂ E03962	TGGATATA CAGGGGCTTG ATGCTATCA GGGCG...TACCG	CTTTGCTGAT TTTTCACATG	TTACCTTT...GTTACAT	TGTCGTGGA	CAGTAGCTAT ACCA	-
	<i>stx</i> ₂ E03959	TGGATATA CAGGGGCTTG ATGCTATCA GGGCG...TACCG	CTTTGCTGAT TTTTCACATG	TTACCTTT...GTTACAT	TGTCGTGGA	CAGTAGCTAT ACCA	-
	<i>stx</i> ₂ X07865	TGGATATA CAGGGGCTTG ATGCTATCA GGGCG...TACCG	CTTTGCTGAT TTTTCACATG	TTACCTTT...GTTACAT	TGTCGTGGA	CAGTAGCTAT ACCA	-
	<i>stx</i> ₂ Y10775	TGGATATA CAGGGGCTTG ATGCTATCA GGGCG...TACCG	CTTTGCTGAT TTTTCACATG	TTACCTTT...GTTACAT	TGTCGTGGA	CAGTAGCTAT ACCA	-
	<i>stx</i> ₂ Z37725	TGGATATA CAGGGGCTTG ATGCTATCA GGGCG...TACCG	CTTTGCTGAT TTTTCACATG	TTACCTTT...GTTACAT	TGTCGTGGA	CAGTAGCTAT ACCA	-
	<i>stx</i> ₂ Z50754	TGGATATA CAGGGGCTTG ATGCTATCA GGGCG...TACCG	CTTTGCTGAT TTTTCACATG	TTACCTTT...GTTACAT	TGTCGTGGA	CAGTAGCTAT ACCA	1077
30	<i>stx</i> ₂ X67514	TGGATATA CAGGGGCTTG ATGCTATCA GGGCG...TACCG	CTTTGCTGAT TTTTCACATG	TTACCTTT...GTTACAT	TGTCGTGGA	CAGTAGCTAT ACCA	-
	<i>stx</i> ₂ L11078	TGGATATA CAGGGGCTTG ATGCTATCA GGGCG...TACCG	CTTTGCTGAT TTTTCACATG	TTACCTTT...GTTACAT	TGTCGTGGA	CAGTAGCTAT ACCA	-
	<i>stx</i> ₂ X65949	TGGATATA CAGGGGCTTG ATGCTATCA GGGCG...TACCG	CTTTGCTGAT TTTTCACATG	TTACCTTT...GTTACAT	TGTCGTGGA	CAGTAGCTAT ACCA	-
	<i>stx</i> ₂ AF043627	TGGATATA CAGGGGCTTG ATGCTATCA GGGCG...TACCG	CTTTGCTGAT TTTTCACATG	TTACCTTT...GTTACAT	TGTCGTGGA	CAGTAGCTAT ACCA	-
35	Selected sequence for amplification primer	ATGTC AGAGGATAG ATCCAGAGGA AGG					1081
40	Selected sequence for hybridization probe		CG CTTTCTGAT TTTTCACATG TTACC				1084
45	Selected sequence for amplification primer*				ACAT TGTCGTGGA CAGTAGCTAT A		1080

The sequence numbering refers to the *Escherichia coli stx*₁ gene fragment (SEQ ID NO. 1076). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches are indicated by lower-case letters. Dots indicate gaps in the sequences displayed.

* This sequence is the reverse-complement of the selected primer.

Annex XXVII: Strategy for the selection of shiga toxin-producing, *Escherichia coli*-specific amplification primers and hybridization probe from *stx*, sequences.

SEQ ID NO.:

		sequences.																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																													
--	--	------------	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--

Selected sequence for
amplification primer

Selected sequence for
hybridization probe

Selected sequence for
amplification primer^a

The sequence numbering refers to the *Escherichia coli stx* gene fragment (SEQ ID NO. 1077). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches are indicated by lower-case letters. Dots indicate gaps in the sequences displayed.
^a This sequence is the reverse-complement of the selected primer.

Annex XXVIII: Strategy for the selection of *vanA*-specific amplification primers from *van* sequences.

Accession #	926	952	1230	1255	SEQ ID NO.:
5	<i>vanA</i> X56895	GTCAAT AGCGCGGACG AATTGGACTA C...GT AGAGGTCTAG	CCCCGTGTGGA	TATG	1139
	<i>vanA</i> M97297	GTCAAT AGCGCGGACG AATTGGACTA C...GT AGAGGTCTAG	CCCCGTGTGGA	TATG	1141
	-	GTCAAT AGCGCGGACG AATTGGACTA C...GT AGAGGTCTAG	CCCCGTGTGGA	TATG	1051
	-	GTCAAT AGCGCGGACG AATTGGACTA C...GT AGAGGTCTAG	CCCCGTGTGGA	TATG	1052
	-	GTCAAT AGCGCGGACG AATTGGACTA C...GT AGAGGTCTAG	CCCCGTGTGGA	TATG	1053
	-	GTCAAT AGCGCGGACG AATTGGACTA C...GT AGAGGTCTAG	CCCCGTGTGGA	TATG	1054
10	-	GTCAAT AGCGCGGACG AATTGGACTA C...GT AGAGGTCTAG	CCCCGTGTGGA	TATG	1055
	-	GTCAAT AGCGCGGACG AATTGGACTA C...GT AGAGGTCTAG	CCCCGTGTGGA	TATG	1056
	-	GTCAAT AGCGCGGACG AATTGGACTA C...GT AGAGGTCTAG	CCCCGTGTGGA	TATG	1057
	-	GTCAAT AGCGCGGACG AATTGGACTA C...GT AGAGGTCTAG	CCCCGTGTGGA	TATG	1049
	-	GTCAAT AGCGCGGACG AATTGGACTA C...GT AGAGGTCTAG	CCCCGTGTGGA	TATG	1050
15	-	GTCAAT AGCGCGGACG AATTGGACTA C...GT AGAGGTCTAG	CCCCGTGTGGA	TATG	1117
	U94526	GTA AAC GGTaCGGAG AACTaAACGC T...GC AGAGGCTTG	CCCCGTGTGGA	TCTT	-
	U94527	GTA AAC AGTaCGGAG AACTaAACGC T...GC AGAGGCTTG	CCCCGTGTGGA	TCTT	-
	U94528	GTA AAC GGTaCGGAG AACTaAACGC T...GC AGAGGCTTG	CCCCGTGTGGA	TCTT	-
	U94529	GTA AAC GGTaCGGAG AACTaAACGC T...GC AGAGGCTTG	CCCCGTGTGGA	TCTT	-
20	U94530	GTA AAC GGTaCGGAG AACTaAACGC T...GC AGAGGCTTG	CCCCGTGTGGA	TCTT	-
	283305	GTA AAC GGTaCGGAG AACTaAACGC T...GC AGAGGCTTG	CCCCGTGTGGA	TCTT	-
	U81452	GTA AAC GGTaCGGAG AACTaAACGC T...GC AGAGGCTTG	CCCCGTGTGGA	TCTT	-
	U35369	GTA AAC AGTaCGGAG AACTaAACGC T...GC AGAGGCTTG	CCCCGTGTGGA	TCTT	-
25	U72704	GTA AAC GGTaCGGAG AACTaAACGC T...GC AGAGGCTTG	CCCCGTGTGGA	TCTT	-
	L06138	GTA AAC AGTaCGGAG AACTaAACGC T...GC AGAGGCTTG	CCCCGTGTGGA	TCTT	-
	L15304	GTA AAC GGTaCGGAG AACTaAACGC T...GC AGAGGCTTG	CCCCGTGTGGA	TCTT	-
	U00456	GTA AAC AGTaCGGAG AACTaAACGC T...GC AGAGGCTTG	CCCCGTGTGGA	TCTT	-
	AF130997	GTA TGC AGGCaGAG AACTaAACGC A...GC AGAGGCTTG	CCCCGTGTGGA	cCTG	-
30	AF136925	GTA Gaa caaaaagtG ATtTaTaaA A...GC AaAGGatTAG	CgaGaaTcGA	cTTT	-
	Selected sequence for amplification primer	AAT AGCGCGGACG AATTGGAC			1090
35	Selected sequence for amplification primer*	GAGGTCTAG CCCGTGTGGA T			1089

The sequence numbering refers to the *Enterococcus faecium vanA* gene fragment (SEQ ID NO. 1139). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches are indicated by lower-case letters. Dots indicate gaps in the sequences displayed.

* This sequence is the reverse-complement of the above selected primer.

Annex XXIX: Strategy for the selection of vanB-specific amplification primers from van sequences.

	Accession #	470	495	608	633	SEQ ID NO.
5	vanA	X56895	A CGCaATTGAA tCGGCAAGAC AATAT...ACG	GaATCTTTtCG	tATtCATCAG GAA	1139
	vanA	M97297	A CGCaATTGAA tCGGCAAGAC AATAT...ACG	GaATCTTTtCG	tATtCATCAG GAA	1141
	vanA	-	A CGCaATTGAA tCGGCAAGAC AATAT...ACG	GaATCTTTtCG	tATtCATCAG GAA	1051
	vanA	-	A CGCaATTGAA tCGGCAAGAC AATAT...ACG	GaATCTTTtCG	tATtCATCAG GAA	1052
10	vanA	-	A CGCaATTGAA tCGGCAAGAC AATAT...ACG	GaATCTTTtCG	tATtCATCAG GAA	1053
	vanA	-	A CGCaATTGAA tCGGCAAGAC AATAT...ACG	GaATCTTTtCG	tATtCATCAG GAA	1054
	vanA	-	A CGCaATTGAA tCGGCAAGAC AATAT...ACG	GaATCTTTtCG	tATtCATCAG GAA	1055
	vanA	-	A CGCaATTGAA tCGGCAAGAC AATAT...ACG	GaATCTTTtCG	tATtCATCAG GAA	1056
15	vanA	-	A CGCaATTGAA tCGGCAAGAC AATAT...ACG	GaATCTTTtCG	tATtCATCAG GAA	1057
	vanA	-	A CGCaATTGAA tCGGCAAGAC AATAT...ACG	GaATCTTTtCG	tATtCATCAG GAA	1049
	vanB	U94526	C TCGCATAGAA tCGGCAAGAC AATAT...ACG	GaATCTTTtCG	tATtCATCAG GAA	1050
	vanB	U94527	C TCGCATAGAA tCGGCAAGAC AATAT...ACG	GaATCTTTtCG	tATtCATCAG GAA	1117
20	vanB	U94528	C TCGCATAGAA tCGGCAAGAC AATAT...ACG	GaATCTTTtCG	tATtCATCAG GAA	-
	vanB	U94529	C TCGCATAGAA tCGGCAAGAC AATAT...ACG	GaATCTTTtCG	tATtCATCAG GAA	-
	vanB	U94530	C TCGCATAGAA tCGGCAAGAC AATAT...ACG	GaATCTTTtCG	tATtCATCAG GAA	-
	vanB	Z83305	C TCGCATAGAA tCGGCAAGAC AATAT...ACG	GaATCTTTtCG	tATtCATCAG GAA	-
25	vanB	U81452	C TCGCATAGAA tCGGCAAGAC AATAT...ACG	GaATCTTTtCG	tATtCATCAG GAA	-
	vanB	U35369	C TCGCATAGAA tCGGCAAGAC AATAT...ACG	GaATCTTTtCG	tATtCATCAG GAA	-
	vanB	U72704	C TCGCATAGAA tCGGCAAGAC AATAT...ACG	GaATCTTTtCG	tATtCATCAG GAA	-
	vanB	L06138	C TCGCATAGAA tCGGCAAGAC AATAT...ACG	GaATCTTTtCG	tATtCATCAG GAA	-
30	vanB	L15304	C TCGCATAGAA tCGGCAAGAC AATAT...ACG	GaATCTTTtCG	tATtCATCAG GAA	-
	vanB	U00456	C TCGCATAGAA tCGGCAAGAC AATAT...ACG	GaATCTTTtCG	tATtCATCAG GAA	-
	vanD	AF130997	C AGCaATCGAA GaAGCAAGAA AATAT...ACG	GctTtTtTaa	gATtCATCAG GAA	-
	vanE	AF136925	A AGCaATAGAC GaAGCtTtCaA AATAT...ATG	GctTtTtTCga	CtatgAagAG AAA	-
	Selected sequence for amplification primer	CGATAGAA GCAGCAGGAC AA				1095
35	Selected sequence for amplification primer ^a	GTATCTTTtCG CATCCATCAG				1096

The sequence numbering refers to the *Enterococcus faecium* vanB gene fragment (SEQ ID NO. 1117). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches are indicated by lower-case letters. Dots indicate gaps in the sequences displayed.

^a This sequence is the reverse-complement of the above vanB sequence.

Annex XXX: Strategy for the selection of vanC-specific amplification primers from vanC sequences.

	Accession #	929	957	1064	1092	SEQ ID NO.:			
5	vanC1	-	GT CGACGGCTTT	TTTGATTTTG	AAGAGAA...ACGGGTC	TGGCTCGCAAT	CGATTTTTTC	GT	1058
	vanC1	-	GT CGACGGCTTT	TTTGATTTTG	AAGAGAA...ACGGGTC	TGGCTCGCAAT	CGATTTTTTC	GT	1059
	vanC1	M75132	GT CGACGGCTTT	TTTGATTTTG	AAGAGAA...ACGGGTC	TGGCTCGCAAT	CGATTTTTTC	GT	1138
	vanC2	-	GT AGACGGCTTT	TTTGATTTTG	AAGAAAA...AAAGGTC	TGGCTCGCAT	CGACTTTTTT	GT	1060
	vanC2	-	GT AGACGGCTTT	TTTGATTTTG	AAGAAAA...AAAGGTC	TGGCTCGCAT	CGACTTTTTT	GT	1061
10	vanC2	-	GT AGACGGCTTT	TTTGATTTTG	AAGAAAA...AAAGGTC	TGGCTCGCAT	CGACTTTTTT	GT	1062
	vanC2	-	GT AGACGGCTTT	TTTGATTTTG	AAGAAAA...AAAGGTC	TGGCTCGCAT	CGACTTTTTT	GT	1063
	vanC2	L29638	GT AGACGGCTTT	TTTGATTTTG	AAGAAAA...AAAGGTC	TGGCTCGCAT	CGACTTTTTT	GT	-
	vanC2	L29638	GT AGACGGCTTT	TTTGATTTTG	AAGAAAA...AAAGGTC	TGGCTCGCAT	CGACTTTTTT	GT	-
15	vanC3	-	GT AGACGGCTTT	TTTGATTTTG	AAGAAAA...AAAGGTC	TGGCTCGCAT	CGACTTTTTT	GT	1064
	vanC3	-	GT AGACGGCTTT	TTTGATTTTG	AAGAAAA...AAAGGTC	TGGCTCGCAT	CGACTTTTTT	GT	1065
	vanC3	-	GT AGACGGCTTT	TTTGATTTTG	AAGAAAA...AAAGGTC	TGGCTCGCAT	CGACTTTTTT	GT	1066
	vanC3	L29639	GT AGACGGCTTT	TTTGATTTTG	AAGAAAA...AAAGGTC	TGGCTCGCAT	CGACTTTTTT	GT	-
20	Selected sequence for resistance primer		GACGGYTTT	TTTGATTTTG	AAGA				1101
	Selected sequence for resistance primer ^a					GGTC	TKGCTCGMAT	CGATTTTTT	1102

25 The sequence numbering refers to the vanC1 gene fragment (SEQ ID NO. 1138). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches are indicated by lower-case letters. Dots indicate gaps in the sequence displayed.

30 "R" "Y" "M" "K" "W" and "S" designate nucleotide positions which are degenerated. "R" stands for A or G; "Y" stands for C or T; "M" stands for A or C; "K" stands for G or T; "W" stands for A or T; "S" stands for C or G. "I" stands for inosine which is a nucleotide analog that can bind to any of the four nucleotides A, C, G or T.

^a This sequence is the reverse-complement of the selected sequence.

Annex XXXI: Strategy for the selection of *Streptococcus pneumoniae*-specific amplification primers and hybridization probes from *pbpla* sequences.

	Accession #	453	505	678	706	SEQ ID NO.:
5	<i>pbpla</i>	M90528	A TTGACTATCC AAGCATGTCAT TATGCTAATG CCAATTCGAG TAATACAAAC GA...TATATG ATGACCGACA TGATGAAAAC CGT...			-
	<i>pbpla</i>	X67873	A TCGACTATCC AAGCATGTCAT TATGCTAATG CCAATTCGAG TAATACAAAC GA...TATATG ATGACCGACA TGATGAAAAC AGT...			-
	<i>pbpla</i>	AB006868	A TCGACTATCC AAGCATGTCAT TATGCTAATG CCAATTCGAG TAATACAAAC GA...TATATG ATGACCGACA TGATGAAAAC AGT...			-
	<i>pbpla</i>	AF046234	A TCGACTATCC AAGCATGTCAT TATGCTAATG CCAATTCGAG TAATACAAAC GA...TATATG ATGACCGACA TGATGAAAAC TGT...			-
10	<i>pbpla</i> ...		A TCGACTATCC AAGCATGTCAT TATGCTAATG CCAATTCGAG TAATACAAAC GA...TATATG ATGACCGACA TGATGAAAAC TGT...			1014
	<i>pbpla</i>	AB006873	A TCGACTATCC AAGCATGTCAT TATGCTAATG CCAATTCGAG TAATACAAAC GA...TATATG ATGACCGACA TGATGAAAAC TGT...			1017
	<i>pbpla</i>	AF139883	A TCGACTATCC AAGCATGTCAT TATGCTAATG CCAATTCGAG TAATACAAAC GA...TATATG ATGACCGACA TGATGAAAAC AGT...			-
	<i>pbpla</i>		A TCGACTATCC AAGCATGTCAT TATGCTAATG CCAATTCGAG TAATACAAAC GA...TATATG ATGACCGACA TGATGAAAAC AGT...			1169
15	<i>pbpla</i>		A TCGACTATCC AAGCATGTCAT TATGCTAATG CCAATTCGAG TAATACAAAC GA...TATATG ATGACCGACA TGATGAAAAC AGT...			1004
	<i>pbpla</i>		A TCGACTATCC AAGCATGTCAT TATGCTAATG CCAATTCGAG TAATACAAAC GA...TATATG ATGACCGACA TGATGAAAAC AGT...			1007
	<i>pbpla</i>		A TCGACTATCC AAGCATGTCAT TATGCTAATG CCAATTCGAG TAATACAAAC GA...TATATG ATGACCGACA TGATGAAAAC AGT...			1008
	<i>pbpla</i>		A TCGACTATCC AAGCATGTCAT TATGCTAATG CCAATTCGAG TAATACAAAC GA...TATATG ATGACCGACA TGATGAAAAC AGT...			1009
	<i>pbpla</i>		A TCGACTATCC AAGCATGTCAT TATGCTAATG CCAATTCGAG TAATACAAAC GA...TATATG ATGACCGACA TGATGAAAAC AGT...			1011
20	<i>pbpla</i>	AF159448	A TCGACTATCC AAGCATGTCAT TATGCTAATG CCAATTCGAG TAATACAAAC GA...TATATG ATGACCGACA TGATGAAAAC AGT...			-
	<i>pbpla</i>		A TCGACTATCC AAGCATGTCAT TATGCTAATG CCAATTCGAG TAATACAAAC GA...TATATG ATGACCGACA TGATGAAAAC AGT...			1005
	<i>pbpla</i>		A TCGACTATCC AAGCATGTCAT TATGCTAATG CCAATTCGAG TAATACAAAC GA...TATATG ATGACCGACA TGATGAAAAC AGT...			1015
	<i>pbpla</i>		A TCGACTATCC AAGCATGTCAT TATGCTAATG CCAATTCGAG TAATACAAAC GA...TATATG ATGACCGACA TGATGAAAAC AGT...			1016
	<i>pbpla</i>		A TCGACTATCC AAGCATGTCAT TATGCTAATG CCAATTCGAG TAATACAAAC GA...TATATG ATGACCGACA TGATGAAAAC AGT...			1012
25	<i>pbpla</i>	X67867	A TCGACTATCC AAGCATGTCAT TATGCTAATG CCAATTCGAG TAATACAAAC GA...TATATG ATGACCGACA TGATGAAAAC TGT...			-
	<i>pbpla</i>	249094	A TCGACTATCC AAGCATGTCAT TATGCTAATG CCAATTCGAG TAATACAAAC GA...TATATG ATGACCGACA TGATGAAAAC TGT...			1010
	<i>pbpla</i>		A TCGACTATCC AAGCATGTCAT TATGCTAATG CCAATTCGAG TAATACAAAC GA...TATATG ATGACCGACA TGATGAAAAC TGT...			-
	<i>pbpla</i>		A TCGACTATCC AAGCATGTCAT TATGCTAATG CCAATTCGAG TAATACAAAC GA...TATATG ATGACCGACA TGATGAAAAC TGT...			1013
	<i>pbpla</i>	X67870	A TCGACTATCC AAGCATGTCAT TATGCTAATG CCAATTCGAG TAATACAAAC GA...TATATG ATGACCGACA TGATGAAAAC TGT...			1016
30	<i>pbpla</i>		A TCGACTATCC AAGCATGTCAT TATGCTAATG CCAATTCGAG TAATACAAAC GA...TATATG ATGACCGACA TGATGAAAAC TGT...			-
	<i>pbpla</i>	AJ002290	A TTGATATACC AAGCATGTCAT TATGCTAATG CCAATTCGAG TAATACAAAC GA...TATATG ATGACCGACA TGATGAAAAC TGT...			1018
	<i>pbpla</i>	X67871	A TCGACTATCC AAGCATGTCAT TATGCTAATG CCAATTCGAG TAATACAAAC GA...TATATG ATGACCGACA TGATGAAAAC AGT...			-
35	Selected sequences for amplification primers		GAATATCC AAGCATGTCAT TATG		ATG ATGACCGACA TGATGAAAAC	1130 1129
40	Selected sequence for hybridization probe		CAACAG CCAATTCGAG TAATACAAAC			1197

The sequence numbering refers to the *Streptococcus pneumoniae pbpla* gene fragment (SEQ ID NO. 1004). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches are indicated by lower-case letters. Dots indicate gaps in the sequences displayed.

"R" "Y" "W" "K" "W" and "S" designate nucleotide positions which are degenerated. "R" stands for A or G; "Y" stands for C or T; "W" stands for A or C; "K" stands for G or T; "S" stands for A or T; "W" stands for C or G. "I" stands for inosine which is a nucleotide analog that can bind to any of the four nucleotides A, C, G or T.

Annex XXXI: Strategy for the selection of *Streptococcus pneumoniae*-specific amplification primers and hybridization probes from *pbpla* sequences (continued).

5	Accession #	756	783	813	840	SEQ ID NO.:
	<i>pbpla</i>	...GCTGGTAA	...GCTGGTAA	...GCTGGTAA	...GCTGGTAA	-
	<i>pbpla</i>	M90528	TCGAACCTATA...A	ATACGGGTTA	TGTAGCTCCG	-
	<i>pbpla</i>	X67873	...GCTGGTAA	...GCTGGTAA	...GCTGGTAA	-
	<i>pbpla</i>	AB006868	...GCTGGTAA	...GCTGGTAA	...GCTGGTAA	-
	<i>pbpla</i>	AF046234	...GCTGGTAA	...GCTGGTAA	...GCTGGTAA	-
10	<i>pbpla</i>GCTGGTAA	...GCTGGTAA	...GCTGGTAA	1014
	<i>pbpla</i>GCTGGTAA	...GCTGGTAA	...GCTGGTAA	1017
	<i>pbpla</i>	AB006873	...GCTGGTAA	...GCTGGTAA	...GCTGGTAA	-
	<i>pbpla</i>	AF1139883	...GCTGGTAA	...GCTGGTAA	...GCTGGTAA	1169
15	<i>pbpla</i>GCTGGTAA	...GCTGGTAA	...GCTGGTAA	1004
	<i>pbpla</i>GCTGGTAA	...GCTGGTAA	...GCTGGTAA	1007
	<i>pbpla</i>GCTGGTAA	...GCTGGTAA	...GCTGGTAA	1008
	<i>pbpla</i>GCTGGTAA	...GCTGGTAA	...GCTGGTAA	1009
	<i>pbpla</i>GCTGGTAA	...GCTGGTAA	...GCTGGTAA	1011
20	<i>pbpla</i>	AF159448	-
	<i>pbpla</i>GCTGGTAA	...GCTGGTAA	...GCTGGTAA	1005
	<i>pbpla</i>GCTGGTAA	...GCTGGTAA	...GCTGGTAA	1015
	<i>pbpla</i>GCTGGTAA	...GCTGGTAA	...GCTGGTAA	1006
	<i>pbpla</i>GCTGGTAA	...GCTGGTAA	...GCTGGTAA	1012
25	<i>pbpla</i>	X67867	-
	<i>pbpla</i>GCTGGTAA	...GCTGGTAA	...GCTGGTAA	1010
	<i>pbpla</i>	Z49094	-
	<i>pbpla</i>GCTGGTAA	...GCTGGTAA	...GCTGGTAA	1013
	<i>pbpla</i>GCTGGTAA	...GCTGGTAA	...GCTGGTAA	1016
30	<i>pbpla</i>	X67870	-
	<i>pbpla</i>GCTGGTAA	...GCTGGTAA	...GCTGGTAA	1018
	<i>pbpla</i>	AJ002290	-
	<i>pbpla</i>	X67871	-
35	Selected sequence for hybridization probe	GCTAA	GACAGGTACT	TCTAACT		1193
40	Selected sequence for amplification primer ^a				ACTGGGTTA	1131

The sequence numbering refers to the *Streptococcus pneumoniae* *pbpla* gene fragment (SEQ ID NO. 1004). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches are indicated by lower-case letters. Dots indicate gaps in the sequences displayed. "R" "Y" "W" and "S" designate nucleotide positions which are degenerated. "R" stands for A or G; "Y" stands for C or T; "W" stands for A or T; "S" stands for C or G. "I" stands for inosine which is a nucleotide analog that can bind to any of the four nucleotides A, C, G or T.

^a This sequence is the reverse-complement of the selected primer.

Annex XXXII: Specific and ubiquitous primers for nucleic acid amplification (*stx* sequences).

			Originating DNA fragment	
5	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	<u>Toxin gene:</u> <i>stx₁</i>			
	1081	5'-ATG TCA GAG GGA TAG ATC CA	1076 ^a	233-252
	1080 ^b	5'-TAT AGC TAC TGT CAC CAG ACA ATG T	1076 ^a	394-418
15	<u>Toxin gene:</u> <i>stx₂</i>			
	1078	5'-AGT TCT GCG TTT TGT CAC TGT C	1077 ^a	546-567
	1079 ^b	5'-CGG AAG CAC ATT GCT GAT T	1077 ^a	687-705
20	<u>Toxin genes:</u> <i>stx₁</i> and <i>stx₂</i>			
	1082	5'-TTG ARC RAA ATA ATT TAT ATG TG	1076 ^a	287-309
	1083 ^b	5'-TGA TGA TGR CAA TTC AGT AT	1076 ^a	790-809

25

^a Sequences from databases.

^b These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

**Ann x XXXIII: Mol cular beacon internal probes for hybridization
and specific detection of toxin sequenc s.**

5			Originating DNA fragment	
	SEQ ID NO.	Nucleotide sequence ^a	SEQ ID NO.	Nucleotide position
10	<u>Toxin gene:</u> <i>stx₁</i>			
15	1084	5'- <u>CCA CGC</u> CGC TTT GCT GAT TTT TCA CAT GTT ACC <u>GCG TGG</u>	1076 ^b	346-372
20	<u>Toxin gene:</u> <i>stx₂</i>			
	1085	5'- <u>CCA CGC</u> CAC TGT CTG AAA CTG CTC CTG TG <u>CGT GG</u>	1077 ^b	617-638

^a Underlined nucleotides indicate the molecular beacon's stem.

^b Sequences from databases.

Annex XXXIV: Specific and ubiquitous primers for nucleic acid amplification (van sequences).

5	SEQ ID NO. Nucleotide sequence		Originating DNA fragment	
			SEQ ID NO.	Nucleotide position
10	Resistance gene: vanA			
	1086	5'-CTA CTC CCG CCT TTT GGG TT	1049-1057 ^a	513-532 ^b
	1087 ^c	5'-CTC ACA GCC CGA AAC AGC CT	1049-1057 ^a	699-718 ^b
15	1086	5'-CTA CTC CCG CCT TTT GGG TT	1049-1057 ^a	513-532 ^b
	1088 ^c	5'-TGC CGT TTC CTG TAT CCG TC	1049-1057 ^a	885-904 ^b
	1086	5'-CTA CTC CCG CCT TTT GGG TT	1049-1057 ^a	513-532 ^b
20	1089 ^c	5'-ATC CAC ACG GGC TAG ACC TC	1049-1057 ^a	933-952 ^b
	1090	5'-AAT AGC GCG GAC GAA TTG GAC	1049-1057 ^a	629-649 ^b
	1091 ^c	5'-AAC GCG GCA CTG TTT CCC AA	1049-1057 ^a	734-753 ^b
	1090	5'-AAT AGC GCG GAC GAA TTG GAC	1049-1057 ^a	629-649 ^b
25	1089 ^c	5'-ATC CAC ACG GGC TAG ACC TC	1049-1057 ^a	933-952 ^b
	1092	5'-TCG GCA AGA CAA TAT GAC AGC	1049-1057 ^a	662-682 ^b
	1088 ^c	5'-TGC CGT TTC CTG TAT CCG TC	1049-1057 ^a	885-904 ^b
30	Resistance gene: vanB			
	1095	5'-CGA TAG AAG CAG CAG GAC AA	1117 ^d	473-492
	1096 ^c	5'-CTG ATG GAT GCG GAA GAT AC	1117 ^d	611-630
35	Resistance gene: vanAB			
	1112	5'-GGC TGY GAT ATT CAA AGC TC	1049-1057, 1117 ^a	437-456 ^b
	1113 ^c	5'-ACC GAC CTC ACA GCC CGA AA	1049-1057, 1117 ^a	705-724 ^b
40	1112	5'-GGC TGY GAT ATT CAA AGC TC	1049-1057, 1117 ^a	437-456 ^b
	1114 ^c	5'-TCW GAG CCT TTT TCC GGC TCG	1049-1057, 1117 ^a	817-837 ^b
	1115	5'-TTT CGG GCT GTG AGG TCG GBT GHG CG	1049-1057, 1117 ^a	705-730 ^b
45	1114 ^c	5'-TCW GAG CCT TTT TCC GGC TCG	1049-1057, 1117 ^a	817-837 ^b
	1116	5'-TTT CGG GCT GTG AGG TCG GBT GHG CGG	1049-1057, 1117 ^a	705-731 ^b
	1114 ^c	5'-TCW GAG CCT TTT TCC GGC TCG	1049-1057, 1117 ^a	817-837 ^b
50	1112	5'-GGC TGY GAT ATT CAA AGC TC	1049-1057, 1117 ^a	437-456 ^b
	1118 ^c	5'-TTT TCW GAG CCT TTT TCC GGC TCG	1049-1057, 1117 ^a	817-840 ^b

^a These sequences were aligned to derive the corresponding primer.

^b The nucleotide positions refer to the *vanA* sequence fragment (SEQ ID NO. 1051).

^c These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

^d Sequences from databases.

Annex XXXIV: Specific and ubiquitous primers for nucleic acid amplification (van s quenc s) (continued).

5			Originating DNA fragment	
	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	Resistance gene: vanAB (continued)			
	1115	5'-TTT CGG GCT GTG AGG TCG GBT GHG CG	1049-1057,1117 ^a	705-730 ^b
	1118 ^c	5'-TTT TCW GAG CCT TTT TCC GGC TCG	1049-1057,1117 ^a	817-840 ^b
15	1116	5'-TTT CGG GCT GTG AGG TCG GBT GHG CGG	1049-1057,1117 ^a	705-731 ^b
	1118 ^c	5'-TTT TCW GAG CCT TTT TCC GGC TCG	1049-1057,1117 ^a	817-840 ^b
	1119	5'-TTT CGG GCT GTG AGG TCG GBT GHG C	1049-1057,1117 ^a	705-729 ^b
20	1118 ^c	5'-TTT TCW GAG CCT TTT TCC GGC TCG	1049-1057,1117 ^a	817-840 ^b
	1120	5'-TTT CGG GCT GTG AGG TCG GBT GHG	1049-1057,1117 ^a	705-728 ^b
	1118 ^c	5'-TTT TCW GAG CCT TTT TCC GGC TCG	1049-1057,1117 ^a	817-840 ^b
	1121	5'-TGT TTG WAT TGT CYG GYA TCC C	1049-1057,1117 ^a	408-429 ^b
25	1111 ^c	5'-CTT TTT CCG GCT CGW YTT CCT GAT G	1049-1057,1117 ^a	806-830 ^b
	1112	5'-GGC TGY GAT ATT CAA AGC TC	1049-1057,1117 ^a	437-456 ^b
	1111 ^c	5'-CTT TTT CCG GCT CGW YTT CCT GAT G	1049-1057,1117 ^a	806-830 ^b
30	1123	5'-TTT CGG GCT GTG AGG TCG GBT G	1049-1057,1117 ^a	705-726 ^b
	1111 ^c	5'-CTT TTT CCG GCT CGW YTT CCT GAT G	1049-1057,1117 ^a	806-830 ^b
	1112	5'-GGC TGY GAT ATT CAA AGC TC	1049-1057,1117 ^a	437-456 ^b
35	1124 ^c	5'-GAT TTG RTC CAC YTC GCC RAC A	1049-1057,1117 ^a	757-778 ^b
	Resistance gene: vanC1			
	1103	5'-ATC CCG CTA TGA AAA CGA TC	1058-1059 ^a	519-538 ^d
40	1104 ^c	5'-GGA TCA ACA CAG TAG AAC CG	1058-1059 ^a	678-697 ^d
	Resistance gene: vanC1, vanC2, vanC3			
	1097	5'-TCY TCA AAA GGG ATC ACW AAA GTM AC	1058-1066 ^a	607-632 ^d
45	1098 ^c	5'-TCT TCA AAA TCG AAA AAG CCG TC	1058-1066 ^a	787-809 ^d
	1099	5'-TCA AAA GGG ATC ACW AAA GTM AC	1058-1066 ^a	610-632 ^d
	1100 ^c	5'-GTA AAK CCC GGC ATR GTR TTG ATT TC	1058-1066 ^a	976-1001 ^d
	1101	5'-GAC GGY TTT TTY GAT TTT GAA GA	1058-1066 ^a	787-809 ^d
50	1102 ^c	5'-AAA AAR TCG ATK CGA GCM AGA CC	1058-1066 ^a	922-944 ^d
	Resistance gene: vanC2-vanC3			
	1105	5'-CTC CTA CGA TTC TCT TGA YAA ATC A	1060-1066,1140 ^a	487-511 ^e
55	1106 ^c	5'-CAA CCG ATC TCA ACA CCG GCA AT	1060-1066,1140 ^a	690-712 ^e

^a These sequences were aligned to derive the corresponding primer.

^b The nucleotide positions refer to the vanA sequence fragment (SEQ ID NO. 1051).

^c These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

^d The nucleotide positions refer to the vanC1 sequence fragment (SEQ ID NO. 1058).

^e The nucleotide positions refer to the vanC2 sequence fragment (SEQ ID NO. 1140).

Annex XXXIV: Sp cific and ubiquitous primers for nucleic acid amplification (van sequences) (continued).

5			Originating DNA fragment	
	SEQ ID NO.	Nucleotide sequence SEQ ID	Nucleotide NO.	position
10	Sequencing primers (vanAB)			
	1112	5'-GGC TGY GAT ATT CAA AGC TC	1139 ^a	737-756
	1111 ^b	5'-CTT TTT CCG GCT CGW YTT CCT GAT G	1139 ^a	1106-1130
15	Sequencing primers (vanA, vanX, vanY)			
	1150	5'-TGA TAA TCA CAC CGC ATA CG	1141 ^a	860-879
	1151 ^b	5'-TGC TGT CAT ATT GTC TTG CC	1141 ^a	1549-1568
20	1152	5'-ATA AAG ATG ATA GGC CGG TG	1141 ^a	1422-1441
	1153 ^b	5'-CTC GTA TGT CCC TAC AAT GC	1141 ^a	2114-2133
	1154	5'-GTT TGA AGC ATA TAG CCT CG	1141 ^a	2520-2539
25	1155 ^b	5'-CAG TGC TTC ATT AAC GTA GTC	1141 ^a	3089-3109
	Sequencing primers (vanC1)			
	1110	5'-ACG AGA AAG ACA ACA GGA AGA CC	1138 ^a	122-144
30	1109 ^b	5'-ACA TCG TGA TCG CTA AAA GGA GC	1138 ^a	1315-1337
	Sequencing primers (vanC2-vanC3)			
	1108	5'-GTA AGA ATC GGA AAA GCG GAA GG	1140 ^a	1-23
35	1107 ^b	5'-CTC ATT TGA CTT CCT CCT TTG CT	1140 ^a	1064-1086

^a Sequences from databases.

^b These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

Annex XXXV: Internal probes for nucleic acid hybridization and specific detection of van sequences.

5			Originating DNA fragment	
	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	Resistance gene: <i>vanA</i>			
	1170	5'-ACG AAT TGG ACT ACG CAA TT	1049-1057 ^a	639-658 ^b
15	Resistance gene: <i>vanB</i>			
	1171	5'-ACG AGG ATG ATT TGA TTG TC	1117 ^c	560-579

20

^a These sequences were aligned to derive the corresponding primer.

^b The nucleotide positions refer to the *vanA* sequence fragment (SEQ ID NO. 1051).

^c Sequences from databases.

Annex XXXVI: Specific and ubiquitous primers for nucleic acid amplification (pbp sequences).

5			Originating DNA fragment	
	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	Resistance gene: <i>pbp1a</i>			
	1129	5'-ATG ATG ACC GAM ATG ATG AAA AC	1004-1018 ^a	681-703 ^b
	1131 ^c	5'-CAT CTG GAG CTA CRT ARC CAG T	1004-1018 ^a	816-837 ^b
15	1130	5'-GAC TAT CCA AGC ATG CAT TAT G	1004-1018 ^a	456-477 ^b
	1131	5'-CAT CTG GAG CTA CRT ARC CAG T	1004-1018 ^a	816-837 ^b
	Sequencing primers (<i>pbp1a</i>)			
20	1125	5'-ACT CAC AAC TGG GAT GGA TG	1169 ^d	873-892
	1126 ^c	5'-TTA TGG TTG TGC TGG TTG AGG	1169 ^d	2140-2160
	1125	5'-ACT CAC AAC TGG GAT GGA TG	1169 ^d	873-892
25	1128 ^c	5'-GAC GAC YTT ATK GAT ATA CA	1169 ^d	1499-1518
	1127	5'-KCA AAY GCC ATT TCA AGT AA	1169 ^d	1384-1403
	1126 ^c	5'-TTA TGG TTG TGC TGG TTG AGG	1169 ^d	2140-2160
	Sequencing primers (<i>pbp2b</i>)			
30	1142	5'-GAT CCT CTA AAT GAT TCT CAG GTG G	1172 ^d	1-25
	1143 ^c	5'-CAA TTA GCT TAG CAA TAG GTG TTG G	1172 ^d	1481-1505
	1142	5'-GAT CCT CTA AAT GAT TCT CAG GTG G	1172 ^d	1-25
35	1145 ^c	5'-AAC ATA TTK GGT TGA TAG GT	1172 ^d	793-812
	1144	5'-TGT YTT CCA AGG TTC AGC TC	1172 ^d	657-676
	1143 ^c	5'-CAA TTA GCT TAG CAA TAG GTG TTG G	1172 ^d	1481-1505
40	Sequencing primers (<i>pbp2x</i>)			
	1146	5'-GGG ATT ACC TAT GCC AAT ATG AT	1173 ^d	219-241
45	1147 ^c	5'-AGC TGT GTT AGC VCG AAC ATC TTG	1173 ^d	1938-1961
	1146	5'-GGG ATT ACC TAT GCC AAT ATG AT	1173 ^d	219-241
	1149 ^c	5'-TCC YAC WAT TTC TTT TTG WG	1173 ^d	1231-1250
	1148	5'-GAC TTT GTT TGG CGT GAT AT	1173 ^d	711-730
50	1147 ^c	5'-AGC TGT GTT AGC VCG AAC ATC TTG	1173 ^d	1938-1961

^a These sequences were aligned to derive the corresponding primer.

^b The nucleotide positions refer to the *pbp1a* sequence fragment (SEQ ID NO. 1004).

^c These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

^d Sequences from databases.

Annex XXXVII: Internal probes for nucleic acid hybridization and specific detection of *pbp* sequences.

		Originating DNA fragment	
SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
<u>Resistance gene:</u> <i>pbp1a</i>			
1132	5'-AGT GAA AAR ATG GCT GCT GC	1004-1018 ^a	531-550 ^b
1133	5'-CAT CAA GAA CAC TGG CTA YGT AG	1004-1018 ^a	806-828 ^b
1134	5'-CTA GAT AGA GCT AAA ACC TTC CT	1004-1018 ^a	417-439 ^b
1135	5'-CAT TAT GCA AAC GCC ATT TCA AG	1004-1018 ^a	471-493 ^b
1192	5'-GGT AAA ACA GGA ACC TCT AAC T	1004-1018 ^a	759-780 ^b
1193	5'-GGT AAG ACA GGT ACT TCT AAC T	1004-1018 ^a	759-780 ^b
1194	5'-CAT TTC AAG TAA TAC AAC AGA ATC	1004-1018 ^a	485-508 ^b
1195	5'-CAT TTC AAG TAA CAC AAC TGA ATC	1004-1018 ^a	485-508 ^b
1196	5'-GCC ATT TCA AGT AAT ACA ACA GAA	1004-1018 ^a	483-506 ^b
1197	5'-CAA ACG CCA TTT CAA GTA ATA CAA C	1004-1018 ^a	478-502 ^b
1094	5'-GGT AAA ACA GGT ACT TCT AAC TA	1004-1018 ^a	759-781 ^b
1214	5'-GGT AAA ACA GGT ACC TCT AAC TA	1004-1018 ^a	759-781 ^b
1216	5'-GGT AAG ACT GGT ACA TCA AAC TA	1004-1018 ^a	759-781 ^b
1217	5'-CAA ATG CCA TTT CAA GTA ACA CAA C	1004-1018 ^a	478-502 ^b
1218	5'-CAA ACG CCA TTT CAA GTA ACA CAA C	1004-1018 ^a	478-502 ^b
1219	5'-CAA ATG CTA TTT CAA GTA ATA CAA C	1004-1018 ^a	478-502 ^b
1220	5'-CAA ACG CCA TTT CAA GTA ATA CGA C	1004-1018 ^a	478-502 ^b

^a These sequences were aligned to derive the corresponding primer.

^b The nucleotide positions refer to the *pbp1a* sequence fragment (SEQ ID NO. 1004).

Annex XXXVIII: Strategy for the selection of *vanAB*-specific amplification primers and specific hybridization probes *vana* and *vanB* from *van* sequences.

Accession #	734	759	936	961	SEQ ID NO.:
5	<i>vana</i> X56895	GTAGGCT GCGATATTCA AAGCTCAGC...CGGACGAAAT	GGACTACGCA ATTGAA...	1139	
	<i>vana</i> M97297	GTAGGCT GCGATATTCA AAGCTCAGC...CGGACGAAAT	GGACTACGCA ATTGAA...	1141	
	<i>vana</i>	GTAGGCT GCGATATTCA AAGCTCAGC...CGGACGAAAT	GGACTACGCA ATTGAA...	1051	
10	<i>vana</i>	GTAGGCT GCGATATTCA AAGCTCAGC...CGGACGAAAT	GGACTACGCA ATTGAA...	1052	
	<i>vana</i>	GTAGGCT GCGATATTCA AAGCTCAGC...CGGACGAAAT	GGACTACGCA ATTGAA...	1053	
	<i>vana</i>	GTAGGCT GCGATATTCA AAGCTCAGC...CGGACGAAAT	GGACTACGCA ATTGAA...	1054	
	<i>vana</i>	GTAGGCT GCGATATTCA AAGCTCAGC...CGGACGAAAT	GGACTACGCA ATTGAA...	1055	
	<i>vana</i>	GTAGGCT GCGATATTCA AAGCTCAGC...CGGACGAAAT	GGACTACGCA ATTGAA...	1056	
	<i>vana</i>	GTAGGCT GCGATATTCA AAGCTCAGC...CGGACGAAAT	GGACTACGCA ATTGAA...	1057	
15	<i>vana</i>	GTAGGCT GCGATATTCA AAGCTCAGC...CGGACGAAAT	GGACTACGCA ATTGAA...	1049	
	<i>vanB</i> U94526	GTAGGCT GCGATATTCA AAGCTCAGC...CGGACGAAAT	GGACTACGCA ATTGAA...	1050	
	<i>vanB</i> U94527	GTAGGCT GCGATATTCA AAGCTCAGC...CGGACGAAAT	GGACTACGCA ATTGAA...	1117	
	<i>vanB</i> U94528	GTAGGCT GCGATATTCA AAGCTCAGC...CGGACGAAAT	GGACTACGCA ATTGAA...	-	
20	<i>vanB</i> U94529	GTAGGCT GCGATATTCA AAGCTCAGC...CGGACGAAAT	GGACTACGCA ATTGAA...	-	
	<i>vanB</i> U94530	GTAGGCT GCGATATTCA AAGCTCAGC...CGGACGAAAT	GGACTACGCA ATTGAA...	-	
	<i>vanB</i> Z83305	GTAGGCT GCGATATTCA AAGCTCAGC...CGGACGAAAT	GGACTACGCA ATTGAA...	-	
	<i>vanB</i> U81452	GTAGGCT GCGATATTCA AAGCTCAGC...CGGACGAAAT	GGACTACGCA ATTGAA...	-	
	<i>vanB</i> U35369	GTAGGCT GCGATATTCA AAGCTCAGC...CGGACGAAAT	GGACTACGCA ATTGAA...	-	
25	<i>vanB</i> U72704	GTAGGCT GCGATATTCA AAGCTCAGC...CGGACGAAAT	GGACTACGCA ATTGAA...	-	
	<i>vanB</i> L06138	GTAGGCT GCGATATTCA AAGCTCAGC...CGGACGAAAT	GGACTACGCA ATTGAA...	-	
	<i>vanB</i> L15304	GTAGGCT GCGATATTCA AAGCTCAGC...CGGACGAAAT	GGACTACGCA ATTGAA...	-	
	<i>vanB</i> U00456	GTAGGCT GCGATATTCA AAGCTCAGC...CGGACGAAAT	GGACTACGCA ATTGAA...	-	
	<i>vand</i> AF130997	GTAGGCT GCGATATTCA AAGCTCAGC...CGGACGAAAT	GGACTACGCA ATTGAA...	-	
30	<i>vane</i> AF136925	GTAGGCT GCGATATTCA AAGCTCAGC...CGGACGAAAT	GGACTACGCA ATTGAA...	-	
	Selected sequence for amplification primer	GGCT GCGATATTCA AAGCTC		1112	
35	Selected sequence for hybridization probe	ACGAAAT GGACTACGCA ATT		1170	

The sequence numbering refers to the *Enterococcus faecium* *vana* gene fragment (SEQ ID NO. 1139). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches are indicated by lower-case letters. Dots indicate gaps in the sequences displayed.

"R" "Y" "W" "K" "W" and "S" designate nucleotide positions which are degenerated. "R" stands for A or G; "Y" stands for C or T; "W" stands for A or C; "K" stands for G or T; "S" stands for A or T; "W" stands for C or G. "I" stands for inosine which is a nucleotide analog that can bind to any of the four nucleotides A, C, G or T.

Annex XXXVIII: Strategy for the selection of vanAB-specific amplification primers and specific hybridization probes vanA and vanB from van^s sequences (continued).

	Accession #	1038	1063	1103	1133	SEQ ID NO.:
5	vanA X56895	GAACAAGT	GCCGCGTTAG	TTGTTGGC...ATT	CATCAGGAAAG	TCGAGCCGGA AAAAGGCT
	vanA M97297	GAACAAGT	GCCGCGTTAG	TTGTTGGC...ATT	CATCAGGAAAG	TCGAGCCGGA AAAAGGCT
	vanA	GAACAAGT	GCCGCGTTAG	TTGTTGGC...ATT	CATCAGGAAAG	TCGAGCCGGA AAAAGGCT
	vanA	GAACAAGT	GCCGCGTTAG	TTGTTGGC...ATT	CATCAGGAAAG	TCGAGCCGGA AAAAGGCT
10	vanA	GAACAAGT	GCCGCGTTAG	TTGTTGGC...ATT	CATCAGGAAAG	TCGAGCCGGA AAAAGGCT
	vanA	GAACAAGT	GCCGCGTTAG	TTGTTGGC...ATT	CATCAGGAAAG	TCGAGCCGGA AAAAGGCT
	vanA	GAACAAGT	GCCGCGTTAG	TTGTTGGC...ATT	CATCAGGAAAG	TCGAGCCGGA AAAAGGCT
	vanA	GAACAAGT	GCCGCGTTAG	TTGTTGGC...ATT	CATCAGGAAAG	TCGAGCCGGA AAAAGGCT
15	vanA	GAACAAGT	GCCGCGTTAG	TTGTTGGC...ATT	CATCAGGAAAG	TCGAGCCGGA AAAAGGCT
	vanB U94526	GGAAACAG	GATGATTTCG	TTGTCGGC...ATC	CATCAGGAAAG	TCGAGCCGGA AAAAGGCT
	vanB U94527	GGAAACAG	GATGATTTCG	TTGTCGGC...ATC	CATCAGGAAAG	TCGAGCCGGA AAAAGGCT
	vanB U94528	GGAAACAG	GATGATTTCG	TTGTCGGC...ATC	CATCAGGAAAG	TCGAGCCGGA AAAAGGCT
	vanB U94529	GGAAACAG	GATGATTTCG	TTGTCGGC...ATC	CATCAGGAAAG	TCGAGCCGGA AAAAGGCT
	vanB U94530	GGAAACAG	GATGATTTCG	TTGTCGGC...ATC	CATCAGGAAAG	TCGAGCCGGA AAAAGGCT
	vanB 283305	GGAAACAG	GATGATTTCG	TTGTCGGC...ATC	CATCAGGAAAG	TCGAGCCGGA AAAAGGCT
	vanB U81452	GGAAACAG	GATGATTTCG	TTGTCGGC...ATC	CATCAGGAAAG	TCGAGCCGGA AAAAGGCT
	vanB U35369	GGAAACAG	GATGATTTCG	TTGTCGGC...ATC	CATCAGGAAAG	TCGAGCCGGA AAAAGGCT
25	vanB U72704	GGAAACAG	GATGATTTCG	TTGTCGGC...ATC	CATCAGGAAAG	TCGAGCCGGA AAAAGGCT
	vanB L06138	GGAAACAG	GATGATTTCG	TTGTCGGC...ATC	CATCAGGAAAG	TCGAGCCGGA AAAAGGCT
	vanB L15304	GGAAACAG	GATGATTTCG	TTGTCGGC...ATC	CATCAGGAAAG	TCGAGCCGGA AAAAGGCT
	vanB U00456	GGAAACAG	GATGATTTCG	TTGTCGGC...ATC	CATCAGGAAAG	TCGAGCCGGA AAAAGGCT
	vanD AF130997	GGAAACGGA	AATGATTTGA	TTGTCGGC...ATT	CATCAGGAAAG	cacAGCCGGA AAAAGGCT
30	vanE AF136925	GGAA...t	GAACATTTAG	TTGTCGGA...TAT	GAAGAGAAAT	ACAA.....TT
			ACAG	GATGATTTCG	TTGTC	
	Selected sequence for hybridization probe					1171
35	Selected sequence for amplification primer*					1111

The sequence numbering refers to the *Enterococcus faecium* varA gene fragment (SEQ ID NO. 1139). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches are indicated by lower-case letters. Dots indicate gaps in the sequences displayed.

"R" and "W" designate nucleotide positions which are degenerated. "R" stands for A or G; "W" stands for A or T

^a This sequence is the reverse-complement of the above selected primer.

Annex XXXIX: Internal probe for nucleic acid hybridization and specific detection of *mecA*.

5	SEQ ID NO. Nucleotide sequence		Originating DNA fragment	
	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	<u>Resistance gene:</u>			
	<i>mecA</i>			
15	1177	5'-GCT CAA CAA GTT CCA GAT TA	1178 ^a	1313-1332

^a Sequence from databases.

Annex XL: Specific and ubiquitous primers for nucleic acid amplification (*hexA* sequences).

5			Originating DNA fragment	
	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	<hr/>			
	<u>Bacterial species:</u>	<i>Streptococcus pneumoniae</i>		
	1179	5'-ATT TGG TGA CGG GTG ACT TT	1183 ^a	431-450
15	1181 ^b	5'-AGC AGC TTA CTA GAT GCC GT	1183-1191 ^c	652-671 ^d
	Sequencing primers			
	1179	5'-ATT TGG TGA CGG GTG ACT TT	1183 ^a	431-450
20	1182 ^b	5'-AAC TGC AAG AGA TCC TTT GG	1183 ^a	1045-1064
	<hr/>			

^a Sequences from databases.

^b These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

^c These sequences were aligned to derive the corresponding primer.

^d The nucleotide positions refer to the *hexA* sequence fragment (SEQ ID NO. 1183).

Annex XLI: Internal probe for nucleic acid hybridization and specific detection of hexA sequence s.

5

		Originating DNA fragment	
SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position

10

| Bacterial species: | | ***Streptococcus pneumoniae*** | |
| 1180^a | 5'-TCC ACC GTT GCC AAT CGC A | 1183-1191^b | 629-647^c |

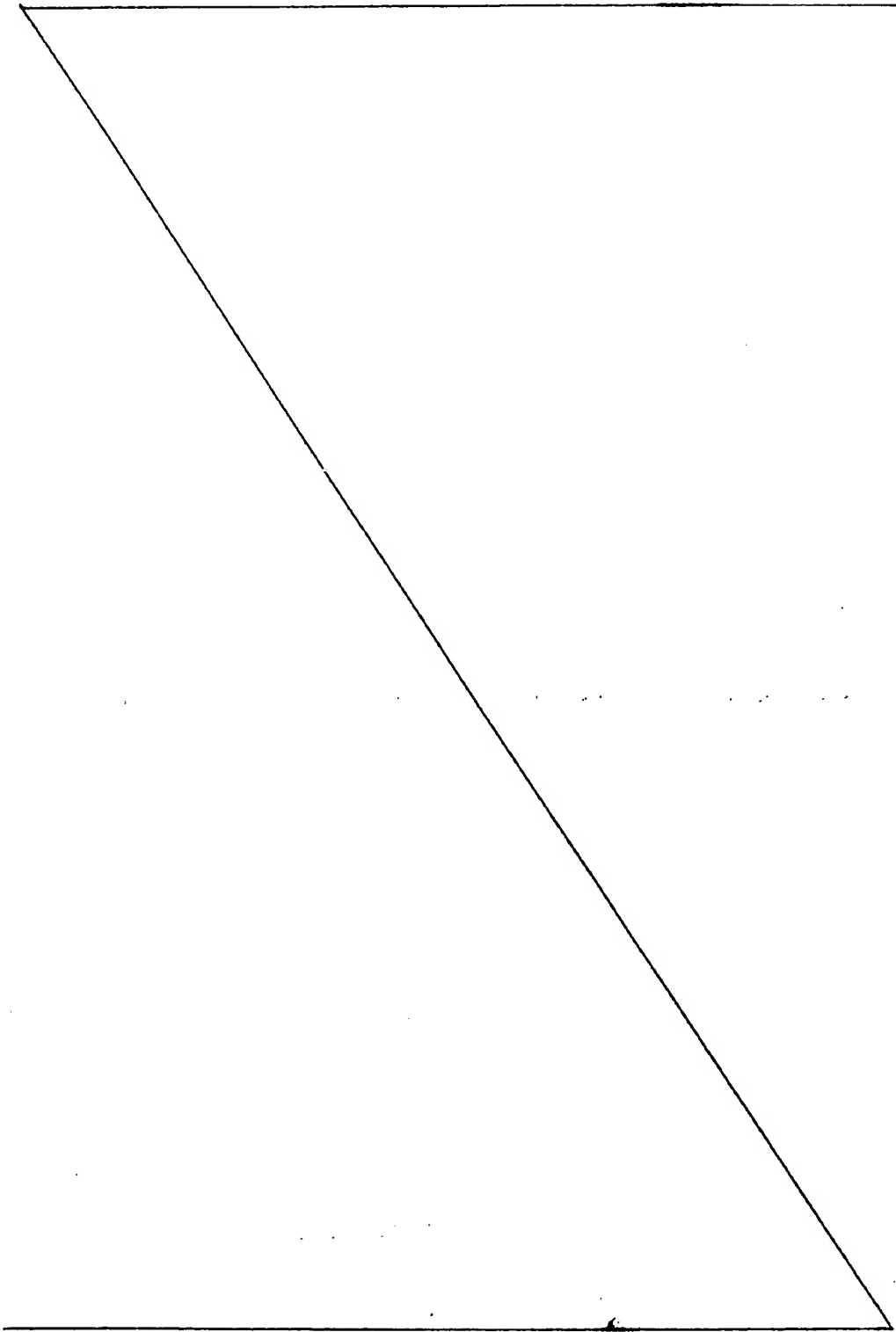
15

20

^a This sequences is from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

^b These sequences were aligned to derive the corresponding primer.

^c The nucleotide positions refer to the *hexA* sequence fragment (SEQ ID NO. 1183).



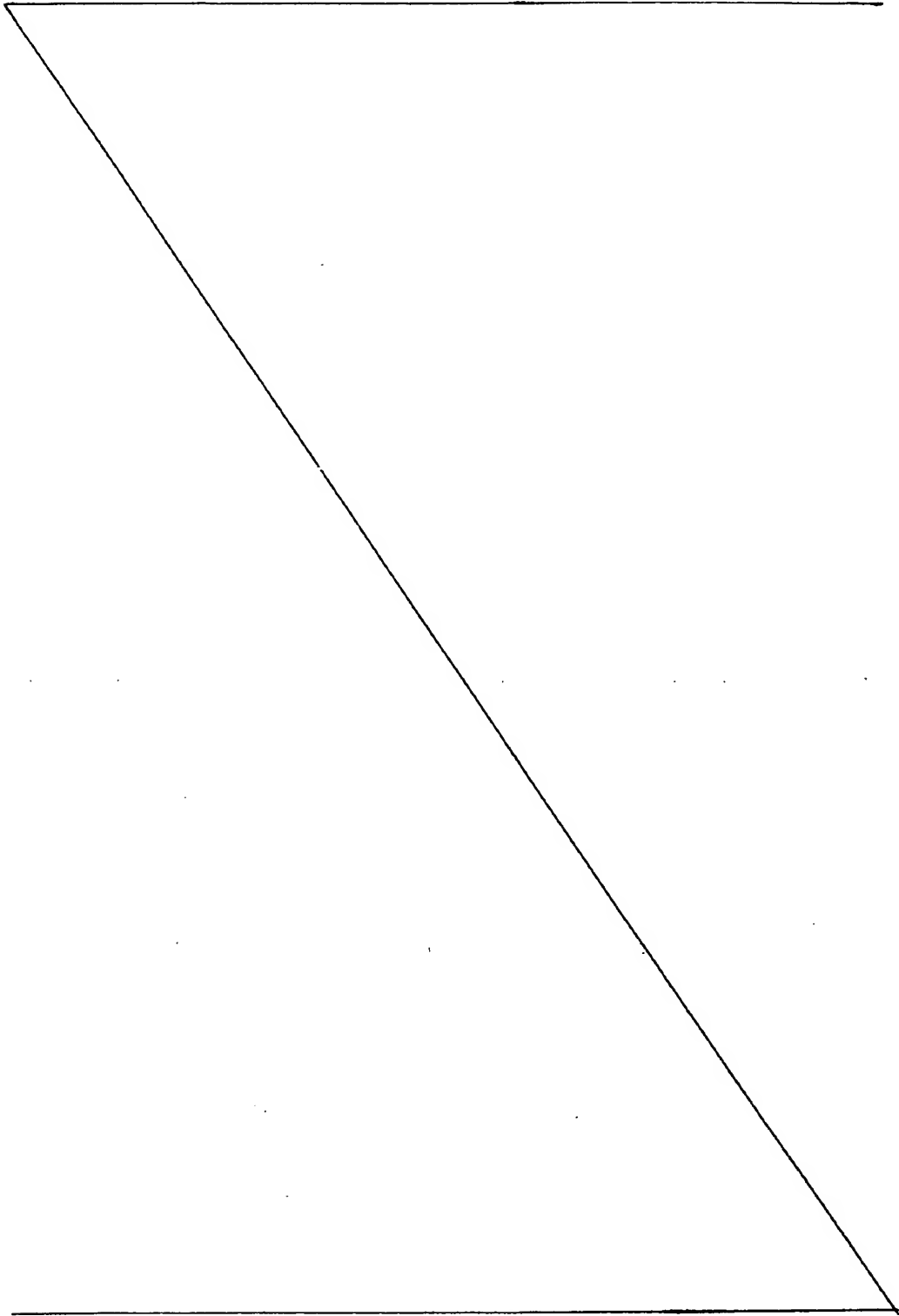
Ann x XLII: Strategy for the selection of *Streptococcus pneumoniae* species-sp cific amplification primers and hybridization probe from hexA sequences.

5

	428	453	626	674	1042	1067	SEQ ID NO.:
<i>S. pneumoniae</i>	TGG ATTGCTGAC GGGTGACTTT	TAT...ATTG CGATTGGCAA	CGGTGGAGCA AACGGCATCT	AGTAAGCTGC	TCCA...AATCCAAAG	GAATCTCTGC	1183
<i>S. pneumoniae</i>	---	-----TGAC GGGTGACTTT	TAT...ATTG CGATTGGCAA	CGGTGGAGCA AACGGCATCT	AGTAAGCTGC	TCCA...AATCCAAAG	1184
<i>S. pneumoniae</i>	---	-----TGAC GGGTGACTTT	TAT...ATTG CGATTGGCAA	CGGTGGAGCA AACGGCATCT	AGTAAGCTGC	TCCA...AATCCAAAG	1185
<i>S. pneumoniae</i>	---	-----TGAC GGGTGACTTT	TAT...ATTG CGATTGGCAA	CGGTGGAGCA AACGGCATCT	AGTAAGCTGC	TCCA...AATCCAAAG	1186
<i>S. pneumoniae</i>	---	-----TGAC GGGTGACTTT	TAT...ATTG CGATTGGCAA	CGGTGGAGCA AACGGCATCT	AGTAAGCTGC	TCCA...AATCCAAAG	1187
<i>S. oralis</i>	---	-----TGAC GGGTGACTTT	TAT...ATTG CGATTGGCAA	CGGTGGAGCA AACGGCATCT	AGTAAGCTGC	TCCA...AATCCAAAG	1188
<i>S. mitis</i>	---	-----TGAC GGGTGACTTT	TAT...ATTG CGATTGGCAA	CGGTGGAGCA AACGGCATCT	AGTAAGCTGC	TCCA...AATCCAAAG	1189
<i>S. mitis</i>	---	-----TGAC GGGTGACTTT	TAT...ATTG CGATTGGCAA	CGGTGGAGCA AACGGCATCT	AGTAAGCTGC	TCCA...AATCCAAAG	1190
<i>S. mitis</i>	---	-----TGAC GGGTGACTTT	TAT...ATTG CGATTGGCAA	CGGTGGAGCA AACGGCATCT	AGTAAGCTGC	TCCA...AATCCAAAG	1191
Selected sequence for amplification primer	ATTGCTGAC GGGTGACTTT						1179
Selected sequences for amplification primers*				ACGGCATCT	AGTAAGCTGC	T	1181
					CCAAAG	GAATCTCTGC	1182
Selected sequence for hybridization probe		TG	CGATTGGCAA	CGGTGGAA			1180

The sequence numbering refers to the *Streptococcus pneumoniae* hexA gene fragment (SEQ ID NO. 1183). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches are indicated by lower-case letters. Dots indicate gaps in the sequences displayed. "*" indicate incomplete sequence data.

* This sequence is the reverse-complement of the selected primer.



Annex XLIII: Specific and ubiquitous primers for nucleic acid amplification (pcp sequence).

5

		Originating DNA fragment	
SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position

10

Bacterial species: ***Streptococcus pyogenes***			
1211	5'-ATT CTT GTA ACA GGC TTT GAT CCC	1215^a	291-314
1210^b	5'-ACC AGC TTG CCC AAT ACA AAG G	1215^a	473-494

15

| | | | |

20

^a Sequences from databases.

^b These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

Annex XLIV: Specific and ubiquitous primers for nucleic acid amplification (*S. saprophyticus* unknown gene sequences).

5	<hr/>			
			Originating DNA fragment	
	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	<hr/>			
	Bacterial species: <i>Staphylococcus saprophyticus</i>			
15	1208	5'-TCA AAA AGT TTT CTA AAA AAT TTA C	74,1093, 1198 ^b	169-193 ^c
	1209 ^a	5'-ACG GGC GTC CAC AAA ATC AAT AGG A	74,1093, 1198 ^b	355-379 ^c
20	<hr/>			
	^a This sequence is from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.			
	^b These sequences were aligned to derive the corresponding primer.			
25	^c The nucleotide positions refer to the <i>S. saprophyticus</i> unknown gene sequence fragment (SEQ ID NO. 1198).			

Annex XLV: Molecular beacon internal probes for hybridization and specific detection of antibiotic resistance gene sequences.

5

		Originating DNA fragment	
SEQ ID NO.	Nucleotide sequence ^a	SEQ ID NO.	Nucleotide position
<hr/>			
<u>Resistance gene:</u> <i>mecA</i>			
1231	5'-GCG AGC CCG AAG ATA AAA AAG AAC CTC TGC TGC TCG C	1178 ^b	1291-1315
<u>Resistance gene:</u> <i>vanA</i>			
1239	5'-GCG AGC GCA GAC CTT TCA GCA GAG GAG GCT CGC	1051	860-880
1240	5'-GCG AGC CGG CAA GAC AAT ATG ACA GCA AAA TCG CTC GC	1051	663-688
<u>Resistance gene:</u> <i>vanB</i>			
1241	5'-GCG AGC GGG GAA CGA GGA TGA TTT GAT TGG CTC GC	1117	555-577

10

15

20

25

30

^a Underlined nucleotides indicate the molecular beacon's stem.

^b Sequence from databases.

Annex XLVI: Molecular beacon internal probe for hybridization and specific detection of an unknown *S. aureus* gene sequence.

5				
			Originating DNA fragment	
	SEQ ID NO.	Nucleotide sequence ^a	SEQ ID NO.	Nucleotide position
10				
	<u>Bacterial species:</u> <i>S. aureus</i>			
15	1232	5'-GGA GCC GCG CGA TTT TAT AAA TGA ATG TTG ATA ACC GGC TCC	1244	53-80

^a Underlined nucleotides indicate the molecular beacon's stem.

Annex XLVII: Molecular beacon internal probes for hybridization and specific detection of *tuf* sequences.

5			Originating DNA fragment	
	SEQ ID NO.	Nucleotide sequence ^a	SEQ ID NO.	Nucleotide position
10	Bacterial species: <i>Enterococcus faecalis</i>			
	1236	5'- <u>GCG</u> <u>AGC</u> CGT GGT GAA GTT CGC GTT GGT GGC TCG C	883	370-391
15	Bacterial species: <i>Enterococcus faecium</i>			
	1235	5'- <u>GCG</u> <u>AGC</u> CGA AGT TGA AGT TGT TGG TAT TGC TGG <u>CTC</u> GC	64	412-437
20	Bacterial species: <i>Staphylococcus</i> sp. other than <i>S. aureus</i>			
25	1233	5'- <u>GCG</u> <u>AGC</u> GTT ACT GGT GTA GAA ATG TTC CGG <u>CTC</u> GC	878	372-394

^a Underlined nucleotides indicate the molecular beacon's stem.

Annex XLVIII: Molecular beacon internal probes for hybridization and specific detection of *ddl* and *mtl* genes.

5			Originating DNA fragment	
	SEQ ID NO.	Nucleotide sequence ^a	SEQ ID NO.	Nucleotide position
10				
	<u>Bacterial species:</u> <i>E. faecium</i> (<i>ddl</i>)			
15	1237	5'-GCG AGC CGC GAA ATC GAA GTT GCT GTA TTA GGG CTC GC	1242	334-359
	<u>Bacterial species:</u> <i>E. faecalis</i> (<i>mtl</i>)			
20	1238	5'-GCG AGC GGC GTT AAT TTT GGC ACC GAA GAA GAG CTC GC	1243	631-656

^a Underlined nucleotides indicate the molecular beacon's stem.

Annex XLIX: Internal probe for nucleic acid hybridization and specific detection of an unknown *S. aureus* gene sequence.

		Originating DNA fragment	
SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
Bacterial species: <i>Staphylococcus aureus</i>			
1234	5'-ACT AAA TAA ACG CTC ATT CG	1244	35-54

What is claimed is:

1. A repertoire of nucleic acid sequences used for the detection and/or identification of a bacterial, fungal or parasitical species, genus, family or group, which repertoire is created by amplifying the nucleic acids of a plurality of determined bacterial, fungal and parasitical species with any combination of the primer pairs shown in annexes I, II, XXI, XXII, XXXII, XXXIV, XXXVI, XL, XLIII and XLIV.
2. A nucleic acid used for universal detection of any bacterium, fungus or parasite which is derived from the repertoire of claim 1.
3. A nucleic acid used for universal detection as set forth in claim 2, which has a nucleic acid sequence of at least 12 nucleotides capable of hybridizing with said any bacterium, fungus or parasite and with any one of SEQ ID NOs.: 543, 556-574, 636-655, 658-661, 664, 681-683, 694, 696-697, 699-700, 708, 812-815, 911-917, 919-922, 935-938, 1203-1207, 1212-1213, 1221-1229.
4. A nucleic acid used for the specific and ubiquitous detection and for identification of a bacterial, fungal or parasital species, genus, family or group, which is derived from the repertoire of claim 1.
5. A nucleic acid as set forth in claim 4, which has a nucleic acid sequence of at least 12 nucleotides capable of hybridizing with the nucleic acids of said bacterial, fungal or parasitical species, genus, family or group and with any one of :

SEQ ID NOs.:

- | | |
|--|--|
| 539, 540 | for the detection and/or identification of <i>Mycobacteriaceae</i> family |
| 541, 542, 544 | for the detection and/or identification of <i>Pseudomonads</i> group |
| 545, 546 | for the detection and/or identification of <i>Corynebacterium</i> sp. |
| 547, 548, 1202 | for the detection and/or identification of <i>Streptococcus</i> sp. |
| 549, 550, 582, 583, 625, 626, 627, 628, 1199 | for the detection and/or identification of <i>Streptococcus agalactiae</i> |
| 551, 552 | for the detection and/or identification of <i>Neisseria gonorrhoeae</i> |
| 553, 575, 605, 606, 707, 1175, 1176, 1233 | for the detection and/or identification of <i>Staphylococcus</i> sp. |
| 554, 555 | for the detection and/or identification of <i>Chlamydia trachomatis</i> |
| 576, 631, 632, 633, 634, 635, 1163, 1164, 1167 | for the detection and/or identification of <i>Candida</i> sp. |
| 577, 1156, 1160 | for the detection and/or identification of <i>Candida albicans</i> |
| 578, 1166, 1168 | for the detection and/or identification of <i>Candida dubliniensis</i> |

579	for the detection and/or identification of <i>Escherichia coli</i>
580, 603, 1174, 1236, 1238	for the detection and/or identification of <i>Enterococcus faecalis</i>
581	for the detection and/or identification of <i>Haemophilus influenzae</i>
5 584, 585, 586, 587, 588, 1232, 1234	for the detection and/or identification of <i>Staphylococcus aureus</i>
589, 590, 591, 592, 593	for the detection and/or identification of <i>Staphylococcus epidermidis</i>
10 594, 595	for the detection and/or identification of <i>Staphylococcus haemolyticus</i>
596, 597, 598	for the detection and/or identification of <i>Staphylococcus hominis</i>
599, 600, 601, 695, 1208, 1209	for the detection and/or identification of <i>Staphylococcus saprophyticus</i>
602, 1235, 1237	for the detection and/or identification of <i>Enterococcus faecium</i>
15 604	for the detection and/or identification of <i>Enterococcus gallinarum</i>
620, 1122	for the detection and/or identification of <i>Enterococcus casseliflavus</i> , <i>E. flavescens</i> and <i>E. gallinarum</i>
629, 630	for the detection and/or identification of <i>Chlamydia pneumoniae</i>
656, 657, 271, 20 1136, 1137	for the detection and/or identification of <i>Enterococcus</i> sp.
701, 702	for the detection and/or identification of <i>Leishmania</i> sp.
703, 704, 705, 706, 793	for the detection and/or identification of <i>Entamoeba</i> sp.
794, 795	for the detection and/or identification of <i>Trypanosoma cruzi</i>
25 796, 797, 808, 809, 810, 811	for the detection and/or identification of <i>Clostridium</i> sp.
798, 799, 800, 801, 802, 803, 804, 805, 806,	
30 807	for the detection and/or identification of <i>Cryptosporidium parvum</i>
816, 817, 818, 819	for the detection and/or identification of <i>Giardia</i> sp.
820, 821, 822	for the detection and/or identification of <i>Trypanosoma brucei</i>
823, 824	for the detection and/or identification of <i>Trypanosoma</i> sp.
35 825, 826	for the detection and/or identification of <i>Bordetella</i> sp.
923, 924, 925, 926, 927, 928	for the detection and/or identification of <i>Trypanosomatidae</i> family
933, 934	for the detection and/or identification of <i>Enterobacteriaceae</i> group
935, 938	for the detection and/or identification of platelets contaminants group: <i>Abiotrophia adiacens</i> , <i>Abiotrophia defectiva</i> , <i>Acinetobacter baumannii</i> , <i>Acinetobacter lwoffii</i> , <i>Aerococcus viridans</i> , <i>Bacillus anthracis</i> , <i>Bacillus cereus</i> , <i>Bacillus subtilis</i> , <i>Brucella abortus</i> , <i>Burkholderia cepacia</i> , <i>Citrobacter diversus</i> , <i>Citrobacter freundii</i> , <i>Enterobacter aerogenes</i> , <i>Enterobacter agglomerans</i> , <i>Enterobacter cloacae</i> , <i>Enterococcus avium</i> , <i>Enterococcus casseliflavus</i> , <i>Enterococcus dispar</i> , <i>Enterococcus durans</i> , <i>Enterococcus faecalis</i> , <i>Enterococcus faecium</i> , <i>Enterococcus flavescens</i> , <i>Enterococcus gallinarum</i> ,
40	
45	

- 5 *Enterococcus mundtii*, *Enterococcus raffinosus*, *Enterococcus solitarius*, *Escherichia coli*, *Gemella morbillorum*, *Haemophilus ducreyi*, *Haemophilus haemolyticus*, *Haemophilus influenzae*, *Haemophilus parahaemolyticus*, *Haemophilus parainfluenzae*, *Hafnia alvei*, *Kingella kingae*, *Klebsiella oxytoca*, *Klebsiella pneumoniae*, *Legionella pneumophila*, *Megamonas hypermegale*, *Moraxella atlantae*, *Moraxella catarrhalis*, *Morganella morganii*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Pasteurella aerogenes*, *Pasteurella multocida*, *Peptostreptococcus magnus*, *Proteus mirabilis*, *Providencia alcalifaciens*, *Providencia rettgeri*, *Providencia rustigianii*, *Providencia stuartii*, *Pseudomonas aeruginosa*, *Pseudomonas fluorescens*, *Pseudomonas stutzeri*,
10 *Salmonella bongori*, *Salmonella choleraesuis*, *Salmonella enteritidis*, *Salmonella gallinarum*, *Salmonella typhimurium*, *Serratia liquefaciens*, *Serratia marcescens*, *Shigella flexneri*, *Shigella sonnei*, *Staphylococcus aureus*, *Staphylococcus capitis*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Staphylococcus hominis*, *Staphylococcus lugdunensis*, *Staphylococcus saprophyticus*, *Staphylococcus simulans*,
15 *Staphylococcus warneri*, *Stenotrophomonas maltophilia*, *Streptococcus acidominimus*, *Streptococcus agalactiae*, *Streptococcus anginosus*, *Streptococcus bovis*, *Streptococcus constellatus*, *Streptococcus cricetus*, *Streptococcus cristatus*, *Streptococcus dysgalactiae*, *Streptococcus equi*, *Streptococcus ferus*, *Streptococcus gordonii*, *Streptococcus intermedius*, *Streptococcus macacae*, *Streptococcus mitis*, *Streptococcus mutans*,
20 *Streptococcus oralis*, *Streptococcus parasanguinis*, *Streptococcus parauberis*, *Streptococcus pneumoniae*, *Streptococcus pyogenes*, *Streptococcus rattii*, *Streptococcus salivarius*, *Streptococcus sanguinis*, *Streptococcus sobrinus*, *Streptococcus uberis*, *Streptococcus vestibularis*, *Vibrio cholerae*, *Yersinia enterocolitica*, *Yersinia pestis*, *Yersinia pseudotuberculosis*.
- 25 994, 995, 996,
997, 998, 999,
1000, 1001, 1200,
1210, 1211 for the detection and/or identification of *Streptococcus pyogenes*
1157 for the detection and/or identification of *Candida parapsilosis*
- 30 1158, 1159 for the detection and/or identification of *Candida glabrata*
1160 for the detection and/or identification of *Candida tropicalis*
1161 for the detection and/or identification of *Candida krusei*
1162 for the detection and/or identification of *Candida guilliermondii*
1162 for the detection and/or identification of *Candida lusitanae*
- 35 1165 for the detection and/or identification of *Candida zeylanoides*
1201 for the detection and/or identification of *Streptococcus pneumoniae*.

6. A nucleic acid as set forth in claim 4, which has a nucleic acid sequence of at least 12 nucleotides capable of hybridizing with the nucleic acids of said bacterial, fungal or parasitical species, genus,
40 family, group or universal, and using the former in conjunction with any nucleic acid sequence of at least 12 nucleotides capable of hybridizing with a bacterial antibiotic resistance gene and/or toxin gene respectively listed in Tables 5 and 6.
7. Nucleic acids as set forth in claim 6 where the nucleic acid capable of hybridizing with a bacterial
45 antibiotic resistance gene and/or toxin gene is any one of :

SEQ ID NOs.:

- 1078, 1079, 1085 for the detection and/or identification of the Shiga-like toxin 2 (*stx*₂) gene
 1080, 1081, 1084 for the detection and/or identification of the Shiga-like toxin 1 (*stx*₁) gene
 1082, 1083 for the detection and/or identification of Shiga-like toxins 1 (*stx*₁) and 2 (*stx*₂) genes
- 5 1086, 1087, 1088,
 1089, 1090, 1091,
 1092, 1170, 1239,
 1240 for the detection and/or identification of the *vanA* resistance gene
 1171, 1241 for the detection and/or identification of the *vanB* resistance gene
- 10 1111, 1112, 1113,
 1114, 1115, 1116,
 1118, 1119, 1120,
 1121, 1123, 1124 for the detection and/or identification of the *vanAB* resistance genes
 1103, 1104, 1109,
- 15 1110 for the detection and/or identification of the *vanC1* resistance gene
 1105, 1106, 1107,
 1108 for the detection and/or identification of the *vanC2* and *vanC3* resistance genes
 1097, 1098, 1099,
 1100, 1101, 1102 for the detection and/or identification of the *vanC1*, *vanC2* and *vanC3* resistance genes
- 20 1150, 1153, 1154,
 1155 for the detection and/or identification of the *vanAXY* resistance genes
 1094, 1125, 1126,
 1127, 1128, 1129,
 1130, 1131, 1132,
- 25 1133, 1134, 1135,
 1192, 1193, 1194,
 1195, 1196, 1197,
 1214, 1216, 1217,
 1218, 1219, 1220 for the detection and/or identification of the *S. pneumoniae pbp1a* gene
- 30 1142, 1143, 1144
 1145 for the detection and/or identification of the *S. pneumoniae pbp2b* gene
 1146, 1147, 1148
 1149 for the detection and/or identification of the *S. pneumoniae pbp2x* gene
 1177 for the detection and/or identification of the *mecA* resistance gene.
- 35
8. A method for the specific detection or identification of a bacterial, fungal or parasitological species, genus, family or group in a sample, using a panel of probes or amplification primers or both, each individual probe or primer being derived from a nucleic acid as defined in claim 4, the method comprising the step of contacting the nucleic acids of the sample with said primers or probes under suitable conditions of hybridization or of amplification and detecting the presence of hybridized probes or amplified products as an indication of the presence of said specific bacterial, fungal or parasitological species, genus, family or group.
- 40
9. A method as set forth in claim 8, which further comprises probes or primers, or both, for the detection of at least one of the antibiotic resistance genes listed in Table 5.
- 45

10. A method as set forth in claim 8 or 9, which further comprises probes or primers, or both, for the detection of at least one of the toxin genes listed in Table 6.
- 5 11. A method as defined in claim 8, which further comprises the universal detection of any bacterium, fungus or parasite.
12. A nucleic acid having the nucleotide sequence of any one of the *tuf* sequences listed in Table 7 or in Table 11, or a part of thereof and variants thereof, which can be used as target nucleic acids for the
10 detection and identification of microbial species.
13. A nucleic acid having the nucleotide sequence of any one of the *atpD* sequences listed in Table 7 or in Table 11, or a part of thereof and variants thereof, which can be used as target nucleic acids for the detection and identification of microbial species.
- 15 14. A nucleic acid having the nucleotide sequence of any one of the *recA* sequences listed in Table 7 or in Table 11, or a part of thereof and variants thereof, which can be used as target nucleic acids for the detection and identification of microbial species.
- 20 15. A nucleic acid having the nucleotide sequence of any one of the antibiotic-resistance genes sequences determined by us which are listed in Table 7, or a part of thereof and variants thereof, which can be used as target nucleic acids for the detection and identification of microbial species.
- 25 16. A nucleic acid having the nucleotide sequence of any one of the antibiotic resistance genes sequences listed in Table 5, or a part of thereof and variants thereof, which can be used as target nucleic acids for the detection and identification of microbial species.
- 30 17. A nucleic acid having the nucleotide sequence of any one of the toxin genes sequences listed in Table 6, a part of thereof and variants thereof, which can be used as target nucleic acids for the detection and identification of toxins in microbial species.
18. A repertory of *hexA* nucleic acid sequences used for the detection and/or identification of *Streptococcus pneumoniae*, which repertory is created by amplifying the nucleic acid of any streptococcal species with any combination of primers SEQ ID NOs. 1179, 1181 and 1182.
- 35 19. A nucleic acid used for the specific and ubiquitous detection and for identification of *Streptococcus pneumoniae*, which is derived from the repertory of claim 18.

20. A nucleic acid used for detection as set forth in claim 19 which has a nucleic acid sequence of at least 12 nucleotides capable of hybridizing with said any *Streptococcus pneumoniae* and with any one of SEQ ID NOs. 1184 to 1187.
- 5 21. A nucleic acid as set forth in claim 19, which has a nucleic acid sequence of at least 12 nucleotides capable of hybridizing with the nucleic acids of *Streptococcus pneumoniae* and with any one of SEQ ID NOs. 1179, 1180, 1181, 1182.
- 10 22. A peptide sequence derived from the translation of the nucleic acid sequences from the repertory of claim 1.
23. The use of the peptide sequences of claim 22 as part of a vaccine.
24. The use of the peptide sequences of claim 22 as targets of antimicrobial agents.
- 15 25. The use of the peptide sequences of claim 22 to design or improve antimicrobial agents.
26. The use of *tuf* sequences to identify any of the microorganisms listed in table 15.
- 20 27. The use of *atpD* sequences to identify any of the microorganisms listed in table 15.
28. The use of *recA* sequences to identify any of the microorganisms listed in table 15.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANTS:

5 BERGERON, Michel G. ¹, 1145 des Érables, Québec City,
 Québec, Canada, G2K 1T8
 BOISSINOT, Maurice ¹, 109 Jean-Bruchési, St-Augustin-
 de-Desmaures, Québec, Canada, G3A 2N2
 10 HULETSKY, Ann ¹, 1231 Av des Pins, Sillery, Québec,
 Canada, G1S 4J3
 MÉNARD, Christian ¹, 1174 Rue du Pont, St-Lambert-de-
 Lévis, Québec, Canada, G0S 2W0
 OUELLETTE, Marc ¹, 1035 de Ploërmel, Sillery, Québec,
 Canada, G1S 3S1
 15 PICARD, François J. ¹, 1245 de la Sapinière, Cap-Rouge,
 Québec, Canada, G1Y 1A1
 ROY, Paul H. ², 28 Charles Garnier, Loretteville,
 Québec, Canada, G2A 2X8

20 ¹:Canadian citizenship
²:American citizenship

(ii) TITLE OF THE INVENTION: HIGHLY CONSERVED GENES AN THEIR USE
 25 TO GENERATE SPECIES-SPECIFIC, GENUS-SPECIFIC AND UNIVERSAL
 NUCLEIC ACID PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY
 DETECT AND IDENTIFY BACTERIAL, FUNGAL AND PARASITICAL
 PATHOGENS FROM CLINICAL SPECIMENS FOR DIAGNOSIS

(iii) NUMBER OF SEQUENCES: 940

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE:
 (B) STREET:
 35 (C) CITY:
 (D) STATE:
 (E) COUNTRY:
 (F) ZIP:

(v) COMPUTER READABLE:

(A) MEDIUM TYPE:
 (B) COMPUTER:
 (C) OPERATING:
 45 (D) SOFTWARE:

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION:
 50 (B) FILING DATE:
 (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

55 (A) APPLICATION:
 (B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME:
- (B) REGISTRATION NUMBER:

5

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE:
- (B) TELEFAX:

2) INFORMATION FOR SEQ ID NO: 1

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 750 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Acinetobacter baumannii*
 (B) STRAIN: ATCC 19606

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1

CAA	ACTCGTG	AGC	ACATCCT	TCT	TTCTCGT	CAG	G	TAGGTG	TAC	CTTACAT	50
CAT	CGTATTC	TTA	ACAAAT	GCG	ACCTTGT	TG	ATGACGAA	GA	ATTACTTG	100	
AAT	TAGTAGA	AAT	GGAAGTA	CGT	GAACTTC	TTT	CTACTTA	TG	ACTTCCCA	150	
GGT	GATGACA	CTC	CAGTAAT	CCG	TGGTTCA	GCT	CTTGCAG	CG	CTTAACGG	200	
TGA	AGCTGGT	CCT	TACGGTG	AAG	AATCAGT	TCT	TGCTCTT	GT	AGCAGCAC	250	
TTG	ACTCTTA	CAT	CCCAGAG	CC	AGAGCGTG	CA	ATCGACAA	AG	CATTCTTG	300	
ATG	CCAATCG	AAG	ACGTATT	CT	CAATTTCT	GGT	CGTGGTA	CAG	TAGTAAC	350	
AGG	CCGTGTT	GA	AGCTGGTA	TC	ATCAAAGT	TGG	TGAAGAA	GT	AGAGATCG	400	
TTG	GATATTAA	AG	ATACAGTT	AAA	ACAACTG	TA	ACTGGCGT	AG	AAATGTTT	450	
CGT	AACTTTC	TTG	ACGAAGG	CCG	TGCAGGT	GAG	AACTGTG	GT	ATCTTACT	500	
TCG	TGGTACT	AAG	CGTGAAG	AAG	TACAACG	TGG	CAAGTA	CT	TGCTAAAC	550	
CAG	G	TACAAT	CAAGCCGCAC	ACT	AAATTCG	ACG	CAGAAGT	AT	ACGTACTT	600	
TCT	AAAGAAG	AAG	GTGGTCG	TC	ACACTCCA	TT	CTTAAATG	GT	TACCGTCC	650	
AC	AGTTCTAC	TT	CCGTACAA	CT	GACGTAAC	TG	GTGCRATC	CAG	TTGAAAG	700	
AAG	GCGTTGA	AAT	GGTAATG	CC	AGGTGACA	AC	GTTGAAAT	GT	CAGTAGAA	750	

2) INFORMATION FOR SEQ ID NO: 2

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 826 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Actinomyces meyeri*
 (B) STRAIN: ATCC 35568

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2

CGG	TGCGATC	CTC	GTGGTCG	CCG	CGACCGA	CGG	CCCCATG	GCC	CAGACCC	50
GCG	AGCACGT	CCT	GTCTCGC	CGT	CAGGTCG	GCG	TTCCAC	CAT	CCTCATC	100
GCC	CTCAACA	AGT	CCGACAT	GGT	TGACGAC	GAG	GAAATGA	TGG	AACTGGT	150
CGA	GAGGAG	TGC	CGCGACC	TG	CTGGAGTC	CC	AGGACTTC	GAT	CGCGATG	200
CCCC	GATCGT	CC	AGGTTTCC	GCT	CTGAAGG	CC	CTCGAGGG	CG	ACGCGGAG	250
TGG	GTTGCCA	AG	ATCGAGGA	GCT	CATGGAG	GCT	TGGATT	CCT	ACATCCC	300
CAC	CCCCGAG	CG	CGATATGG	ACA	AGCCCTT	CCT	CATGCCG	AT	CAGGACG	350
TCT	TACGAT	CAC	AGGTCGT	GG	CACGGTCG	TC	ACGGGGCG	TG	TTGAGCGT	400
GG	CAAGCTGC	CG	ATCAACTC	CG	AGGTCGAG	AT	CCTCGGTA	TCC	GTGATCC	450

	CCAGAAGACC	ACGGTCACCG	GCATCGAGAT	GTTCCACAAG	TCGATGGACG	500
	AGGCATGGGC	CGGCGAGAAC	TGTGGCCTGC	TGCTGCGCGG	TACCAAGCGC	550
	GATGAGGTTG	AGCGCGGCCA	GGTTGTGGCC	ATTCCC GGCT	CCATCACGCC	600
	TCACACCGAG	TTCGAGGGCC	AGGTTTACAT	CCTCAAGAAG	GAAGAGGGCG	650
5	GCCGTCACAA	CCCGTTCTTC	TCGAACTACC	GTCCGCAGTT	CTACTTCCGT	700
	ACCACGGACG	TGACCGGCGT	CATCACCTC	CCCGAGGGCA	CCGACATGGT	750
	CATGCCTGGC	GACACCACCG	AGATCTCCGT	TCAGCTGATC	CAGCCCATCG	800
	CCATGGAGCC	CGGCTGGGCT	TCGCCA			826

10

2) INFORMATION FOR SEQ ID NO: 3

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aerococcus viridans*
 (B) STRAIN: ATCC 11563

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3

	TGGTGCGATC	TTAGTAGTAT	CTGCTGCTGA	TGGTCCAATG	CCACAAACTC	50
	GTGAGCACAT	CCTTTTAGCT	GGCCAAATCG	GTGTTCCCTGC	ATTCGTAGTA	100
30	TTCTTAAACA	AAGTTGACCA	AGTTGACGAT	GAAGAATTAC	TAGAATTAGT	150
	TGAAATGGAA	GTTCGTGACT	TATTATCTGA	GTACAACTAC	CCAGGTGACG	200
	ATCTACCTGT	AATCGCTGGT	TCTGCTTTAT	TAGCATTACA	AGGCGATGAA	250
	GCTCAAGAAG	CTAAAATCAT	GGAATTAATG	GAAGCTGTAG	ACTCTTACAT	300
	TCCAGAACCA	GAACGTGACA	ACGACAAACC	ATTCATGATG	CCAATTGAGG	350
35	ATGTATTCTC	AATCACTGGT	CGTGGTACTG	TTGCTACAGG	TCGTGTTGAA	400
	CGTGGTGAAG	TTCGTACAGG	TGACGAAGTT	GACATCGTTG	GTATTGCTGA	450
	ACAAATCGGT	AAATCAGTTG	TAAGTGGTGT	TGAAATGTTT	CGTAAAAACT	500
	TAGACTACGC	TCAAGCTGGT	GACAACATCG	GTGCATTATT	ACGTGGTGTT	550
	CAACGTGAAG	ACATCCAACG	TGGTCAAGTA	TTGGCTGCTC	CTGGTTCAAT	600
40	CATCCACAT	ACTAAATTTA	AAGCGCAAGT	TTACGTTTTA	TCTAAAGAAG	650
	AAGGTGGACG	TCATACACCA	TTCTTAACTA	ACTACCGTCC	ACAATTCTAC	700
	TTCCGTACTA	CTGACATTAC	TGGTGTTATC	ACTTTACCAG	AAGACGTAGC	750
	TATGGTTATG	CCTGGTGACA	ACGTTGATAT	GGACGTTGAA	TTGATTCACC	800
45	CAGTTGCGAT	CGAAGATGGT	ACTAAATTCT	CTATC		835

2) INFORMATION FOR SEQ ID NO: 4

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 827 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Achromobacter xylosoxidans* subsp. *denitrificans*

60

(B) STRAIN: ATCC 15173

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4

```

5  CCTGGTGGTG TCGGCCGCTG ACGGCCCCGAT GCCGCAAACG CGCGAACACA      50
   TCCTGCTGAG CCGCCAGGTT GCGGTGCCGT ACATCATCGT CTCCTGAAC      100
   AAGGCCGACA TGGTTGACGA CGCCGAGCTG CTTGAGCTGG TGGAAATGGA      150
   AGTTCGCGAR CTGCTGAGCA AGTACGACTT CCCGGGCGAC GACACCCCGA      200
   TCGTGAAGGG TTCGGCCAAG CTGGCGCTGG AAGGCGACAA GGGCGAACTG      250
10  GGCGAACAGG CCATCATGGC GCTGGCCGCT GCGCTGGACT CGTACATCCC      300
   GACGCCTGAG CGTGCCGTTG ACGGCGCGTT CCTGATGCCG GTTGAAGACG      350
   TGTTCCTCGAT CTCGGGTCGC GGCACCGTGG TGACCGGCCG TATCGAACGC      400
   GGCATCATCA AGGTCGGCGA GGAAATCGAA ATCGTCGGTC TGGTGCCGAC      450
   GGTGAAGACG ACCTGCACGG GCGTGGAAT GTTCCGCAAG CTGCTGGACC      500
15  AAGGTCAAGC CGGCGACAAC GTGGGCATCC TRCTGCGCGG CACCAAGCGT      550
   GAAGACGTCC AGCGCGGCCA GGTTCCTGGCC AAGCCGGGCT CGATCACCCC      600
   GCACACGGAC TTCACGTCCG AGGTGTACAT CCTGTCCAAG GAAGAAGGCG      650
   GCCGTCACAC TCCGTTCTTC CAAGGCTATC GTCCCCAGTT CTACTTCCGC      700
   ACGACGGACG TGACGGGCAC GATCGAGCTG CCGGCCGACA AGGAAATGGT      750
20  CCTGCCGGGC GACAACGTGG CCATGACGGT CAAGCTGCTG GCTCCGATCG      800
   CCATGGAAGA AGGCCTGCGT TCGCCAC      827

```

25 2) INFORMATION FOR SEQ ID NO: 5

(i) SEQUENCE CHARACTERISTICS:

```

    (A) LENGTH: 823 bases
    (B) TYPE: Nucleic acid
30  (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

```

    (A) ORGANISM: Anaerorhabdus furcosus
    (B) STRAIN: ATCC 25662

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5

```

40  TGGATCAATC CTAGTAGTTG CTGCAACTGA TGGACCAATG CCTCAAATC      50
   GTGAACATAT CTTACTTGCT CGTCAAGTAG GTGTTCCAAG AATGGTTGTA      100
   TTCTTGAACA AATGCGACAT GGTGGAAGAT GAAGAATTAA TCGACCTTGT      150
   TGAAATGGAA GTTCGTGAAC TTCTAAGTGC TTACGGTTTC GAAGGTGATG      200
45  ATACACCAGT TATCCGTGGT TCTGCATTAA AATCTCTTGA AGGAAATGCT      250
   GATTGGGAAG CAAAAGTTGC TGAATTAATG GATGCAGTTG ACTCTTGGAT      300
   TCCAATCCA ACTCATGAAA CAGACAAACC ATTCTTAATG GCTGTTGAAG      350
   ATGTATTAC AATTACAGGT CGTGGTACAG TTGCTACTGG ACGTGTTGAA      400
   CGTGGACACT TAAACCTTAA CGAAGAAGTT GAAATCGTTG GTATTCATGA      450
50  TACTAAGAAA TCAGTTGTTA CTGGTATCGA AATGTTCCGT AAATTATTAG      500
   ACTATGCTGA AGCAGGAGAC AACATTGGTG CATTATTACG TGGTGTTTCT      550
   CGTGATGAAA TCGAACGTGG ACAATGTCTA GCTAAACCTG GATCAGTTAC      600
   TCCACATACA GCTTTCAAAG CTCAAGTATA CGTATTAACT AAAGAAGAAG      650
   GTGGACGTCA TACACCATTG GTAACCTAAT ACCGTCCTCA ATTCTATTTC      700
55  CGTACAATG ACGTAACAGG AGTTGTTAAA CTTCTGAAG GTACTGAAAT      750
   GGTATGCCT GGAGACAACA TCGAAATGAT CGTTGAATTA ATCGCTCCAA      800
   TCGCTGTTGA ACAAGGAAC AAG      823

```

60

2) INFORMATION FOR SEQ ID NO: 6

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus anthracis*
 (B) STRAIN: 4229

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6

CGGCGGTATC	TTAGTAGTAT	CTGCTGCTGA	TGGCCCAATG	CCTCAAAC	50
GTGAGCACAT	CCTTCTTTCT	CGTCAAGTAG	GTGTACCTTA	CATCGTTGTA	100
TTCTTAAACA	AATGCGACAT	GGTAGACGAC	GAAGAATTAT	TAGAATTAGT	150
AGAAATGGAA	GTTGCGGACC	TATTATCTGA	ATACGGATTC	CCAGGCGACG	200
ACATTCCTGT	AATCAAAGGT	TCTGCTCTTA	AAGCTCTTCA	AGGAGAAGCT	250
GATTGGGAAG	CAAAAATCAT	TGAATTAATG	GCTGAAGTTG	ATGCTTACAT	300
CCCAACTCCA	GAACGTGAAA	CTGACAAACC	ATTCTTAATG	CCTGTAGAGG	350
ACGTATTCTC	TATCACAGGT	CGTGGTACAG	TTGCTACTGG	TCGTGTTGAG	400
CGCGGTATCG	TTAAAGTTGG	TGACGTAGTA	GAAATCATCG	GTCTTGCTGA	450
AGAAAATGCT	TCTACAAC	TAAGTGGTGT	AGAGATGTTT	CGTAAACTTC	500
TTGACCAAGC	TCAAGCTGGA	GACAACATCG	GTGCTTTACT	TCGTGGGGTT	550
GCTCGTGAAG	ACATCCAACG	TGGACAAGTA	CTTGCAAAAA	GCGGTTCTGT	600
AAAAGCTCAC	GCTAAATTCA	AAGCTGAAGT	TTTCGTATTA	TCTAAAGAAG	650
AAGGTGGACG	TCACACTCCA	TTCTTCGCTA	ACTACCGTCC	TCAGTTCTAC	700
TTCCGTACAA	CTGACGTAAC	TGGTATCATC	CAATTACCAG	AAGGTACTGA	750
AATGGTAATG	CCTGGTGACA	ACATCGAAAT	GACTATCGAA	CTTATCGCTC	800
CAATCGCTAT	CGAAGAGGGA	ACTAA			825

2) INFORMATION FOR SEQ ID NO: 7

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus cereus*
 (B) STRAIN: ATCC 14579

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7

CGGCGGTATC	TTAGTAGTAT	CTGCTGCTGA	TGGCCCAATG	CCTCAAACAC	50
GTGAGCACAT	CCTTCTTTCT	CGTCAAGTAG	GTGTTCTCTTA	CATCGTTGTA	100
TTCTTAAACA	AATGCGACAT	GGTAGATGAC	GAAGAATTAT	TAGAATTAGT	150
AGAAATGGAA	GTTGCGGACC	TATTATCTGA	ATACGGATTC	CCAGGCGACG	200
ACATTCCTGT	AATCAAAGGT	TCTGCTCTTA	AAGCTCTTCA	AGGAGAAGCT	250
GATTGGGAAG	CAAAAATCAT	TGAATTAATG	GCTGAAGTTG	ATGCTTACAT	300
CCCAACTCCA	GAACGTGAAA	CTGACAAACC	ATTCTTAATG	CCTGTAGAGG	350
ACGTATTCTC	TATCACAGGT	CGTGGTACAG	TTGCTACTGG	TCGTGTTGAG	400

5 CGCGGTATCG TTAAAGTTGG TGACGTAGTA GAAATCATCG GTCTTGCTGA 450
 AGAAAAATGCT TCTACAACCTG TAAGTGGTGT AGAGATGTTC CGTAAACTTC 500
 TTGACCAAGC TCAAGCTGGA GACAACATCG GTGCTTTACT TCGTGGGGTT 550
 GCTCGTGAAG ACATCCAACG TGGACAAGTA CTTGCAAAAA GCGGTTCTGT 600
 AAAAGCTCAC GCTAAATTCA AAGCTGAAGT TTTCGTATTA TCTAAAGAAG 650
 AAGGTGGACG TCACACTCCA TTCTTCGCTA ACTACCGTCC TCAGTTCTAC 700
 TTCCGTACAA CTGACGTAAC TGGTATCATC CAATTACCAG AAGGTACTGA 750
 AATGGTAATG CCTGGTGACA ACATTGAAAT GACTATCGAA CTTATCGCTC 800
 CAATCGCTAT CGAAGAGGGA ACTAAATTC 829

2) INFORMATION FOR SEQ ID NO: 8

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 818 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 20 (ii) MOLECULE TYPE: Genomic DNA
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Bacteroides distasonis*
 25 (B) STRAIN: ATCC 8503

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8

30 CGGTGCTATC ATCGTAGTTG CTGCTACTGA TGGTCCTATG CCTCAAACCTC 50
 GCGAGCACAT CCTTTTGGCT CGTCAGGTAA ACGTTCCGAG ATTGGTTGTA 100
 TTGATGAACA AGTGTGACAT GGTGACGAC GAGGAAATGT TGGAATTGGT 150
 TGAGATGGAG ATGAGAGAGT TGCTTTCATT CTATCAATTC GACGGTGACA 200
 ACACTCCGAT CATCCGTGGT TCTGCTCTTG GTGCATTGAA CGGTGATGCT 250
 CAATGGGAAG ATAAAGTAAT GGAGTTGATG GAAGCTTGTC ATACTTGAT 300
 35 TCCTCTGCCT CCGCGCGAAA TCGACAAGCC GTTCTTGATG CCGGTTGAGG 350
 ACGTATTCTC AATCACGGGT CGTGGTACTG TTGCTACAGG TCGTATCGAG 400
 ACAGGTATTG TTAAGGTTGG TGAGGAAGTT CAGATCATCG GTCTTGCGCG 450
 TGCTGGTAAG AAATCTGTTG TTACAGGTGT TGAGATGTTC CGTAAGTTAT 500
 TGGATCAAGG TGAGGCTGGT GATAACGTTG GTTTGTTGCT TCGCGGTATC 550
 40 GATAAGAATG AGATCAAGCG TGGTATGGTA ATCTGCCACC CGGGTCAGGT 600
 TAAAGAGCAT TCTAAGTTCA AGGCTGAGGT TTATATCTTG AAGAAAGAGG 650
 AAGGTGGTCG TCACACTCCG TTCCACAACA AATATCGTCC TCAGTTCTAT 700
 ATCCGTACAT TGGATGTAAC TGGTGAGATC ACTTTGCCGG AAGGAACTGA 750
 AATGGTAATG CCGGGTGATA ACGTAACGAT CGAGGTTGAG TTGATCTATC 800
 45 CGGTAGCATG TAGCGTAG 818

2) INFORMATION FOR SEQ ID NO: 9

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 639 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 55 (D) TOPOLOGY: Linear
 (ii) MOLECULE TYPE: Genomic DNA
 (vi) ORIGINAL SOURCE:
 60 (A) ORGANISM: *Enterococcus casseliflavus*

(B) STRAIN: R763

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9

5	GGTCCTATGC	CTCAAACACG	TGAACACATC	TTGTTATCAC	GTAACGTTGG	50
	TGTACCATAC	ATCGTTGTTT	TCTTAAACAA	AATGGATATG	GTGATGACG	100
	AAGAATTACT	AGAATTAGTT	GAAATGGAAG	TTCGTGA	ATTGTCAGAA	150
	TATGACTTCC	CAGGCGACGA	TGTTCTTGTA	ATCGCTGGT	CTGCTTTGAA	200
	AGCTCTTGAA	GGCGATGCTT	CATACGAAGA	AAAAATCATG	GAATTAATGG	250
10	CTGCAGTTGA	CGAATACGTT	CCAACTCCAG	AACGTGACAC	TGACAAACCA	300
	TTCATGATGC	CAGTCGAAGA	CGTATTCTCA	ATCACTGGAC	GTGGTACTGT	350
	TGCTACAGGC	CGTGTTGAAC	GTGGACAAGT	TCGCGTTGGT	GACGAAGTTG	400
	AAATCGTTGG	TATTGCTGAA	GAAACTGCTA	AAACA	AACTGGTGTT	450
	GAAATGTTCC	GTAAATTGTT	AGACTATGCT	GAAGCAGGGG	ATAACATTGG	500
15	TGCATTGCTA	CGTGGTGTTG	CTCGTGAAGA	CATCCAACGT	GGACAAGTAT	550
	TGGCTAAAGC	TGGTACAATC	ACACCTCATA	CAAAATTTAA	AGCTGAAGTT	600
	TACGTTTAA	CAAAAGAAGA	AGGTGGACGT	CACACACCA		639

20

2) INFORMATION FOR SEQ ID NO: 10

(i) SEQUENCE CHARACTERISTICS:

25	(A)	LENGTH: 692 bases
	(B)	TYPE: Nucleic acid
	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30

(vi) ORIGINAL SOURCE:

(A)	ORGANISM: <i>Staphylococcus saprophyticus</i>
(B)	STRAIN: CSG 197

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10

	GAACACATTC	TTTTATCACG	TAACGTTGGT	GTTCCAGCAT	TAGTTGTATT	50
	CTTAAACAAA	GTTGACATGG	TTGACGATGA	AGAATTATTA	GAATTAGTAG	100
	AAATGGAAGT	TCGTGACTTA	TTAAGCGAAT	ATGACTTCCC	AGGTGACGAT	150
40	GTACCTGTAA	TCTCTGGTTC	TGCATTAAAA	GCTTTAGAAG	GCGACGCTGA	200
	CTATGAGCAA	AAAATCTTAG	ACTTAATGCA	AGCTGTTGAT	GACTTCATT	250
	CAACACCAGA	ACGTGATTCT	GACAAACCAT	TCATGATGCC	AGTTGAGGAC	300
	GTATTCTCAA	TC	ACTGGTTCG	TGGTACTGTT	GCTACAGGCC	350
	TGGTCAAATC	AAAGTCGGTG	AAGAAATCGA	AATCATCGGT	ATGCAAGAAG	400
45	AATCAAGCAA	AACA	ACTGTTGTT	AAATGTTCCG	TAAATTATTA	450
	GACTACGCTG	AAGCTGGTGA	CAACATTGGT	GCATTATTAC	GTGGTGTTC	500
	ACGTGATGAC	GTACAACGTG	GTCAAGTTT	AGCTGCTCCT	GGTACTATTA	550
	CACCACATAC	AAAATTCAAA	GCGGATGTTT	ACGTTTATC	TAAAGATGAA	600
	GGTGGTCGTC	ATACACCATT	CTTCACTAAC	TACCGCCAC	AATTCTATTT	650
50	CCGTACTACT	GACGTA	ACTG	CTTACCAGAA	GG	692

2) INFORMATION FOR SEQ ID NO: 11

55

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 821 bases
	(B)	TYPE: Nucleic acid
	(C)	STRANDEDNESS: Double
60	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Bacteroides ovatus*
(B) STRAIN: ATCC 8483

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11

10	CGGTGCTATC	ATCGTTTGTG	CTGCAACTGA	TGGTCCGATG	CCTCAAACATC	50
	GCGAACACAT	TCTGTTAGCT	CGTCAGGTAA	ACGTACCTCG	TCTGGTTGTA	100
	TTCTTGAACA	AATGCGATAT	GGTAGACGAC	GAAGAAATGT	TGGAATCGT	150
	TGAAATGGAA	ATGAGAGAAC	TCCTTTCATT	CTATGATTTC	GATGGTGACA	200
	ATACTCCTAT	CATCCGTGGT	TCTGCTCTTG	GCGCATTGAA	CGGTGTTGAA	250
15	AAATGGGAAG	ACAAAGTTAT	GGAAGTGATG	GATGCAGTTG	ATAACTGGAT	300
	TCCACTGCCT	CCGCGCGATG	TTGATAAACC	ATTCTTGATG	CCGGTTGAAG	350
	ACGTGTTCTC	TATCACAGGT	CGTGGTACTG	TAGCAACAGG	TCGTATCGAA	400
	ACAGGTGTCA	TCCACGTTGG	TGATGAAGTC	GAAATTCTTG	GTTTAGGTGA	450
	AGATAAGAAA	TCAGTTGTAA	CTGGTGTGTA	AATGTTCCGT	AAACTGTTGG	500
20	ATCAAGGTGA	AGCTGGTGAC	AACGTAGGTC	TTTGCTTCG	TGGTATTGAC	550
	AAGAACGAAA	TCAAACGTGG	TATGGTTCTT	TGTAAACCAG	GTCAGATTAA	600
	ACCGCACTCT	AAATTCAAAG	CTGAGGTTTA	TATCTTGAAG	AAAGAAGAAG	650
	GTGGTCGTCA	CACCTCCGTT	CACAACAAAT	ACCGTCCTCA	GTTCTACTTG	700
	CGTACTATGG	ACTGTACAGG	TGAAATCACT	TTGCCGGAAG	GAACAGAAAT	750
25	GGTAATGCCG	GGTGATAACG	TAATATTAC	AGTTGAGTTG	ATTTACCCAG	800
	TAGCATTGAA	CCCGGGCTTC	G			821

30 2) INFORMATION FOR SEQ ID NO: 12

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 838 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bartonella henselae*
(B) STRAIN: ATCC 49882

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12

45	TGGTGCGATT	TTGGTTGTTT	CAGCTGCTGA	TGGTCCGATG	CCTCAAACAC	50
	GTGAGCATAT	TCTTCTTGCC	CGTCAGGTTG	GTGTTCCAGC	GATTGTTGTT	100
	TTTCTTAATA	AGGTTGATCA	GGTTGATGAT	GCTGAGCTTT	TGGAGCTTGT	150
	TGAGCTTGAA	GTTTCGGGAGT	TATTGTGCGAA	ATATGATTTT	CCAGGAGACG	200
50	ATATTCCGAT	CGTTAAAGGT	TCTGCTTTGG	CAGCGCTTGA	AGATAAAGAT	250
	AAAAGCATTG	GTGAAGATGC	GGTTCGTCTT	TTGATGAGTG	AAGTTGATAA	300
	TTATATACCG	ACGCCTGAAC	GTCCTGTTGA	TCAGCCGTTT	TTGATGCCAA	350
	TTGAAGATGT	TTTTTCGATT	TCGGGTCGTG	GAAGTTGTTG	GACGGGTCGT	400
	GTTGAGCGTG	GTGTTATTAA	GGTTGGTGAA	GAAGTTGAGA	TTATCGGCAT	450
55	TCGTCCAAC	TCTAAGACAA	CAGTTACAGG	GGTTGAAATG	TTCCGCAAGC	500
	TTTTAGATCA	GGGGCAAGCG	GGTGATAATA	TTGGAGCGCT	GCTTCGTGGT	550
	ATTGATCGTG	AAGGGATTGA	GCGTGGACAA	GTTTTGGCGA	AGCCTGCTTC	600
	GGTTACACCT	CATACGAGAT	TTAAAGCAGA	GGCTTACATT	TTGACGAAAG	650
	ATGAAGGTGG	TCGTCATACT	CCATTTTTC	CGAATTATCG	TCCTCAGTTT	700
60	TATTTCCGTA	CTACGGATGT	AACGGGAATT	GTTACGCTTC	CAGAAGGTAC	750

AGAGATGGTT ATGCCTGGTG ATAATGTTGC TATGGATGTC TCTCTGATTG 800
 TTCCAATTGC CATGGAAGAA AACTTCGTT TTGCTATC 838

5

2) INFORMATION FOR SEQ ID NO: 13

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 839 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bifidobacterium adolescentis*
 (B) STRAIN: ATCC 15703

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13

TGGCGCCATC CTTGTTGTGG CCGCCACCGA CGGCCCGATG GCTCAGACCC 50
 GCGAGCACGT GCTGCTCGCT CGTCAGGTGG GCGTCCCGAA GATCCTCGTC 100
 GCTCTGAACA AGTGCATAT GGTTCGACGAC GACGAGCTCA TCGAGCTCGT 150
 25 TGAGGAAGAG GTCCGTGACC TCCTCGACGA AAATGGCTTC GATCGCGATT 200
 GCCCGGTCAT CCACGTGTCC GCTTACGGCG CACTGCACGA TGACGCTCCG 250
 GACCACGAGA AGTGGGTTGA GCAGATCAAG AAGCTCATGG ACGCCGTCGA 300
 TGA CTACATC CCGACCCCGG TCCACGATCT GGACAAGCCG TTCCTGATGC 350
 CGATCGAAGA TGTCTTCACC ATCTCCGGCC GTGGCACCGT GGTGACCGGC 400
 30 CGTGTCTGAGC GTGGTAAGCT CCCGGTCAAC TCCAACGTCG AGATCGTCGG 450
 CATCCGTCCG ACCCAGACCA CCACCGTCAC CTCCATCGAG ACCTTCCACA 500
 AGCAGATGGA CGAGTGCGAG GCTGGCGACA ACACCGGTCT GCTGCTCCGC 550
 GGCATCAACC GTGACCAGGT CGAGCGTGGC CAGGTTCTGG CTGCTCCGGG 600
 CTCCGTGACC CCGCACACCA AGTTCGAGGG CGAAGTCTAC GTGCTGACCA 650
 35 AGGACGAAGG CGGCCGTCAC TCGCCGTTCT TCTCCAATA CCGTCCGCAG 700
 TTCTACTTCC GTACCACCGA CGTCACCGGC GTCATACCC TGCCGGAAGG 750
 CGTTGAGATG GTGCAGCCGG GCGATCACGC TACCTTCGGC GTTGAGCTGA 800
 TCCAGCCGAT CGCTATGGAA GAGGGCCTGA CCTTCGCAG 839

40

2) INFORMATION FOR SEQ ID NO: 14

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 839 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bifidobacterium dentium*
 (B) STRAIN: ATCC 27534

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14

TGGCGCTATC CTCGTTGTGG CCGCCACCGA CGGCCCGATG GCTCAGACCC 50
 GCGAGCACGT GCTGCTCGCT CGTCAGGTGG GCGTGCCGCG TATCCTCGTC 100
 60 GCCCTGAACA AGTGCATAT GGTTCGACGAC GAAGAGCTCA TCGAGCTCGT 150

5 TGAGGAAGAG GTCCGTGACC TCCTCGACGA AAACGGCTTC GATCGCGATT 200
 GCCCGGTCAT CCACACCTCC GCCTACGGCG CGCTGCACGA TGACGCTCCG 250
 GACCACGACA AGTGGGTTGA GTCCGTCAAG GAACTCATGA AGGCCGTCGA 300
 CGAGTACATC CCGACCCCGA CCCACGATCT GGACAAGCCG TTCCTGATGC 350
 CGATCGAAGA TGTGTTTACC ATCTCCGGCC GTGGCACCCT GGTACCCTGC 400
 CGTGTCTGAGC GTGGTAAGCT CCCGGTCAAC TCCAACGTTG AGATCGTCGG 450
 CATCCGTCCG ACCCAGACCA CCACCGTCAC CTCCATCGAG ACCTTCCACA 500
 AGCAGATGGA CGAGTCCGAG GCTGGCGACA ACACCGGTCT GCTGCTCCGC 550
 GGCATCAACC GTGACCAGGT CGAGCGTGGC CAGGTTCTGG CTGCTCCGGG 600
 10 CTCCGTGACC CCGCACACCA AGTTCGAGGG CGAAGTCTAC GTGCTGACCA 650
 AGGACGAAGG CGGCCGTCAC TCGCCGTTCT TCTCCAACCTA CCGTCCGCAG 700
 TTCTACTTCC GTACCACCGA CGTCACCGGC GTCATCACC TGCCGGAAGG 750
 CGTTGAGATG GTGCAGCCGG GCGATCACGC TACCTTCGGC GTTGAGCTGA 800
 TCCAGCCGAT CGCTATGGAA GAGGGCCTGA CCTTCGCAG 839
 15

2) INFORMATION FOR SEQ ID NO: 15

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 838 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

30 (A) ORGANISM: *Brucella abortus*
 (B) STRAIN: S2308

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15

35 TGGCGCGATC CTGGTGGTTT CGGCTGCTGA CGGCCCCGATG CCGCAGACCC 50
 GCGAGCACAT CCTGCTTGCC CGTCAGGTTG GCGTTCCGGC GATCGTCGTG 100
 TTCCTCAACA AGTGCGACCA GGTGACGAT GCAGAACTGC TCGAACTGGT 150
 TGAAGTGGAA GTGCGCGAAC TTCTGTGCGA GTACGAATTC CCCGGCGACG 200
 AAATCCCGAT CATCAAGGGC TCGGCTCTTG CTGCTCTGGA AGATTCTTCC 250
 AAGGAAGTGG GCGAAGATGC CATCCGCAAC CTGATGGACG CCGTTGACAG 300
 40 CTACATTCCG ACCCCGGAAC GCCCGATCGA CCAGCCGTTT CTGATGCCGA 350
 TCGAAGACGT GTTCTCGATC TCCGGCCGTG GTACGGTTGT GACGGGTCCG 400
 GTTGAGCGCG GTATCGTTAA GGTCCGTGAA GAAGTTGAAA TCGTCGGCAT 450
 CAAGGCGACG ACGAAGACCA CGGTTACCGG CGTTGAAATG TTCCGCAAGC 500
 TGCTCGACCA GGGCCAGGCT GGCAGACAAC TTGGCGCGCT GATCCGCGGC 550
 45 GTTGGCCGTG AAGACGTTGA ACGCGGCCAG GTTCTCTGCA AGCCGGGTTC 600
 TGTGAAGCCG CACACCAAGT TTAAGGCAGA AGCCTATATT CTGACCAAGG 650
 ACGAAGGTGG CCGTCATACG CCGTTCTTCA CCAACTACCG TCCGCAGTTC 700
 TACTTCCGTA CGACGGACGT GACGGGTGTT GTGACGCTTC CGGCTGGCAC 750
 50 GGAAATGGTC ATGCCTGGCG ATAACGTCGC CATGGACGTT ACCCTGATCG 800
 TGCCGATCGC CATGGAAGAG AAGCTTCGCT TCGCTATC 838

2) INFORMATION FOR SEQ ID NO: 16

55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 771 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 60 (D) TOPOLOGY: Linear

(ii)MOLECULE TYPE: Genomic DNA

(vi)ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Burkholderia cepacia*
(B) STRAIN: LSPQ 2217

(xi)SEQUENCE DESCRIPTION: SEQ ID NO: 16

10	GGCAGCAGAC	GGCCCCGATGC	CGCAAACGCG	TGAGCACATC	CTGCTGGCGC	50
	GTCAGGTTGG	CGTTCCGTAC	ATCATCGTGT	TCCTGAACAA	GTGCGACATG	100
	GTGGACGACG	CCGAACGTCT	CGAGCTGGTC	GAGATGGAAG	TTCGCGAACT	150
	CCTGTGGAAG	TACGACTTCC	CGGGCGACGA	CACGCCGATC	GTGAAGGGTT	200
	CGGCGAAGCT	GGCGCTGGAA	GGCGACACGG	GCGAGCTGGG	CGAAGTGGCG	250
15	ATCATGAGCC	TGGCCGACGC	GCTGGACACG	TACATCCCGA	CGCCGGAGCG	300
	TGCAGTTGAC	GGCGCGTTCC	TGATGCCCGT	GGAAGACGTG	TTCTCGATCT	350
	CGGGCCGCGG	TACGGTGGTG	ACGGGTCGTG	TCGAGCGCGG	CATCGTGAAG	400
	GTCGGCGAAG	AAATCGAAAT	CGTCGGTATC	AAGCCGACGG	TGAAGACGAC	450
	CTGCACGGGC	GTTGAAATGT	TCCGCAAGCT	GCTGGACCAA	GGTCAAGCAG	500
20	GCGACAACGT	TGGTATCCTG	CTGCGCGGCA	CGAAGCGTGA	AGACGTGGAG	550
	CGTGGCCAGG	TTCTGGCGAA	GCCGGGTTCG	ATCACGCCGC	ACACGCACTT	600
	CACGGCTGAA	GTGTACGTGC	TGAGCAAGGA	CGAAGGCGGC	CGTCACACGC	650
	CGTTCTTCAA	CAACTACCGT	CCGCAGTTCT	ACTTCCGTAC	GACGGACGTG	700
	ACGGGCTCGA	TCGAGCTGCC	GAAGGACAAG	GAAATGGTGA	TGCCGGGCCGA	750
25	CAACGTGTCTG	ATCACGGTGA	A			771

2) INFORMATION FOR SEQ ID NO: 17

(i)SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
35 (D) TOPOLOGY: Linear

(ii)MOLECULE TYPE: Genomic DNA

(vi)ORIGINAL SOURCE:

- 40 (A) ORGANISM: *Cedecea davisae*
(B) STRAIN: ATCC 33431

(xi)SEQUENCE DESCRIPTION: SEQ ID NO: 17

45	GGCGCTATCC	TGGTTGTTGC	TGCGACTGAT	GGCCCAATGC	CACAGACCCG	50
	TGAGCACATC	CTGCTGGGTC	GTCAGGTTGG	CGTTCCGTAC	ATCATCGTGT	100
	TCCTGAACAA	ATGCGACATG	GTTGATGACG	AAGAGCTGCT	GGAAGTGGTA	150
	GAAATGGAAG	TTCGTGAACT	TCTGTCCCAG	TACGACTTCC	CGGGCGACGA	200
	TACTCCAATC	GTTCTGTGGT	CTGCTCTGAA	AGCGCTGGAA	GGCGAAGCAG	250
50	AGTGGGAAGC	TAAATTCGTT	GAGCTGGCTG	GCTACCTGGA	TTCTTACATC	300
	CCTGAGCCAG	AGCGTGCTAT	CGATAAGCCG	TTCCTGCTGC	CAATCGAAGA	350
	CGTATTCTCC	ATCTCCGGCC	GTGGTACCGT	TGTTACCGGT	CGTGTAGAGC	400
	GCGGTATCAT	CAAAGTTGGT	GAAGAAGTTG	AAATCGTTGG	TATCAAAGAT	450
	ACTGCGAAAT	CTACCTGTAC	CGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	500
55	CGAAGGCCGT	GCTGGTGAGA	ACGTTGGTGT	TCTGCTGCGT	GGTATCAAAC	550
	GTGAAGAAAT	CGAACGTGGT	CAGGTACTGG	CTAAGCCAGG	CTCTATCAAG	600
	CCACACACCA	AGTTCGAATC	TGAAGTGATC	ATCCTGTCCA	AAGACGAAGG	650
	CGGCCGTCAT	ACTCCGTTCT	TCAAAGGCTA	CCGTCCACAG	TTCTACTTCC	700
	GTACAACTGA	CGTGACCGGC	ACCATCGAAT	TGCCAGAAGG	CGTTGAGATG	750
60	GTAATGCCTG	GCGACAACAT	CAAAATGGTT	GTTACCCTGA	TCCACCCAAT	800

CGCGATGGAT GACGGTCTGC GTTTCGCAA

829

5 2) INFORMATION FOR SEQ ID NO: 18

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 824 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cedecea neteri*
 (B) STRAIN: ATCC 33855

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18

20 CGCTATCCTG GTTGGTTGCTG CGACTGACGG CCCTATGCCT CAGACCCGTG 50
 AGCACATCCT GCTGGGTCGT CAGGTTGGCG TTCCTTACAT CATCGTGTTC 100
 CTGAACAAAT GTGACATGGT TGATGACGAA GAGCTGCTGG AGCTGGTTGA 150
 AATGGAAGTT CGTGAAC TTC TGTCTCAGTA CGACTTCCCG GGCGATGACA 200
 25 CTCCAATCAT CCGTGGTTCT GCTCTGAAAG CGCTGGAAGG CGAAGCAGAG 250
 TGGGAAGCTA AAATYGTGA GCTGGCTGGC TTCCTGGATT CCTACATCCC 300
 AGAACCAGTA CGTGCAATCG AYCTGCCGTT CCTGCTGCCA ATCGAAGACG 350
 TATTCTCCAT CTCCGGCCGT GGTACCGTTG TTACCGGTCG TGTAGAGCGC 400
 GGTATCGTTA AAGTGGGCGA AGAAGTAGAA ATCGTTGGTA TCAAAGATAC 450
 30 TGCGAAATCT ACCTGTACCG GCGTTGAAAT GTTCCGCAA CTGCTGGACG 500
 AAGGCCGTGC TGGTGAGAAC GTTGGTGTTC TGCTGCGTGG TATCAAACGT 550
 GAAGAAATCG AACGTGGTCA GGTCTGGCT AAGCCAGGCT CTATCAAGCC 600
 GCACACCAAG TTCGAATCTG AAGTGACAT CCTGTCCAA GACGAAGGCG 650
 GCCGTCATAC TCCGTTCTTC AAAGGCTACC GTCCACAGT CTACTTCCGT 700
 35 ACAACTGACG TGACCGGTAC CATCGAACTG CCAGAAGGCG TAGAGATGGT 750
 AATGCCAGGC GACAACATCA AAATGGTTGT TACCCTGATC CACCCAATCG 800
 CGATGGACGA CGGTCTGCGT TTCG 824

40 2) INFORMATION FOR SEQ ID NO: 19

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 827 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cedecea lapagei*
 (B) STRAIN: ATCC 33432

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19

60 CGCTATTCTG GTTGGTTGCTG CAACTGACGG CCCTATGCCT CAGACCCGTG 50
 AGCACATCCT GCTGGGTCGC CAGGTTGGCG TTCCTTACAT CATCGTGTTC 100
 CTGAACAAAT GTGACATGGT TGATGACGAA GAGCTGCTGG AGCTGGTAGA 150
 AATGGAAGTT CGTGAAC TTC TGTCTCAGTA CGACTTCCCA GGCGATGATA 200

CCCCCAATCAT CCGTGGTTCT GCTCTGAAAG CGCTGGAAGG CGAAGCAGAG 250
 TGGGAAGCTA AAATCGTTGA GCTGGCTGGC TTCCTGGATT CCTACATCCC 300
 AGAACCAGTA CGTGCAATCG ACCTGCCGTT CCTGCTGCCA ATCGAAGACG 350
 TATTCTCCAT CTCCGGCCGT GGTACCGTTG TKACCGGTCG TGTAAGAGCGC 400
 5 GGTATCGTTA AAGTGGGCGA AGAAGTAGAA ATCGTTGGTA TCAAAGATAC 450
 TGCAGAAATCT ACCTGTACTG GCGTTGAAAT GTTCCGCAA CTGCTGGACG 500
 AAGGCCGTGC TGGTGAGAAC GTTGGTGTTC TGCTGCGTGG TATCAAACGT 550
 GAAGAAATCG AACGTGGTCA GGTTCCTGGCT AAGCCAGGCT CTATCAAGCC 600
 GCACACCAAG TTCGAATCTG AAGTGTACAT CCTGTCCAAA GACGAAGGCG 650
 10 GCCGTCATAC TCCGTTCTTC AARGGCTACC GTCCACAGTT CTACTTCCGT 700
 ACCACTGACG TGACCGGTAC CATCGAACTG CCAGAAGGCG TAGAGATGGT 750
 AATGCCAGGT GACAACATCA AAATGGTTGT TACCTGATC CACCCAATCG 800
 CGATGGACGA CGGTCTGCGT TTCGCAA 827

15

2) INFORMATION FOR SEQ ID NO: 20

(i) SEQUENCE CHARACTERISTICS:
 20 (A) LENGTH: 831 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Chlamydia pneumoniae*
 (B) STRAIN: CWL 029

30

--- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20

GCGGAGCTAT CCTAGTCGTT TCAGCTACAG ACGGAGCTAT GCCACAACT 50
 AAAGAACATA TCTTGCTAGC TCGCCAGGTT GGAGTTCCTT ATATCGTTGT 100
 35 TTTCTTGAAT AAAGTAGATA TGATCTCTCA AGAAGATGCT GAACTTATTG 150
 ACCTTGTTGA GATGGAACCTT AGTGAGCTTC TTGAAGAAAA AGGCTACAAA 200
 GGATGCCCTA TTATCCGTGG TTCTGCTTTG AAAGCTCTTG AAGGTGATGC 250
 AAATTATATC GAAAAAGTTC GAGAACTTAT GCAAGCTGTG GATGACAACA 300
 TCCCTACACC AGAAAGAGAA ATTGATAAGC CTTTCTTAAT GCCTATCGAA 350
 40 GACGTATTCT CAATCTCTGG TCGTGGTACT GTGGTTACAG GAAGAATCGA 400
 GCGTGGAATC GTTAAAGTTT CTGATAAAGT TCAGCTCGTG GGATTAGGAG 450
 AGACTAAAGA AACAATCGTT ACTGGAGTCG AAATGTTTCAG GAAAGAAGCTT 500
 CCTGAAGGTC GTGCAGGAGA AAACGTTGGT TTAATCCTCA GAGGTATTGG 550
 AAAGAACGAT GTTGAAAGAG GTATGGTGGT TTGTCAGCCT AACAGCGTGA 600
 45 AGCCTCATAC GAAATTTAAG TCAGCTGTTT ACGTTCTTCA GAAAGAAGAA 650
 GGCGGACGTC ATAAGCCTTT CTTACAGCGGA TACAGACCTC AGTTCTTCTT 700
 CCGTACTACA GACGTGACAG GAGTCGTAAC TCTTCCTGAA GGAAGTGAAG 750
 TGGTAATGCC TGGAGATAAC GTTGAGCTTG ATGTTGAGCT CATTGGAACA 800
 GTTGCTCTTG AAGAAGGAAT GAGATTTGCA A 831

50

2) INFORMATION FOR SEQ ID NO: 21

55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 826 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 60 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Chlamydia psittaci*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21

```

5      TGGAGCGATT CTCGTTGTTT CCGCTACTGA CGGTGCGATG CCTCAGACCA      50
      AAGAACATAT TCTTTTGGCG AGACAGGTTG GTGTTTCCTTA CATCGTTGTT      100
10     TTCCTTAACA AAATCGATAT GATTTCTCAA GAAGATGCTG AGCTCGTAGA      150
      CTTAGTTGAA ATGGAATTGT CCGAACTTCT AGAAGAAAAA GGTTATAAAG      200
      GTTGCCCAAT TATCCGTGGT TCTGCTTTGA AAGCCTTAGA AGGTGATGCA      250
      AGCTACGTTG AAAAAATTCG CGAGTTAATG CAAGCAGTGG ATGATAACAT      300
      CCCTACTCCA GAGCGTGAAG TTGATAAGCC TTTCTTAATG CCTATCGAAG      350
15     ACGTATTCTC TATTTCTGGT CGTGCTACTG TGGTCACAGG ACGTATCGAG      400
      CGTGGAATCG TTAAAGTGGG TGATAAAGTA CAGATTGTTG GTTTAAGAGA      450
      TACTAGAGAG ACAATTGTTA CCGGTGTGGA AATGTTTACA AAAGAACTTC      500
      CAGAAGGTCA AGCAGGGGAA AACGTTGGTT TGCTCCTCAG AGGTATCGGT      550
      AAGAATGACG TTGAACGTGG TATGGTTATC TGCCAACCTA ATAGCGTGAA      600
20     ATCTCACACA CAATTTAAAG GTGCTGTCTA CATCTACAA AAAGAAGAGG      650
      GTGGACCTCA TAAACCTTTC TTTACCGGAT ACAGACCTCA GTTCTTCTTC      700
      CGTACAACAG ATGTTACAGG TGTTGTAACCT CTCCCAGAAG GTACAGAGAT      750
      GGTATGCCA GGCATAACG TTGAATTCTGA AGTTCAATTA ATTAGCCCAG      800
      TAGCTCTAGA AGAAGGTATG AGATTT      826
25

```

2) INFORMATION FOR SEQ ID NO: 22

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Chlamydia trachomatis*
 (B) STRAIN: LGV 12

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22

```

45     GGGGCTATTC TAGTAGTTTC TGCAACAGAC GGAGCTATGC CTCAAACTAA      50
      AGAGCATATT CTTTTGGCAA GACAAGTTGG GGTTCCTTAC ATCGTTGTTT      100
      TTCTCAATAA AATTGACATG ATTTCCGAAG AAGACGCTGA ATTGGTCGAC      150
      TTGGTTGAGA TGGAGTTGGC TGAGCTTCTT GAAGAGAAAG GATACAAAGG      200
      GTGTCCAATC ATCAGAGGTT CTGCTCTGAA AGCTTTGGAA GGGGATGCTG      250
      CATACATAGA GAAAGTTCGA GAGCTAATGC AAGCCGTCGA TGATAATATC      300
50     CCTACTCCAG AAAGAGAAAT TGACAAGCCT TTCTTAATGC CCATTGAGGA      350
      CGTGTTCTCT ATCTCCGGAC GAGGAAGTGT AGTAACTGGA CGTATTGAGC      400
      GTGGAATTGT TAAAGTTTCC GATAAAGTTC AGTTGGTCGG TCTTAGAGAT      450
      ACTAAAGAAA CGATTGTTAC TGGGGTTGAA ATGTTTCAAG AAGAACTCCC      500
      AGAAGGTCGT GCAGGAGAGA ATGTTGGATT GCTCCTCAGA GGTATTGGTA      550
55     AGAACGATGT GGAAAGAGGA ATGGTTGTTT GCTTGCCAAA CAGTGTTAAA      600
      CCTCATACAC GGTTTAAGTG TGCTGTTTAC GTTCTGCAAA AAGAAGAAGG      650
      TGGACGACAT AAGCCTTTCT TCACAGGATA TAGACCTCAA TTCTTCTTCC      700
      GTACAACAGA CGTTACAGGT GTGGTAACTC TGCCTGAGGG AGTTGAGATG      750
      GTCATGCCTG GGGATAACGT TGAGTTTGAA GTGCAGTTGA TTAGCCCTGT      800
60     GGCTTTAGAA GAAGGTATGA GA      822

```

2) INFORMATION FOR SEQ ID NO: 23

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Chryseobacterium meningosepticum*
 (B) STRAIN: CDC B7681

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23

```

20  CGGAGCTATC TTAGTATGTG CTGCTACAGA TGGTCCAATG CCTCAAACATA    50
    GAGAACACAT CCTACTTTGC CGTCAGGTAA ACGTACCTAG AATTGTTGTG    100
    TTCATGAACA AAGTTGACAT GGTAGATGAT CCAGAATTGT TAGAGCTTGT    150
    TGAGCTTGAA CTTAGAGATC TATTATCTAC TTACGAATAT GATGGTGATA    200
    ACTCTCCAGT AATTCAAGGT TCTGCTCTTG GTGCTCTTAA CGGTGATGCT    250
25  AAGTGGGTAG CTACTGTAGA AGCTCTAATG GATGCTGTTG ATACTTGGAT    300
    CGAGCAACCA GTAAGAGATT CTGATAAGCC ATTCTTATG CCAATCGAAG    350
    ACGTATTCTC TATTACAGGT AGAGGTACTG TAGCAACTGG TAGAATCGAG    400
    GCTGGTGTA TCAACACAGG TGATCCTGTT GACATCGTAG GTATGGGTGA    450
    CGAGAAGTTA ACTTCTACTA TTACAGGTGT TGAGATGTTT AGAAAAATCC    500
30  TAGACAGAGG TGAAGCTGGT GATAACGTAG GTCTATTGTT GAGAGGTATT    550
    GAAAAGACTG ACATCAAGAG AGGTATGGTT ATCGCTAAGA AAGATTCAGT    600
    TAAGCCACAC AAGAAATTCA AAGCTGAGGT TTATATCCTT TCTAAAGAAG    650
    AAGGTGGACG TCACACTCCA TTCCACAACA AATACCGTCC TCAGTTCTAT    700
    GTAAGAACTA CTGACGTTAC AGGTGAAATC TTCTTACCAG AAGGTGTAGA    750
35  AATGGTAATG CCTGGTGATA ACTTAACTAT CACTGTAGAA TTGTTACAAC    800
    CAATCGCTCT TAACGAGGGT CTTAGATTCG CGATC                    835

```

2) INFORMATION FOR SEQ ID NO: 24

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 816 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter amalonaticus*
 (B) STRAIN: ATCC 25405

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24

```

55  CGGCGCGATC CTGGTTGTTG CTGCGACTGA CGGCCCGATG CCGCAGACTC    50
    GTGAGCACAT CCTGCTGGGT CGTCAGGTAG GCGTTCCGTA CATCATCGTG    100
    TTCCTGAACA AATGCGACAT GGTTGATGAC GAAGAGCTGC TGGAACTGGT    150
    AGAAATGGAA GTTCGTGAAC TTCTGTCTCA GTACGATTTC CCGGGCGACG    200
60  ACACCCCGAT CGTTCGTGGT TCTGCTCTGA AAGCGCTGGA AGGCGACGCA    250

```

5 GAGTGGGAAG CGAAAATCAT CGAACTGGCC GGCTTCCTGG ATTCTTACAT 300
 CCCGGAACCA GAGCGTGCGA TTGACAAGCC GTTCCTGCTG CCGATCGAAG 350
 ACGTATTCTC CATCTCCGGT CGTGGTACCG TTGTTACCGG TCGTGTAGAA 400
 CGCGGTATCA TCAAAGTGGG CGAAGAAGTT GAAATCGTTG GTATCAAAGA 450
 GACTGCCAAG TCTACCTGTA CTGGCGTTGA AATGTTCCGC AACTGCTGG 500
 ACGAAGGCCG TGCGGGTGAG AACGTTGGTG TTCTGCTGCG TGGTATCAAA 550
 CGTGAAGAAA TCGAACGTGG TCAGGTACTG GCTAAGCCGG GCWCCATCAA 600
 GCCGCACACC ATGTTTCAAT CYGAAGTGTA CATCCTGTCC AAAGACGAAG 650
 GCGGCCGTCA TACTCCGTTC TTCAAAGGCT ACCGTCCGCA GTTCTACTTC 700
 10 CGTACAACCTG ACGTGACTGG CACCATCGAA CTGCCGGAAG GCGTTGAGAT 750
 GGTAATGCCG GGCGACAACA TCAAATGGT TGTTACCCTG ATCCACCCGA 800
 TCGCGATGGA CGACGG 816

15

2) INFORMATION FOR SEQ ID NO: 25

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Citrobacter braakii*
 (B) STRAIN: ATCC 43162

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25

CGCGATCCTG GTTGTGCTG CAACTGACGG CCCGATGCCG CAGACTCGTG 50
 AGCACATCCT GCTGGGTCGY CAGGTAGGCG TTCCGTACAT CATCGTGTTC 100
 CTGAACAAAT GCGACATGGT TGATGACGAA GAGCTGCTGG AACTGGTAGA 150
 35 AATGGAAGTT CGTGAAC TTC TGTCTCAGTA CGATTTCCTG GCGGACGACA 200
 CGCCGATCGT TCGTGGTTCT GCTCTGAAAG CGCTGGAAGG CGAWGCAGAG 250
 TGGGAAGCGA AAATCATCGA ACTGGCTGGC TTCCTGGATT CTTACATCCC 300
 GGAACCAGAG CGTGCGATTG ACAAGCCGTT CCTGCTGCCT ATCGAAGACG 350
 TATTCTCCAT CTCTGGTCGT GGTACCGTTG TTACCGGTCG TGTAAGACGC 400
 40 GGTATCATCA AAGTTGGTGA AGAAGTTGAA ATCGTTGGTA TCAARGACAC 450
 TGCTAAGTCT ACCTGTACTG GCGTTGAAAT GTTCCGCAA CTGCTGGACG 500
 AAGGCCGTGC TGGTGAGAAC GTTGGTGTTT TGCTGCGTGG TATCAAGCGT 550
 GAAGAAATCG AACGTGGTCA GGTACTGGCT AAGCCGGGCT CTATCAAGCC 600
 GCACACCAAG TTCGAATCTG AAGTGTACAT TCTGTCCAAA GACGAAGGCG 650
 45 GCCGTCATAC TCCGTTCTTC AARGGCTACC GTCCGCAGTT CTACTTCCGT 700
 ACTACTGACG TGACTGGTAC CATCGAACTG CCGGAAGGCG TTGAGATGGT 750
 AATGCCGGGC GACAACATCA AAATGGTTGT TACCCTGATC CACCCAATCG 800
 CGATGGACGA CGGTCTGCGT TTCGC 825

50

2) INFORMATION FOR SEQ ID NO: 26

(i) SEQUENCE CHARACTERISTICS:

55 (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Citrobacter koseri*

(B) STRAIN: ATCC 27156

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26

5
10
15
20
25

CGGCGCGATC	CTGGTTGTTG	CTGCGACTGA	CGGCCCGATG	CCGCAGACCC	50
GTGAGCACAT	CCTGCTGGGT	CGTCAGGTAG	GCGTTCCGTA	CATCATCGTG	100
TTCCTGAACA	AATGCGACAT	GGTTGATGAC	GAAGAGCTGC	TGGAAGTGGT	150
TGAGATGGAA	GTGCGTGAAC	TGCTGTCTCA	GTACGATTTC	CCGGGCGACG	200
ACACGCCGAT	CGTTTCGTGGT	TCTGCTCTGA	AAGCGCTGGA	AGGCGAMGCT	250
GAGTGGGAAG	CGAAAATCAT	CGAACTGGCT	GGCTACCTGG	ATTCTTACAT	300
CCCGGAACCA	GAGCGTGCGA	TTGACAAGCC	GTTCTTGCTG	CCGATCGAAG	350
ACGTATTCTC	CATCTCCGGT	CGTGGTACCG	TTGTTACCGG	TCGTGTAGAG	400
CGCGGTATCA	TCAAAGTGGG	CGAAGAAGTT	GAAATYGTG	GTATCAAAGA	450
GACTGCGAAG	TCTACCTGTA	CTGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
ACGAAGGCCG	TGCTGGTGAG	AACGTAGGTG	TTCTGCTGCG	TGGTATCAAA	550
CCGAAGAAA	TCGAACGTGG	TCAGGTACTG	GCTAAGCCGG	GYTCCATCAA	600
GCCGCACACC	AAGTTCGAAT	CTGAAGTGTA	CATYCTGTCY	AAAGATGAAG	650
GCGGCCGTCA	TACTCCGTTC	TTCAAAGGCT	ACCGTCCGCA	GTTCTACTTC	700
CGTACAACCTG	ACGTGACTGG	CACCATCGAA	CTGCCGGAAG	GCGTAGAGAT	750
GGTAATGCCG	GGCGACAACA	TCAAATGGT	TGTTACCCCTG	ATCCACCCGA	800
TCGCGAGGAC	GACGGTCTGC	GTTTCGCAA			829

2) INFORMATION FOR SEQ ID NO: 27

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 827 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Citrobacter farmeri*

(B) STRAIN: ATCC 51112

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27

45
50
55
60

CGCGATCCTG	GTTGTTGCTG	CGACTGACGG	CCCGATGCCG	CAGACTCGTG	50
AGCACATCCT	GCTGGGTCGT	CAGGTAGGCG	TTCCGTACAT	CATCGTGTTC	100
CTGAACAAAT	GCGACATGGT	TGATGACGAA	GAGCTGCTGG	AACTGGTAGA	150
GATGGAAGTT	CGTGAACCTGC	TGTCTCAGTA	CGATTTCCTG	GGCGACGACA	200
CGCCGATCGT	TCGTGGTTCT	GCTCTGAAAG	CGCTGGAAGG	CGACGCAGAG	250
TGGGAAGCGA	AAATCATCGA	ACTGGCAGGC	TTCCTGGATT	CTTACATCCC	300
GGAACCAGAG	CGTGCGATTG	ACAAGCCGTT	CCTGCTGCCG	ATCGAAGACG	350
TATTCTCCAT	CTCTGGTTCGT	GGTACCGTTG	TTACCGGTCG	TGTAGAGCGC	400
GGTATCATCA	AAGTGGGTGA	AGAAGTTGAA	ATCGTTGGTA	TCAAAGAGAC	450
TGCCAAGTCT	ACCTGTACTG	GCGTTGAAAT	GTTCCGCAAA	CTGCTGGACG	500
AAGGCCGTGC	TGGTGAGAAC	GTAGGTGTTT	TGCTGCGTGG	TATCAAACGT	550
GAAGAAATCG	AACGTGGTCA	GGTACTGGCT	AAGCCGGGCW	CCATCAAGCC	600
RCACACTATG	TTCAATCTTG	AAGTGTACAT	TCTGTCCAAA	GACGAAGGCG	650
GCCGTCATAC	TCCGTTCTTC	AAAGGCTACC	GTCCGCAGTT	CTACTTCCGT	700
ACGACTGACG	TGACTGGCAC	CATCGAACTG	CCGGAAGGTG	TTGAGATGGT	750
TATGCCGGGC	GACAACATCA	AAATGGTTGT	TACCCTGATC	CACCCGATCG	800
CGATGGACGA	CGGTCTGCGT	TTTCGCAA			827

2) INFORMATION FOR SEQ ID NO: 28

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 797 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter freundii*
 (B) STRAIN: ATCC 8090

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28

20	CCTGGTTGTT	GCTGCGACTG	ACGGCCCGAT	GCCGCAGACT	CGTGAGCACA	50
	TCCTGCTGGG	TCGTCAGGTA	GGCGTTCCGT	ACATCATCGT	G TTCCTGAAC	100
	AAATGCGACA	TGGTTGATGA	CGAAGAGCTG	CTGGAAGTGG	TAGAAATGGA	150
	AGTTCGTGAA	CTTCTGTCTC	AGTACGATTT	CCCGGGCGAC	GACACTCCGA	200
	TCGTTCTGGG	TTCTGCTCTG	AAAGCGCTGG	AAGGCGAAGC	AGAGTGGGAA	250
25	GCGAAAATCA	TCGAACTGGC	TGGCTTCCTG	GATTCTTACA	TCCCAGAACC	300
	AGAGCGTGCG	ATTGACAAGC	CGTTCCTGCT	GCCTATCGAA	GACGTATTCT	350
	CCATCTCCGG	TCGTGGTACC	GTTGTTACCG	GTCGTGTAGA	GCGCGGTATC	400
	ATCAAAGTTG	GTGAAGAAGT	TGAAATCGTT	GGTATCAAAG	AGACTGCTAA	450
	GTCTACCTGT	ACTGGCGTTG	AAATGTTCCG	CAAAC TGCTG	GACGAAGGCC	500
30	GTGCTGGTGA	GAACGTTGGT	GTTCTGCTGC	GTGGTATCAA	ACGTGAAGAA	550
	ATCGAACGTG	GTCAGGTACT	GGCTAAGCCG	GGCTCTATCA	AGCCGCACAC	600
	CAAGTTTCGAA	TCTGAAGTGT	ACATTCTGTC	CAAAGACGAA	GGCGGCCGTC	650
	ATACTCCGTT	CTTCAAAGGC	TACCGTCCGC	AGTTCTACTT	CCGTACTACT	700
	GACGTGACTG	GTACCATCGA	ACTGCCGGAA	GGCGTAGAGA	TGGTAATGCC	750
35	GGGCGACAAC	ATCAAAATGG	TTGTTACCCT	GATCCACCCA	ATCGCGA	797

2) INFORMATION FOR SEQ ID NO: 29

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 826 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter sedlakii*
 (B) STRAIN: ATCC 51115

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29

55	CGGCGCGATC	CTGGTTGTTG	CCGCGACTGA	CGGCCCGATG	CCGCAGACCC	50
	GTGAGCACAT	CCTGCTGGGT	CGTCAGGTAG	GCGTTCCGTA	CATCATCGTG	100
	TTCCTGAACA	AATGCGACAT	GGTTGATGAC	GAAGAGCTGC	TGGAAGTGGT	150
	AGAGATGGAA	GTTCTGTGAA	TGCTGTCTCA	GTACGATTTT	CCGGGCGACG	200
	ACACGCCGAT	CGTTCGTGGT	TCAGCTCTGA	AAGCGCTGGA	AGGCGACGCA	250
60	GAGTGGGAAG	CGAAAATCAT	CGAACTGGCT	GGCTTCCTGG	ATTCTTACAT	300

```

TCCGGAACCA GAGCGTGCGA TTGACAAGCC GTTCCTGCTG CCGATCGAAG 350
ACGTATTCTC CATCTCCGGT CGTGGTACCG TTGTTACCGG TCGTGTAAG 400
CGCGGTATCA TCAAAGTGGG CGAAGAAGTT GAAATCGTTG GTATCAAAGA 450
GACTGCGAAG TCTACCTGTA CTGGCGTTGA AATGTTCCGC AAAGTCTGCTG 500
5 ACGAAGGCCG TCGGGGTGAG AACGTAGGTG TTCTGCTGCG TGGTATCAAA 550
CGTGAAGAAA TCGAACGTGG TCAGGTACTG GCGAAGCCCG GCACCATCAA 600
GCCGCACACC AAGTTCGAAT CTGAAGTGTA TATTCTGTCC AAAGATGAAG 650
GCGGCCGTCA TACTCCGTTT TTCAAAGGCT ACCGTCCGCA GTTCTACTTC 700
CGTACAACGT ACGTGACTGG CACCATCGAA CTGCCGGAAG GCGTAGAGAT 750
10 GGTAATGCCG GGCACACA TCAAAATGGT TGTTACCCTG ATCCACCCGA 800
TCGCGATGGA CGACGGTCTG CGTTTC 826

```

15 2) INFORMATION FOR SEQ ID NO: 30

(i) SEQUENCE CHARACTERISTICS:

```

20 (A) LENGTH: 823 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

```

    (A) ORGANISM: Citrobacter werkmanii
    (B) STRAIN: ATCC 51114

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30

```

30 GCGATCCTGG TTGTTGCTGC GACTGACGGC CCGATGCCGC AGACTCGTGA 50
   GCACATCCTG CTGGGTCGTC AGGTAGGCGT TCCGTACATC ATCGTGTTCC 100
   TGAACAAATG CGACATGGTT GATGACGAAG AGCTGCTGGA ACTGGTAGAA 150
35 ATGGAAGTTC GTGAACTTCT GTCTCAGTAC GATTTCCCGG GCGACGACAC 200
   TCCGATCGTT CGTGGTTCTG CTCTGAAAGC GCTGGAAGGC GAAGCAGAGT 250
   GGAAGCGAA AATCATCGAA CTGGCTGGCT TTCTGGATTC TTACATCCCG 300
   GAACCAGAGC GTGCGATTGA CAAGCCGTTT CTGCTRCCTA TCGAAGACGT 350
   ATTCTCCATC TCCGGTCGTG GTACCGTTGT TACCGGTCGT GTAGAGCGCG 400
   GTATCATCAA AGTTGGTGAA GAAGTTGAAA TCGTTGGTAT CAAAGACACC 450
40 GCTAAGTCTA CCTGTACCGG CGTTGAAATG TTCCGCAAAC TGCTGGACGA 500
   AGGCCGTGCT GGTGAGAACG TTGGTGTTCT GCTGCGTGGT ATCAAACGTG 550
   AAGAAATCGA ACGTGGTCAG GTACTGGCTA AGCCGGGCTC TATCAAGCCG 600
   CACACCAAGT TCGAATCTGA AGTGATACAT CTGTCCAAAG ACGAAGGCGG 650
   CCGTCATACT CCGTTCTTCA AAGGCTACCG TCCGCAGTTC TACTTCCGTA 700
45 CTACTGACGT GACTGGTACC ATCGAAGTGC CGGAAGGCGT AGAGATGGTA 750
   ATGCCGGGCG ACAACATYAA AATGGTTGTT ACYCTGATCC ACCCGATCGC 800
   GATGGACGAC GGTCTGCGTT TCG 823

```

50

2) INFORMATION FOR SEQ ID NO: 31

(i) SEQUENCE CHARACTERISTICS:

```

55 (A) LENGTH: 826 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Citrobacter youngae*
 (B) STRAIN: ATCC 29935

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31

```

GGCGCGATCC TGGTTGTTGC TGC GACTGAC GGCCCGATGC CGCAGACTCG      50
TGAGCACATC CTGCTGGGTC GTCAGGTAGG CGTTCCGTAC ATCATCGTGT      100
TCCTGAACAA ATGCGACATG GTTGATGACG AAGAGCTGCT GGAAGTGGTA      150
10 GAAATGGAAG TTCGTGAACT TCTGTCTCAG TACGATTTC CGGGCGACGA      200
TACGCCGATC GTTCGTGGTT CTGCTCTGAA AGCGCTGGAA GGCGAAGCAG      250
AGTGGGAAGC GAAAATCATC GAAGTGGCTG GCTTCCTGGA TTCTTACATC      300
CCGGAACCAAG AACGTGCTAT CGATAAGCCG TTCCTGCTGC CAATCGAAGA      350
CGTATTCTCC ATCTCCGGTC GTGGTACCGT TGTTACTGGT CGTGTAGAAC      400
15 GCGGTATCAT CAAAGTTGGT GAAGAAGTTG AAATCGTTGG TATCAAAGAG      450
ACTGCCAAGT CTACCTGTAC TGGCGTTGAA ATGTTCCGCA AACTGCTGGA      500
CGAAGGCCGT GCTGGTGAGA ACGTTGGTGT TCTGCTGCGT GGTATCAAAC      550
GTGAAGAAAT CGAACGTGGT CAGGTACTGG CTAAGCCGGG CTCTATCAAG      600
CCGCACACCA AGTTCGAATC TGAAGTGTAC ATTCTGTCCA AAGACGAAGG      650
20 CGGCCGTCTA ACTCCGTTCT TCAAAGGTAC CCGTCCGCAG TTCTACTTCC      700
GTACTACTGA CGTGACGGGT ACCATCGAAC TGCCGGAAGG CGTAGAGATG      750
GTAATGCCGG GCGACAACAT CAAATGGTT GTTACCCTGA TCCACCCAAT      800
CGCGATGGAT GACGGTCTGC GTTTCG                                     826

```

25

2) INFORMATION FOR SEQ ID NO: 32

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 841 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Clostridium perfringens*
 (B) STRAIN: ATCC 13124

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32

```

CGGAGCTATA TTAGTTTGTT CAGCAGCTGA TGGTCCAATG CCTCAAACAA      50
GAGAGCACAT CTTATTATCA TCAAGAGTTG GAGTTGACCA CATCGTAGTA      100
45 TTCTTAAACA AAGCAGATAT GGTTGACGAC GAAGAATTAT TAGAATTAGT      150
TGAAATGGAA GTTAGAGAGT TATTAAGCGA GTACAACTTC CCAGGAGACG      200
AYATTCCAGT AATCAARGGA TCAGCTTTAG TAGCATTAGA AAACCCAAC      250
GACGAAGCTG CAACAGCTTG TATCAGAGAG TTAATGGATG CTGTAGATAG      300
CTACATCCCA ACACCAGAAA GAGCAACAGA TAAGCCATTC TTAATGCCAG      350
50 TAGAGGACGT ATTACAATC ACTGGTAGAG GAACAGTTGC AACAGGAAGA      400
GTTGAAAGAG GAGTTCTACA TGTAGGAGAC GAAGTAGAAG TAATCGGATT      450
AACTGAAGAA AGAAGAAAAA CTGTTGTAAC AGGAATCGAA ATGTTTCAGAA      500
AGTTATTAGA TGAAGCACA GCTGGAGATA ACATCGGAGC ATTATTAAGA      550
GGTATCCAAA GAACTGAYAT CGAAAGAGGT CAAGTTTGTAG CTCAAGTTGG      600
55 AACAATCAAC CCACACAAAA AATTCTGAGG TCAAGTATAC GTACTTAAAA      650
AAGAAGAAGG TGGAAGACAT ACTCCATTCT TCGATGGATA CAGACCACAA      700
TTCTACTTCA GAACAACAGA CGTTACAGGA TCAATCAAAT TACCAGAAGG      750
AATGGAAATG GTTATGCCTG GAGACCACAT CGACATGGAA GTTGAATTAA      800
TCACAGAAAT CGCTATGGAY GAAGGATTAA GATTGCTAT C                                     841

```

60

2) INFORMATION FOR SEQ ID NO: 33

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Comamonas acidovorans*
 (B) STRAIN: ATCC 15668

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33

20	CGGCGCCATC	CTGGTGTGCT	CGGCCGCTGA	CGGCCCCATG	CCCCAGACCC	50
	GCGAGCACAT	CCTGCTGGCC	CGTCAGGTGG	GCGTGCCCTA	CATCATCGTG	100
	TTCCTGAACA	AGTGCGACAT	GGTGGACGAC	GAAGAGCTGC	TGGAAGTGGT	150
	CGAAATGGAA	GTGCGCGAGC	TGCTTGCCAA	GTACGACTTC	CCCGGCGACG	200
	ACACCCCAT	CATCCGCGGC	TCGGCCAAGC	TGGCCCTGGA	AGGCGACCAG	250
	TCCGACAAGG	GCGAACCTGC	CATCCTGCGC	CTGGCTGAAG	CACTGGACTC	300
25	CTACATCCCC	ACGCCCGAGC	CGCGTGTGGA	CGGCGCCTTT	GCAATGCCCG	350
	TGGAAGACGT	GTTCTCGATC	TCTGGCCGTG	GCACCGTGGT	GACTGGCCGT	400
	ATCGAGCGCG	GCATCATCAA	GGTCGGCGAA	GAAATCGAAA	TCGTCCGTAT	450
	CCGCGACACC	CAGAAGACCA	TCGTCACCGG	CGTGGAAATG	TTCCGCAAGC	500
	TGCTGGACCA	AGGTCAAGCT	GGCGACAACG	TGGGTCTGCT	GCTGCGCGGC	550
30	ACCAAGCGTG	AAGACGTGGA	ACGCGGCCAA	GTGCTGTGCA	AGCCCGGCTC	600
	CATCAAGCCC	CACACCCACT	TCACGGCTGA	GGTGTACGTG	CTGTCCAAGG	650
	ACGAAGGTGG	TCGCCACACT	CCGTTCTTCA	ACAACTACCG	TCCCCAGTTC	700
	TATTTCCGTA	CGACCGACGT	GACCGGCTCC	ATCGAGCTGC	CCGCCGACAA	750
	GGAAATGGTG	ATGCCTGGCG	ACAACGTGTC	GATCACCGTC	AAGCTGATCG	800
35	CCCCCATCGC	CATGGAAGAA	GG			822

2) INFORMATION FOR SEQ ID NO: 34

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 702 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium bovis*
 (B) STRAIN: ATCC 7715

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34

55	GCCGCAGACC	CGTGAGCACG	TCCTCCTGGC	CCGTCAGGTC	GGTGTGCCCT	50
	ACATCCTCGT	CGCCCTCAAC	AAGTGCACGA	TGGTCGACGA	CGAGGACCTC	100
	ATCGAGCTCG	TCGAGATGGA	GGTCCGTGAG	CTCCTCGCCG	AGCAGGACTA	150
	CGACGAGGAC	GCCCCGATCA	TCCACATCTC	CGCCCTCAAG	GCCCTCGAGG	200
	GTGACCCGGA	GTGGACGCAG	CGCATCGTCG	ACCTCATGAA	GGCCTGCGAC	250
60	GACGCCATCC	CGGATCCGGA	GCGCGAGACG	GACAAGCCGT	TCCTCATGCC	300

10
 5
 10
 15
 20
 25
 30
 35
 40
 45
 50
 55
 60
 65
 70
 75
 80
 85
 90
 95
 100
 105
 110
 115
 120
 125
 130
 135
 140
 145
 150
 155
 160
 165
 170
 175
 180
 185
 190
 195
 200
 205
 210
 215
 220
 225
 230
 235
 240
 245
 250
 255
 260
 265
 270
 275
 280
 285
 290
 295
 300
 305
 310
 315
 320
 325
 330
 335
 340
 345
 350
 355
 360
 365
 370
 375
 380
 385
 390
 395
 400
 405
 410
 415
 420
 425
 430
 435
 440
 445
 450
 455
 460
 465
 470
 475
 480
 485
 490
 495
 500
 505
 510
 515
 520
 525
 530
 535
 540
 545
 550
 555
 560
 565
 570
 575
 580
 585
 590
 595
 600
 605
 610
 615
 620
 625
 630
 635
 640
 645
 650
 655
 660
 665
 670
 675
 680
 685
 690
 695
 700
 705
 710
 715
 720
 725
 730
 735
 740
 745
 750
 755
 760
 765
 770
 775
 780
 785
 790
 795
 800
 805
 810
 815
 820
 825
 830
 835
 840
 845
 850
 855
 860
 865
 870
 875
 880
 885
 890
 895
 900
 905
 910
 915
 920
 925
 930
 935
 940
 945
 950
 955
 960
 965
 970
 975
 980
 985
 990
 995
 1000
 1005
 1010
 1015
 1020
 1025
 1030
 1035
 1040
 1045
 1050
 1055
 1060
 1065
 1070
 1075
 1080
 1085
 1090
 1095
 1100
 1105
 1110
 1115
 1120
 1125
 1130
 1135
 1140
 1145
 1150
 1155
 1160
 1165
 1170
 1175
 1180
 1185
 1190
 1195
 1200
 1205
 1210
 1215
 1220
 1225
 1230
 1235
 1240
 1245
 1250
 1255
 1260
 1265
 1270
 1275
 1280
 1285
 1290
 1295
 1300
 1305
 1310
 1315
 1320
 1325
 1330
 1335
 1340
 1345
 1350
 1355
 1360
 1365
 1370
 1375
 1380
 1385
 1390
 1395
 1400
 1405
 1410
 1415
 1420
 1425
 1430
 1435
 1440
 1445
 1450
 1455
 1460
 1465
 1470
 1475
 1480
 1485
 1490
 1495
 1500
 1505
 1510
 1515
 1520
 1525
 1530
 1535
 1540
 1545
 1550
 1555
 1560
 1565
 1570
 1575
 1580
 1585
 1590
 1595
 1600
 1605
 1610
 1615
 1620
 1625
 1630
 1635
 1640
 1645
 1650
 1655
 1660
 1665
 1670
 1675
 1680
 1685
 1690
 1695
 1700
 1705
 1710
 1715
 1720
 1725
 1730
 1735
 1740
 1745
 1750
 1755
 1760
 1765
 1770
 1775
 1780
 1785
 1790
 1795
 1800
 1805
 1810
 1815
 1820
 1825
 1830
 1835
 1840
 1845
 1850
 1855
 1860
 1865
 1870
 1875
 1880
 1885
 1890
 1895
 1900
 1905
 1910
 1915
 1920
 1925
 1930
 1935
 1940
 1945
 1950
 1955
 1960
 1965
 1970
 1975
 1980
 1985
 1990
 1995
 2000
 2005
 2010
 2015
 2020
 2025
 2030
 2035
 2040
 2045
 2050
 2055
 2060
 2065
 2070
 2075
 2080
 2085
 2090
 2095
 2100
 2105
 2110
 2115
 2120
 2125
 2130
 2135
 2140
 2145
 2150
 2155
 2160
 2165
 2170
 2175
 2180
 2185
 2190
 2195
 2200
 2205
 2210
 2215
 2220
 2225
 2230
 2235
 2240
 2245
 2250
 2255
 2260
 2265
 2270
 2275
 2280
 2285
 2290
 2295
 2300
 2305
 2310
 2315
 2320
 2325
 2330
 2335
 2340
 2345
 2350
 2355
 2360
 2365
 2370
 2375
 2380
 2385
 2390
 2395
 2400
 2405
 2410
 2415
 2420
 2425
 2430
 2435
 2440
 2445
 2450
 2455
 2460
 2465
 2470
 2475
 2480
 2485
 2490
 2495
 2500
 2505
 2510
 2515
 2520
 2525
 2530
 2535
 2540
 2545
 2550
 2555
 2560
 2565
 2570
 2575
 2580
 2585
 2590
 2595
 2600
 2605
 2610
 2615
 2620
 2625
 2630
 2635
 2640
 2645
 2650
 2655
 2660
 2665
 2670
 2675
 2680
 2685
 2690
 2695
 2700
 2705
 2710
 2715
 2720
 2725
 2730
 2735
 2740
 2745
 2750
 2755
 2760
 2765
 2770
 2775
 2780
 2785
 2790
 2795
 2800
 2805
 2810
 2815
 2820
 2825
 2830
 2835
 2840
 2845
 2850
 2855
 2860
 2865
 2870
 2875
 2880
 2885
 2890
 2895
 2900
 2905
 2910
 2915
 2920
 2925
 2930
 2935
 2940
 2945
 2950
 2955
 2960
 2965
 2970
 2975
 2980
 2985
 2990
 2995
 3000
 3005
 3010
 3015
 3020
 3025
 3030
 3035
 3040
 3045
 3050
 3055
 3060
 3065
 3070
 3075
 3080
 3085
 3090
 3095
 3100
 3105
 3110
 3115
 3120
 3125
 3130
 3135
 3140
 3145
 3150
 3155
 3160
 3165
 3170
 3175
 3180
 3185
 3190
 3195
 3200
 3205
 3210
 3215
 3220
 3225
 3230
 3235
 3240
 3245
 3250
 3255
 3260
 3265
 3270
 3275
 3280
 3285
 3290
 3295
 3300
 3305
 3310
 3315
 3320
 3325
 3330
 3335
 3340
 3345
 3350
 3355
 3360
 3365
 3370
 3375
 3380
 3385
 3390
 3395
 3400
 3405
 3410
 3415
 3420
 3425
 3430
 3435
 3440
 3445
 3450
 3455
 3460
 3465
 3470
 3475
 3480
 3485
 3490
 3495
 3500
 3505
 3510
 3515
 3520
 3525
 3530
 3535
 3540
 3545
 3550
 3555
 3560
 3565
 3570
 3575
 3580
 3585
 3590
 3595
 3600
 3605
 3610
 3615
 3620
 3625
 3630
 3635
 3640
 3645
 3650
 3655
 3660
 3665
 3670
 3675
 3680
 3685
 3690
 3695
 3700
 3705
 3710
 3715
 3720
 3725
 3730
 3735
 3740
 3745
 3750
 3755
 3760
 3765
 3770
 3775
 3780
 3785
 3790
 3795
 3800
 3805
 3810
 3815
 3820
 3825
 3830
 3835
 3840
 3845
 3850
 3855
 3860
 3865
 3870
 3875
 3880
 3885
 3890
 3895
 3900
 3905
 3910
 3915
 3920
 3925
 3930
 3935
 3940
 3945
 3950
 3955
 3960
 3965
 3970
 3975
 3980
 3985
 3990
 3995
 4000
 4005
 4010
 4015
 4020
 4025
 4030
 4035
 4040
 4045
 4050
 4055
 4060
 4065
 4070
 4075
 4080
 4085
 4090
 4095
 4100
 4105
 4110
 4115
 4120
 4125
 4130
 4135
 4140
 4145
 4150
 4155
 4160
 4165
 4170
 4175
 4180
 4185
 4190
 4195
 4200
 4205
 4210
 4215
 4220
 4225
 4230
 4235
 4240
 4245
 4250
 4255
 4260
 4265
 4270
 4275
 4280
 4285
 4290
 4295
 4300
 4305
 4310
 4315
 4320
 4325
 4330
 4335
 4340
 4345
 4350
 4355
 4360
 4365
 4370
 4375
 4380
 4385
 4390
 4395
 4400
 4405
 4410
 4415
 4420
 4425
 4430
 4435
 4440
 4445
 4450
 4455
 4460
 4465
 4470
 4475
 4480
 4485
 4490
 4495
 4500
 4505
 4510
 4515
 4520
 4525
 4530
 4535
 4540
 4545
 4550
 4555
 4560
 4565
 4570
 4575
 4580
 4585
 4590
 4595
 4600
 4605
 4610
 4615
 4620
 4625
 4630
 4635
 4640
 4645
 4650
 4655
 4660
 4665
 4670
 4675
 4680
 4685
 4690
 4695
 4700
 4705
 4710
 4715
 4720
 4725
 4730
 4735
 4740
 4745
 4750
 4755
 4760
 4765
 4770
 4775
 4780
 4785
 4790
 4795
 4800
 4805
 4810
 4815
 4820
 4825
 4830
 4835
 4840
 4845
 4850
 4855
 4860
 4865
 4870
 4875
 4880
 4885
 4890
 4895
 4900
 4905
 4910
 4915
 4920
 4925
 4930
 4935
 4940
 4945
 4950
 4955
 4960
 4965
 4970
 4975
 4980
 4985
 4990
 4995
 5000
 5005
 5010
 5015
 5020
 5025
 5030
 5035
 5040
 5045
 5050
 5055
 5060
 5065
 5070
 5075
 5080
 5085
 5090
 5095
 5100
 5105
 5110
 5115
 5120
 5125
 5130
 5135
 5140
 5145
 5150
 5155
 5160
 5165
 5170
 5175
 5180
 5185
 5190
 5195
 5200
 5205
 5210
 5215
 5220
 5225
 5230
 5235
 5240
 5245
 5250
 5255
 5260
 5265
 5270
 5275
 5280
 5285
 5290
 5295
 5300
 5305
 5310
 5315
 5320
 5325
 5330
 5335
 5340
 5345
 5350
 5355
 5360
 5365
 5370
 5375
 5380
 5385
 5390
 5395
 5400
 5405
 5410
 5415
 5420
 5425
 5430
 5435
 5440
 5445
 5450
 5455
 5460
 5465
 5470
 5475
 5480
 5485
 5490
 5495
 5500
 5505
 5510
 5515
 5520
 5525
 5530
 5535
 5540
 5545
 5550
 5555
 5560
 5565
 5570
 5575
 5580
 5585
 5590
 5595
 5600
 5605
 5610
 5615
 5620
 5625
 5630
 5635
 5640
 5645
 5650
 5655
 5660
 5665
 5670
 5675
 5680
 5685
 5690
 5695
 5700
 5705
 5710
 5715
 5720
 5725
 5730
 5735
 5740
 5745
 5750
 5755
 5760
 5765
 5770
 5775
 5780
 5785
 5790
 5795
 5800
 5805
 5810
 5815
 5820
 5825
 5830
 5835
 5840
 5845
 5850
 5855
 5860
 5865
 5870
 5875
 5880
 5885
 5890
 5895
 5900
 5905
 5910
 5915
 5920
 5925
 5930
 5935
 5940
 5945
 5950
 5955
 5960
 5965
 5970
 5975
 5980
 5985
 5990
 5995
 6000
 6005
 6010
 6015
 6020
 6025
 6030
 6035
 6040
 6045
 6050
 6055
 6060
 6065
 6070
 6075
 6080
 6085
 6090
 6095
 6100
 6105
 6110
 6115
 6120
 6125
 6130
 6135
 6140
 6145
 6150
 6155
 6160
 6165
 6170
 6175
 6180
 6185
 6190
 6195
 6200
 6205
 6210
 6215
 6220
 6225
 6230
 6235
 6240
 6245
 6250
 6255
 6260
 6265
 6270
 6275
 6280
 6285
 6290
 6295
 6300
 6305
 6310
 6315
 6320
 6325
 6330
 6335
 6340
 6345
 6350
 6355
 6360
 6365
 6370
 6375
 6380
 6385
 6390
 6395
 6400
 6405
 6410
 6415
 6420
 6425
 6430
 6435
 6440
 6445
 6450
 6455
 6460
 6465
 6470
 6475
 6480
 6485
 6490
 6495
 6500
 6505
 6510
 6515
 6520
 6525
 6530
 6535
 6540
 6545
 6550
 6555
 6560
 6565
 6570
 6575
 6580
 6585
 6590
 6595
 6600
 6605
 6610
 6615
 6620
 6625
 6630
 6635
 6640
 6645
 6650
 6655
 6660
 6665
 6670
 6675
 6680
 6685
 6690
 6695
 6700
 6705
 6710
 6715
 6720
 6725
 6730
 6735
 6740
 6745
 6750
 6755
 6760
 6765
 6770
 6775
 6780
 6785
 6790
 6795
 6800
 6805
 6810
 6815
 6820
 6825
 6830
 6835
 6840
 6845
 6850
 6855
 6860
 6865
 6870
 6875
 6880
 6885
 6890
 6895
 6900
 6905
 6910
 6915
 6920
 6925
 6930
 6935
 6940
 6945
 6950
 6955

```

5  GGTGTGTTGCT GCAACCGATG GTCCTATGCC GCAGACCCGC GAGCACGTTC 50
   TTCTGGCTCG CCAGGTTGGC GTTCCTTACA TCCTCGTTGC TCTTAACAAG 100
   TCGGACATGG TTGATGATGA GGAAATCATC GAGCTCGTTG AGATGGAAAT 150
   CCGCGAACTG CTCGCTGAGC AGGACTACGA CGAGGATGCC CCCATCATCC 200
   ACATCTCCGC TCTCAAGGCT CTTGAGGGTG ACGAGAAGTG GGTACAGGCC 250
   ATCGTCGACC TCATGCAGGC CTGCGATGAC TCCATTCCGG ATCCGGAGCG 300
   CGAGACCGAC AAGCCCTTCC TCATGCCTAT CGAGGACATC TTCACCATCA 350
   CCGGCCGCGG TACCGTTGTT ACCGGCCGTG TTGAGCGTGG CGTTTTGAAG 400
10 GTCAACGAGG ATGTTGAGAT CATCGGCATC AAGGAGAAGT CCATCTCCAC 450
   CACCGTTACC GGTATCGAAA TGTTCCGCAA GATGATGGAC TACACCGAGG 500
   CTGGCGACAA CTGTGGTCTG CTCTGCGTG GTACCAAGCG TGAAGAGGTC 550
   GAGCGCGGCC AGGTTGTTAT CAAGCCGGGC GCCTACACCC CCCACACCAA 600
   GTTCGAGGGT TCCGTCTACG TCCTCAAGAA GGAAGAGGGC GGCCGCCACA 650
15 CCCC GTTCAT GGACAACTAC CGTCCGAGT TCTACTTCCG TACCACTGAC 700
   GTGACCGGCG TTGTTACCT GCCTGAGGGC ACCGAGATGG TCATGCCTGG 750
   CGACAACGTT GATATGACCG TTGAGCTCAT CCAGCCCGTC GCTAGGATGA 800
   GGC 804

```

20

2) INFORMATION FOR SEQ ID NO: 37

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 692 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium kutscheri*
 (B) STRAIN: ATCC 15677

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37

```

40 TGCTCAGAC CCGTGAGCAC GTTCTTCTTG CTCGCCAGGT TGGCGTTCCT 50
   TACATCCTCG TTGCTCTTAA CAAGTGCGAC ATGGTTGACG ATGAGGAAAT 100
   CATCGAGCTC GTTGAGATGG AAGTTCGCGA GCTTCTTGCT GAGCAGGAGT 150
   ACGATGAAGA GGCTCCAATC ATCCACATCT CTGCTTTGAA GGCTCTTGAG 200
   GCGGACGAGA AGTGGACTCA GGCCATCATC GACCTCATGC AGGCTTGTGA 250
   TGA TCCATC CCAGATCCAG AGCGTGAGAC CGACAAGCCA TTCCTCATGC 300
   CTATCGAGGA TATCTTCACC ATCACC GGTC GTGGCACC GTTACCGGT 350
45 CGTGTGAGC GCGGTTCTT GAAGGTGAAT GAGGACGTCG AGATCATCGG 400
   CATCAAGGAG AAGTCCACCA CTACTACCGT TACCGGTATC GAAATGTTCC 450
   GTAAGCTTCT TGATTACACC GAAGCTGGCG ATA ACTGTGG TCTGCTTCTT 500
   CGTGGTATCA AGCGCGAAGA CGTTGAGCGT GGTCAGGTTG TTGTTAAGCC 550
   AGGCGCTTAC ACACCTCACA CCGAGTTCGA GGGCTCTGTT TACGTTCTTT 600
50 CCAAGGACGA GGGCGGCCGC CACACCCCAT TCTTCGACAA CTACCGTCCA 650
   CAGTTCTACT TCCGCACCAC TGACGTTACC GGTGTTGTGA AG 692

```

55 2) INFORMATION FOR SEQ ID NO: 38

(i) SEQUENCE CHARACTERISTICS:

- 60 (A) LENGTH: 797 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Corynebacterium minutissimum*

(B) STRAIN: ATCC 23348

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38

10 CCTGGTTGTT GCTGCAACCG ATGGCCCGAT GCCGCAGACC CGCGAGCACG 50
 TTCTTCTGGC CCGCCAGGTT GGCGTTCGGT ACATCCTCGT TGCCTGAAC 100
 AAGTGTGACA TGGTTGACGA TGAGGAAATC ATCGAGCTCG TTGAGATGGA 150
 GATCCGTGAG CTGCTCGCTG AGCAGGACTA CGACGAGGAA GCTCCGATCG 200
 15 TTCACATCTC CGCTCTGAAG GCTCTTGAGG GCGACGAGAA GTGGGCACAG 250
 TCCATCGTTG ACCTGATGCA GGCTTGCGAT GACTCCATCC CGGATCCGGA 300
 GCGCGAGCTG GACAAGCCGT TCCTGATGCC GATCGAGGAC ATCTTCACCA 350
 TTACCGGCCG CGGTACCGTT GTTACCGGCC GTGTTGAGCG TGGCTCCCTG 400
 AACGTTAACG AGGACATCGA GATCATCGGT ATCAAGGACA AGTCCATGTC 450
 20 CACCACCGTT ACCGGTATCG AGATGTTCCG CAAGATGATG GACTACACCG 500
 AGGCTGGCGA CAACTGTGCT CTGCTTCTGC GTGGTACCAA GCGTGAAGAG 550
 GTTGAGCGTG GCCAGGTTTG CATCAAGCCG GCGGCTTACA CCCCACACAC 600
 CAAGTTCGAG GGTTCGCTCT ACGTCCTGAA GAAGGAAGAG GGCGGCCGCC 650
 ACACCCCGTT CATGGACAAC TACCGTCCGC AGTTCTACTT CCGCACCACC 700
 25 GACGTCACCG GTGTCATCAA GCTGCCGGAG GGCACCGAGA TGGTCATGCC 750
 GGGCGACAAC GTTGAGATGT CCGTAGAGCT GATCCAGCCG GTCGCTA 797

30 2) INFORMATION FOR SEQ ID NO: 39

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 702 bases

(B) TYPE: Nucleic acid

35 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Corynebacterium mycetoides*

(B) STRAIN: ATCC 21134

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39

45 GCCGCAGACC CGCGAGCACG TTCTTCTGGC CCGCCAGGTC GGCGTCCCCT 50
 ACATCCTCGT TGCCTGAAC AAGTGCAGCA TGGTTGATGA TGAGGAGATC 100
 ATCGAGCTCG TGGAGATGGA GGTCCGTGAG CTGCTCGGCG AGCAGGACTA 150
 CGACGAGGAC GCCCCATCA TCCACATCTC CGCTCTGAAG GCTCTCGAGG 200
 50 GCGACGAGAA GTGGGTTTCA TCCGTGCTCG ACCTCATGCA GGCGTGCGAC 250
 GACTCCATCC CGGATCCGGT CCGCGAGACC GACCGCGACT TCCTGATGCC 300
 GATCGAGGAC ATCTTCACCA TCTCCGGCCG CGGCACCGTG GTTACCGGTC 350
 GTGTGGAGCG CGGCGTGCTC AACCTCAACG ACGAGGTCGA GATCATCGGC 400
 ATCCGCGACA AGTCCCAGAA GACCACCGTC ACCTCCATCG AGATGTTCAA 450
 55 CAAGCTGCTC GATACCGCTG AGGCAGGCGA CAACGCGGCT CTGCTGCTCC 500
 GCGGTCTGAA GCGCGAGGAC GTGAGCGGTG GCCAGGTTGT CATCAAGCCG 550
 GGCGCCTACA CCCCACACAC CAAGTTCGAG GGTTCGCTCT ACGTCCTGTC 600
 CAAGGACGAG GGCGGCCGCC ACACCCCGTT CTTGACAAC TACCGTCCGC 650
 AGTTCTACTT CCGCACCACC GACGTGACCG GTGTTGTGAA GCTGCCGGAG 700
 60 GG 797

2) INFORMATION FOR SEQ ID NO: 40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 674 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium pseudogenitalium*
 (B) STRAIN: ATCC 33038

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40

```

20  GCTCGCCAGG TTGGCGTTCC TTACATCCTC GTTGCCTGA ACAAGTGCGA      50
    CATGGTTGAT GATGAGGAAA TCATCGAGCT CGTTGAGATG GAGATCCGTG      100
    AGCTGCTCGC AGAGCAGGAT TACGATGAGG AAGCTCCTAT CGTTCACATC      150
    TCCGCTCTGA AGGCCCTCGA GGGCGATGAC AAGTGGGTAC AGTCCGTCGT      200
    TGATCTGATG GAAGCCTGCG ACAACTCCAT CCCGGATCCG GAGCGCGCTA      250
25  CCGACCAGCC GTTCCTGATG CCTATCGAGG ACATCTTCAC CATTACCGGC      300
    CGCGGTACCG TTGTTACCGG CCGTGTTGAG CGTGGCCGTC TGAACGTCAA      350
    CGAGGACGTT GAGATCATCG GTATCCAGGA GAAGTCCCAG ACCACCACCG      400
    TTACCGGTAT CGAGATGTTT CGCAAGATGA TGGACTACAC CGAGGCTGGC      450
    GACAACTGTG GTCTGCTTCT GCGTGTTACC AAGCGTGAGG ACGTTGAGCG      500
30  TGGCCAGGTT GTTATCAAGC CGGGCGCTTA CACCCCGCAC ACCAAGTTCG      550
    AGGGCTCCGT CTACGTCCTG AAGAAGGAAG AGGGCGGCCG CCACACCCCG      600
    TTCATGAACA ACTACCGTCC GCAGTTCTAC TTCCGTACCA CGGACGTTAC      650
    CGGTGTTGTT CACCTGCCAG AGGG

```

2) INFORMATION FOR SEQ ID NO: 41

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 694 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium renale*
 (B) STRAIN: ATCC 19412

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41

```

    TGCCTCAGAC CCGTGAGCAC GTTCTGCTTG CTCGTCAGGT CGGCGTTCCT      50
    TACATCCTCG TTGCACTGAA CAAGTGCGAC ATGGTCGACG ACGAAGAAAT      100
55  CATCGAGCTC GTCGAGATGG AAATCCGTGA ACTGCTCGCA GAGCAGGACT      150
    ACGATGAGGA AGCTCCTATC GTTCACATCT CCGCTCTGGG CGCCCTGAAC      200
    GGCGAGCAGA AGTGGGTGTA CTCCATCGTC GAACTGATGG AAGCTTGCGA      250
    CAACTCCATC CCAGACCCAG TTCGCGACAT CGACCACCCA TTCCTGATGC      300
    CTATCGAGGA CATCTTCACC ATTACCGGTC GCGGTACCGT TGTACCGGC      350
60  CGTGTGAGAG GTGGCCGTCT CAACGTCAAC GAAGAAGTTG AGATCATCGG      400

```

```

TATCAAGGAC AAGTCCCAGA AGACCACCGT CACCGGTATC GAGATGTTCC 450
GCAAGATGCT GGACTACACC GAAGCTGGCG ACAACTGTGG TCTGCTGCTC 500
CGCGGCATCG GCCGTGAGGA TGTCGAGCGT GGCCAGGTTA TCATCAAGCC 550
AGGCGCTTAC ACCCCTCACT CTGAGTTCGA GGGCTCTGTC TACGTCCTGT 600
5 CCAAGGACGA GGGTGGCCGC CACACCCCAT TCTTCGACAA CTACCGTCCA 650
CAGTTCTACT TCCGCACCAC CGACGTGACC GCGTTGTGC ACCT 694

```

10 2) INFORMATION FOR SEQ ID NO: 42

(i) SEQUENCE CHARACTERISTICS:

```

15 (A) LENGTH: 687 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

```

    (A) ORGANISM: Corynebacterium ulcerans
    (B) STRAIN: NCTC 8665

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42

```

25 GCCGCAGACC CGCGAGCACG TTCTGCTGGC TCGCCAGGTT GCGGTTCKT 50
   ACATCCTSGT TGCACGAAAC AAGTCCGACA TGGTTGACGA TGAGGARCTC 100
   CTSGAGCTCG TCGAGATGGA GGTCCGCGAG CTGCTGGCTG AGCAGGACTA 150
   CGACGAGGAA GCTCCGRTCG TTCACATCTC CGCWCTGAAC GCCCTGGACG 200
30 GCGACSAGAA GTGGGCTVAC TCCATCCTCG AGCTGATGCA GGCTTGCGAC 250
   GAGTCCATCC CGGATCCGGA GCGCGAGACC GACAAGCCGT TCCTGATGCC 300
   GATTGAGGAC ATCTTCACCA TTACCGGTCG CGGYACCGTT GTTACCGGCC 350
   GTGTTGAGCG TGGCDTCCTG AACGTSAAAC ACGASGTTGA GATCATGGGY 400
   ATCCGGGAGA AGTCCCAGAA GACCACCGTY ACCKSCATCG AGATGTTCAA 450
35 CAAGMTGMTG GACWCCGCGA AGGCTGCGCA CAACGCTGSW CTGCTGCTGC 500
   GTGGTMTSAA GCGTGAGGAC GTTGAGCGTG GCCAGATCAT CGYTAAGCCG 550
   GCGGCKTACA CCCCACACAC CGAGTTCGAG GGCTCCGTCT ACGTCCTGTC 600
   CAAGGACGAG GGCGGCCGCC ACACCCCGTT CTTGACAAAC TACCGTCCGC 650
40 AGTTCTACTT CCGCACCACC GACGTSACCG GTGTTGT 687

```

2) INFORMATION FOR SEQ ID NO: 43

(i) SEQUENCE CHARACTERISTICS:

```

45 (A) LENGTH: 778 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

```

55 (A) ORGANISM: Corynebacterium urealyticum
    (B) STRAIN: ATCC 43042

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43

```

60 CTGGTTGTTG CTGCAACCGA TGGCCCGATG CCGCAGACCC GTGAGCACGT 50
   TCTGCTGGCT CGCCAGGTTG GCGTTCGTA CATCCTCGTT GCACTGAACA 100

```

```

AGTGCGACAT GGTGACGAT GAGGAGCTCC TCGAGCTCGT CGAGATGGAG 150
GTCCGCGAGC TTCTGGCTGA GCAGGACTAC GACGAGGAGG CTCCGGTCGT 200
CCCGATCTCC GCACTGGGCG CCCTGGACGG CGATCAGAAAG TGGGTCGACT 250
CCATCCTCGA GCTCATGAAG GCTTGCGACG AGTCCATCCC GGACCCGGAG 300
5 CGCGAGACCG ACAAGCCGTT CCTGATGCCG GTTGAGGACA TCTTCACCAT 350
TACCGGTCGC GGCACCGTCG TTACCGGCCG TGTGAGCGT GGCGTCCTGA 400
ACCTGAACGA CGAGGTCGAG ATCCTGGGCA TCCGCGAGAA GTCCACCAAG 450
ACCACCGTCA CCTCCATCGA GATGTTCAAC AAGCTGCTGG ACACCGCAGA 500
GGCTGGCGAC AACGCTGCAC TGCTGCTGCG TGGTCTGAAG CGTGAGGACG 550
10 TCGAGCGAGG CCAGATCATC GCTAAGCCGG GCGCTTACAC CCCGCACACC 600
GAGTTCGAGG GCTCCGTCTA CGTCTGTGCC AAGGACGAGG GCGGCCGTCA 650
CACCCCGTTC TTCGACAACT ACCGTCCGCA GTTCTACTTC CGTACCACCG 700
ACGTCACCGG TGTCGTTACC CTGCCAGAGG GCACCGACAT GGTTCATGCCG 750
GGCGACAACG TTGAGATGAG CGTCAAGC 778
15

```

2) INFORMATION FOR SEQ ID NO: 44

```

20 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 703 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear
25
(ii) MOLECULE TYPE: Genomic DNA
(vi) ORIGINAL SOURCE:
    (A) ORGANISM: Corynebacterium xerosis
30    (B) STRAIN: ATCC 373

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44

```

35 CGCAGACCCG TGAGCACGTC CTCCTGGCCC GCCAGGTCGG CGTCCCCTAC 50
ATCCTCGTCG CCCTGAACAA GTGCGACATG GTCGACGATG AGGAGATCAT 100
CGAGCTCGTG GAGATGGAGG TGCGTGAGCT TCTCGCCGAG CAGGACTACG 150
ACGAGGAGGC CCCGATCGTG CACATCTCCG CCCTGGGCGC CCTCAATGGC 200
GAAGAGAAGT GGGTCGACTC CATCGTCGAG CTCATGAACG CCGTCGACGA 250
GAACGTTCCG GACCCGGTCC GCGAGACCGA CAAGCCGTTC CTGATGCCCCG 300
40 TCGAGGACAT CTTACCATC ACCGGCCGCG GCACCGTCGC CACCGGTCGC 350
GTGGAGCGCG GCACCCTGAA GGTC AACGAC GAGGTCGAGA TCCTGGGCAT 400
CCAGGAGAAG TCCCAGACCA CCACCGTCAC CGGCATCGAG ATGTTCCGCA 450
AGCTGCTGGA CTCCGCCGAG GCCGGCGACA ACTGTGGCCT GCTGCTCCGC 500
GGCATCAAGC GCGAGGACAT CGAGCGCGCG CAGATCATCG CGAAGCCGGG 550
45 CGCCTACACC CCGCACACCG AGTTCGAGGG CTCGCTCTAC ATCCTGGCCA 600
AGGACGAGGG CGGCCGCCAC ACCCCGTTCT TCGACAATA CCGTCCGCAG 650
TTCTACTTCC GCACCACCGA CGTCACCGGC GTCGTGAAGC TGCCGGAGGG 700
CAC 703
50

```

2) INFORMATION FOR SEQ ID NO: 45

```

55 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 832 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear
60 (ii) MOLECULE TYPE: Genomic DNA

```


(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Coxiella burnetii*

(B) STRAIN: Nine Mile phase II

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45

5
10
15
20
25

GGAGCGATAT	TGGTGGTGAG	CGCAGCGGAC	GGCCCGATGC	CGCAAACGCG	50
GGAACACATT	GTATTGGCGA	AGCAAGTGGG	TGTTCCGAAC	ATAGTGGTTT	100
ACTTGAACAA	AGCGGACATG	GTGGATGACA	AAGAGCTGTT	GGAATTAGTG	150
GAAATGGAAG	TGAGGGATTT	ATTGAACAGT	TATGATTTCC	CTGGGGATGA	200
GACGCCGATA	ATAGTGGGGT	CAGCGTTAAA	GGCGTTAGAA	GGTGACAAGA	250
GTGAGGTTGG	GGAGCCATCG	ATAATCAAAT	TAGTGGAAC	GATGGACACG	300
TACTTCCCGC	AGCCGGAGCG	AGCGATAGAC	AAACCGTTTT	TAATGCCGAT	350
CGAAGATGTG	TTTTTCGATAT	CGGGCCGAGG	GACGGTGGTG	ACGGGACGCG	400
TAGAGCGAGG	GATCATCAAA	GTGGGCGACG	AGATAGAGAT	TGTGGGGATC	450
AAGGACACGA	CGAAGACGAC	GTGCACGGGC	GTTGAGATGT	TTCGCAAATT	500
ATTGGATGAA	GGTCAAGCGG	GTGACAACGT	AGGAATTTTA	TTGAGAGGGA	550
CGAAACGCGA	AGAAGTGGAG	CGTGGTCAAG	TATTGGCGAA	ACCGGGATCG	600
ATCACGCCAC	ACAAGAAATT	TGAGGCGGAG	ATTTATGTGT	TGTCAAGGA	650
AGAAGGGGGA	CGCCGACAC	CGTTTTTACA	AGGCTATCGA	CCGCAATTTT	700
ATTTCCGCAC	GACGGACGTG	ACGGGCCAGT	TATTGAGTTT	ACCGGAGGGG	750
ATAGAGATGG	TGATGCCGGG	AGATAACGTG	AAAGTGACGG	TTGAATTGAT	800
TGCGCCGCTA	GCGATGGATG	AAGGGCTACG	AT		832

2) INFORMATION FOR SEQ ID NO: 46

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 816 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Edwardsiella hoshinae*

(B) STRAIN: ATCC 33379

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46

45
50
55
60

GGCGCTATCC	TGGTTGTTGC	TGCGACTGAC	GGCCCGATGC	CGCAGACCCG	50
TGAGCACATC	CTGCTGGGTC	GCCAGGTAGG	CGTTCCGTAC	ATCATCGTGT	100
TCCTGAACAA	GTGCGACATG	GTTGATGACG	AAGAGCTGCT	GGAAGTGGTT	150
GAGATGGAAG	TTCGCGAACT	GCTGTCTCAG	TACGATTTCC	CGGGCGACGA	200
TACGCCGGTA	ATCCGCGGTT	CTGCGCTGAA	AGCGCTGGAA	GGCGAAGCCG	250
AGTGGGAAGC	GAAGATCATC	GAAGTGGCTG	AAACGCTGGA	CTCCTACATT	300
CCGGAACCTG	AGCGTGACAT	CGACAAGCCG	TTCCTGCTGC	CGATCGAAGA	350
CGTATTCTCA	ATCTCTGGTC	GTGGTACCGT	TGTTACCGGT	CGTGTAGAGC	400
GCGGTATCAT	CAAGGTAGGC	GACGAAGTTG	AAATCGTAGG	TATCAAGCCG	450
ACCACCAAGA	CTACCTGTAC	TGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	500
CGAAGGCCGT	GCTGGTGAGA	ACGTAGGTGT	TCTGCTGCGT	GGTACCAAGC	550
GTGACGAAAT	CGAAGCTGGT	CAGGTACTGG	CTAAGCCGGG	CACCATCACT	600
CCGCACACCA	AGTTCTGAATC	AGAAGTGTAC	ATCCTGAGCA	AGGATGAAGG	650
CGGCCGTCAT	ACTCCGTTCT	TCAAAGGTTA	CCGTCCGCAG	TTCTACTTCC	700
GTACCACTGA	CGTGACTGGC	ACCATCGAAC	TGCCGGAAGG	CGTAGAGATG	750
GTAATGCCGG	GCGACAACAT	CAAGATGGTT	GTTACCCTGA	TCCACCCGAT	800
CGCCATGGAC	GATGGT				816

2) INFORMATION FOR SEQ ID NO: 47

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 821 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Edwardsiella tarda*
 (B) STRAIN: ATCC 15947

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47

20	GGCGCGATCC	TGGTTGTTGC	TGCGACTGAC	GGCCCGATGC	CGCAGACCCG	50
	TGAGCACATC	CTGTTGGGTC	GCCAGGTAGG	CGTTCCGTAC	ATCATCGTGT	100
	TCCTGAACAA	GTGCGACATG	GTTGATGACG	AAGAGCTGCT	GGAAGTGGTT	150
	GAGATGGAAG	TTCGCGAACT	GCTGTCTCAG	TACGACTTCC	CGGGCGACGA	200
	CACGCCGGTA	ATCCGCGGTT	CTGCGCTGAA	AGCGCTGGAA	GGCGAAGCCG	250
25	AGTGGGAAGC	GAAGATCATC	GAAGTGGCTG	AAACTCTGGA	CTCCTACATC	300
	CCGGAACCTG	AGCGTGACAT	CGACAAGCCG	TTCCTGCTGC	CGATCGAAGA	350
	CGTATTCTCT	ATCTCTGGCC	GTGGTACCGT	TGTTACCGGT	CGTGTAAGC	400
	GCGGTATCAT	CAAGGTAGGC	GACGAAGTTG	AAATCGTTGG	TATCAAGCCG	450
	ACCACCAAGA	CCACCTGTAC	TGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	500
30	CGAAGGCCGT	GCTGGTGAGA	ACGTTGGTGT	TCTGCTGCGT	GGTACTAAGC	550
	GTGACGAAAT	CGAACGTGGT	CAGGTACTGG	CTAAGCCGGG	CACCATCACT	600
	CCGCACACCA	AGTTCGAATC	TGAAGTGTAC	ATCCTGAGCA	AGGATGAAGG	650
	CGGCCGTCAT	ACTCCGTTCT	TCAAAGGCTA	CCGTCCGCAG	TTCTACTTCC	700
	GTACTACTGA	CGTGACTGGT	ACCATCGAAC	TGCCGGAAGG	CGTAGAGATG	750
35	GTAATGCCGG	GCGACAACAT	CAAGATGGTT	GTTACCCTGA	TCCACCCGAT	800
	CGCCATGGAC	GATGGTCTGC	G			821

2) INFORMATION FOR SEQ ID NO: 48

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 830 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Eikenella corrodens*
 (B) STRAIN: ATCC 23834

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48

55	CGGTGCCATC	CTGGTGGTAT	CCGCTGCTGA	CGGCCCCATG	CCTCAGACTC	50
	GCGAACACAT	CCTGTTGGCT	CGTCAGGTAG	GTGTACCCTA	CATCCTCGTA	100
	TTCATGAACA	AATGCGACAT	GGTAGATGAT	GCCGAGCTGC	TTGAGTTGGT	150
	TGAGATGGAA	ATCCGCGACC	TGCTCTCCAG	CTATGACTTC	CCTGGTGACG	200
60	ACTGCCCGAT	CGTACAAGGT	TCCGCTCTCA	AAGCCCTCGA	AGGCGATGCC	250

	GGTTACAAAG	AAAAAATCTT	CGAACTAGCT	GCTGCTTTGG	ATAGCTACAT	300
	CCCCACTCCT	CAACGTGCTG	TAGACAAACC	CTTCCTGTTG	CCGATCGAAG	350
	ACGTATTCTC	TATCTCCGGC	CGTGGTACCG	TAGTAACCGG	TCGTGTAGAG	400
	CGCGGCATCA	TCAAAGTAGG	TGAAGAGATC	GAAATCGTTG	GTCTGAAGCC	450
5	CACTCAGAAA	ACTACCTGTA	CTGGCGTGGA	AATGTTCCGC	AAACTGCTGG	500
	ACGAAGGTCA	GGCCGGTGAC	AACGTAGGCG	TACTGCTGCG	CGGTACCAAA	550
	CGTGAAGAAG	TTGAGCGTGG	TCAAGTATTG	GCTAAACCCG	GCACCATCAC	600
	TCCGCACACC	AAGTTCAAAG	CCGAAGTATA	CGTATTGAGC	AAAGAAGAAG	650
	GTGGTTCGTC	CACCCCGTTC	TTTGCCAACT	ACCGTCCACA	GTTCTACTTC	700
10	CGTACTACTG	ACGTAACCGG	TGCTGTAGAG	CTGGAGCCTG	GTGTAGAAAT	750
	GGTTATGCCT	GGTGAGAACG	TAACCATCAC	CGTAGAACTG	ATTGCTCCGA	800
	TTGCTATGGA	AGAAGGTCTG	CGCTTTGCGA			830

15

2) INFORMATION FOR SEQ ID NO: 49

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 808 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter aerogenes*
 (B) STRAIN: ATCC 13048

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49

	GGCGCGATCC	TGGTTGTTGC	TGCGACTGAC	GGCCCGATGC	CGCAGACTCG	50
	TGAGCACATC	CTGCTGGGTC	GTCAGGTAGG	CGTTCCGTAC	ATCATCGTGT	100
	TCCTGAACAA	ATGCGACATG	GTTGATGACG	AAGAGCTGCT	GGAAGTGGTT	150
35	GAGATGGAAG	TTCGTGAAC	CTGTCTCAG	TACGATTTC	CGGGCGACGA	200
	CACTCCGATC	GTTCTGGGTT	CTGCTTGAA	AGCGCTGGAA	GGCGACGCAG	250
	AGTGGGAAGC	GAAAATCATC	GAAGTGGCTG	GCTTCCTGGA	TTCTTACATC	300
	CCRGAAACCAG	AGCGTGCGAT	TGACAAGCCG	TTCTTGCTGC	CGATCGAAGA	350
	CGTATTCTCC	ATCTCCGGTC	GTGGTACCGT	TGTTACCGGT	CGTGTAGAGC	400
40	GCGGTATCAT	CAAAGTTGGT	GAAGAAGTTG	AAATCGTTGG	TATCAAAGAC	450
	ACCGCGAAAA	CCACCTGTAC	TGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	500
	CGAAGGCCGT	GCTGGTGAGA	ACGTAGGYGT	TCTGCTGCGT	GGTATCAAAC	550
	GTGAAGAAAT	CGAACGTGGT	CAGGTACTGG	CTAAGCCGGG	CAGCATCAAG	600
	CCGCACACCA	AGTTCGAATC	TGAAGTGTAC	ATCCTGTCCA	AAGACGAAGG	650
45	CGGCCGTCAT	ACTCCGTTCT	TCAAAGGCTA	CCGTCCGCAG	TTCTACTTCC	700
	GTACTACTGA	CGTGACTGGT	ACCATCGAAC	TGCCGGAAGG	CGTAGAGRTG	750
	GTAATGCCCG	GCGACAACAT	CAAAATGGTT	GTTACCCTGA	TCCACCCGAT	800
	CGCGATGG					808

50

2) INFORMATION FOR SEQ ID NO: 50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter agglomerans*
 (B) STRAIN: ATCC 27989

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50

```

CGGCGCGATC CTGGTTGTTG CTGCGACTGA CGGCCCCGATG CCGCAGACTC      50
GTGAGCACAT CCTGCTGGGT CGTCAGGTAG GCGTTCCGTA CATCATCGTG      100
10 TTCCTGAACA AATGTGACAT GGTTGATGAC GAAGAGCTGC TGGAACTGGT      150
TGAAATGGAA GTTCGTGAAC TTCTGTCTCA GTACGATTTC CCGGGCGACG      200
ATACTCCGAT CGTTCGTGGT TCTGCTCTGA AAGCGCTGGA AGGCGAMGCW      250
GAGTGGGAAG CGAAAATCAT CGARCTGGCT GGCCACCTGG ATACCTATAT      300
CCCGGAACCA GAGCGTGCGA TTGACAAGCC GTTCCTGCTG CCGATCGAAG      350
15 ACGTATTCTC CATCTCCGGT CGCGGTACCG TTGTTACCGG TCGTGTAGAG      400
CGCGGTATCA TYAAAGTGGG CGAAGAAGTT GAAATCGTTG GTATCAAAGA      450
TACYGCGAAA TCAACCTGTA CCGGCGTTGA AATGTTCCGC AAAGTGCTGG      500
ACGAAGGCCG TGCTGGTGAG AACGTTGGTG TTCTGCTGCG TGGTATCAAA      550
CGTGAAGAAA TCGAACGTGG TCAGGTACTG GCTAAGCCGG GCACCATCAA      600
20 GCCGCACACC AAGTTCGAAT CTGAAGTGTA CATTCTGTCC AAAGATGAAG      650
GCGGTCGTCA CACTCCGTTT TTCAAAGGCT ACCGTCCSCA GTTCTACTTC      700
CGTACAACCTG ACGTGACTGG CACCATCGAA CTGCCGGAAG GCGTAGAGAT      750
GGTAATGCCG GGCGACAACA TCAAATGGT TGTTACCCTG ATCCACCCGA      800
TCGCGATGGA CGACGGTCTG CGTTCGCA      828
25

```

2) INFORMATION FOR SEQ ID NO: 51

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter amnigenus*
 (B) STRAIN: ATCC 33072

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51

```

TGGCGCGATC CTGGTTGTTG CTGCAACTGA TGGCCCTATG CCACAGACGC      50
45 GTGAGCACAT CCTGCTGGGT CGTCAGGTAG GCGTTCCTTA CATCATCGTG      100
TTCTTGAACA AATGCGACAT GGTGATGAC GAAGAGCTGC TGGAACTGGT      150
AGAAATGGAA GTTCGTGAAC TTCTGTCTCA GTACGATTTC CCAGGTGATG      200
ACACTCCAAT CATCCGTGGT TCTGCTCTGA AAGCGCTGGA AGGCGAAGCA      250
GAGTGGGAAG CTAAAATCGT TGAGCTGGCT GGCTACCTGG ATTCTTACAT      300
50 CCCGGAACCA GAACGTGCTA TCGATAAGCC ATTCCTGCTG CCAATCGAAG      350
ACGTATTCTC TATCTCCGGC CGTGGTACTG TTGTAACCGG TCGTGTAGAG      400
CGCGGTATCG TTAAAGTTGG CGAAGAAGTT GAAATCGTTG GTATCAAAGA      450
GACTGCTAAG TCTACCTGTA CTGGCGTTGA AATGTTCCGC AAAGTGCTGG      500
ACGAAGGCCG TGCTGGTGAG AACGTTGGTG TTCTGCTGCG TGGTATCAAA      550
CGTGAAGAAA TCGAACGTGG TCAGGTACTG GCTAAGCCAG GCTCAATCAA      600
GCCGCACACC AAATTCGAAT CTGAAGTTTA TATTCTGTCC AAAGATGAAG      650
GCGGCCGTCA TACTCCGTTT TTCAAAGGCT ACCGTCCACA GTTCTACTTC      700
CGTACAACCTG ACGTGACCGG CACCATCGAA CTGCCAGAAG GCGTAGAGAT      750
GGTAATGCCA GGCGACAACA TTCAGATGGT TGTTACCCTG ATCCACCCAA      800
60 TCGCGATGGA TGACGGTCTG CGTTT      825

```

2) INFORMATION FOR SEQ ID NO: 52

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter asburiae*
 (B) STRAIN: ATCC 35953

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52

20	CGGCGCGATC	CTGGTTGTTG	CTGCGACTGA	CGGCCCAATG	CCTCAGACTC	50
	GTGAGCACAT	CCTGCTGGGT	CGTCAGGTAG	GCGTTCCTTT	CATCATCGTG	100
	TTCCTGAACA	AATGCGACAT	GGTTGATGAC	GAAGAGCTGC	TGGAAGTGGT	150
	AGAGATGGAA	GTTCGTGAAC	TGCTGTCTCA	GTACGATTTC	CCGGGCGACG	200
	ATACTCCAAT	CGTTCGTGGT	TCTGCTCTGA	AAGCGCTGGA	AGGCGACGCA	250
25	GAGTGGGAAG	CGAAAATCAT	CGAACTGGCT	GGCTTCCTGG	ATTCTTACAT	300
	CCCAGAACCA	GAGCGTGCGA	TTGACAAGCC	ATTCTGCTG	CCAATCGAAG	350
	ACGTATTCTC	CATCTCCGGT	CGTGGTACCG	TTGTTACCGG	TCGTGTAGAG	400
	CGCGGTATCA	TCAAAGTTGG	CGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	450
	GACTGCTAAG	TCTACCTGTA	CTGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
30	ACGAAGGCCG	TGCTGGTGAG	AACGTTGGTG	TTCTGCTGCG	TGGTATCAAA	550
	CGTGAAGAAA	TCGAACGTGG	TCAGGTTCTG	GCGAAGCCAG	GCTCAATCAA	600
	GCCACACACC	AAGTTCGAAT	CTGAAGTGTA	CATCCTGTCC	AAAGACGAAG	650
	GCGGCCGTCA	TACTCCGTTT	TTCAAAGGCT	ACCGTCCACA	GTTCTACTTC	700
	CGTACAACCTG	ACGTGACCGG	TACCATCGAA	CTGCCAGAAG	GCGTTGAGAT	750
35	GGTAATGCCA	GGCGACAACA	TCAAGATGGT	TGTGACTCTG	ATCCACCCAA	800
	TCGCGATGGA	CGACGGTCTG	CG			822

2) INFORMATION FOR SEQ ID NO: 53

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 826 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter cancerogenus*
 (B) STRAIN: ATCC 35317

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53

55	CGGCGCGATC	CTGGTTGTTG	CTGCGACTGA	CGGCCCAATG	CCTCAGACTC	50
	GTGAGCACAT	CCTGCTGGGT	CGTCAGGTAG	GCGTTCCTTA	CATCATCGTG	100
	TTCCTGAACA	AGTGCACAT	GGTTGATGAC	GAAGAGCTGC	TGGAAGTGGT	150
	AGAAATGGAA	GTTCGTGAAC	TGCTGTCTCA	GTACGATTTC	CCAGGCGACG	200
60	ACACTCCAAT	CGTTCGTGGT	TCCGCGCTGA	AAGCGCTGGA	AGGCGAAGCT	250

```

5  GAGTGGGAAG CAAAAATCAT CGAACTGGCT GGCTTCCTGG ATTCTTACAT 300
   CCCAGAACCA GAGCGTGCGA TTGACAAGCC ATTCCTGCTG CCAATCGAAG 350
   ACGTATTCTC CATCTCCGGT CGTGGTACCG TTGTTACCGG TCGGTAGAG 400
   CGCGGTATCA TCAAAGTTGG TGAAGAAGTT GAAATCGTTG GTATCAAAGA 450
   TACTGCKAAA TCTACCTGTA CTGGCGTTGA AATGTTCCGC AACTGCTGG 500
   ACGAAGGCCG TGCTGGTGAG AACGTTGGTG TTCTGCTGCG TGGTATCAAA 550
   CGCGAAGAAA TCGAACGTGG TCAGGTTCTG GCGAAGCCAG GCTCAATCAA 600
   GCCACACACC AAGTTCGAAT CTGAAGTGTA CATCCTGTCC AAAGACGAAG 650
   GCGGCCGTCA TACTCCGTTT TTCAAAGGCT ACCGTCCACA GTTCTACTTC 700
10 CGTACAACCTG ACGTGACCGG TACCATCGAA CTGCCAGAAG GCGTAGAGAT 750
   GGTAATGCCA GCGGACAACA TCAAGATGGT TGTGACGCTG ATCCACCCAA 800
   TCGCGATGGA CGACGGTCTG CGTTTC 826

```

15

2) INFORMATION FOR SEQ ID NO: 54

(i) SEQUENCE CHARACTERISTICS:

```

20  (A) LENGTH: 806 bases
   (B) TYPE: Nucleic acid
   (C) STRANDEDNESS: Double
   (D) TOPOLOGY: Linear

```

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

```

   (A) ORGANISM: Enterobacter cloacae
   (B) STRAIN: ATCC 13047

```

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54

```

   GATCCTGGTA GTAGCTGCGA CTGACGGCCC AATGCCTCAG ACTCGTGAGC 50
   ACATCCTGCT GGGTCGTCAG GTAGGCGTTC CTTACATCAT CGTGTTCTTG 100
   AACAAATGCG ACATGGTTGA TGACGAAGAG CTGCTGGAAC TGGTAGAGAT 150
35  GGAAGTTCGT GAACTGCTGT CTCAGTACGA TTTCCCAGGC GACGATACCC 200
   CAATCGTTCTG TGGTTCTGCT CTGAAAGCGC TGAAGGCGA CGCAGAGTGG 250
   GAAGMGAAAA TCATCGAACT GGCTGGCTAC CTGGATTCTT ACATCCCAGA 300
   ACCAGAGCGT GCGATTGAYA AGCCATTCTT GCTGCCAATC GAAGACGTAT 350
   TCTCCATCTC CCGTCGTGGT ACCGTTGTTA CCGGTCGTGT AGAGCGCGGT 400
40  ATCATCAAAG TGGGTGAAGA AGTTGAAATC GTTGGTATCA AAGAGACTGC 450
   GAAGTCTACC TGTACTGGCG TTGAAATGTT CCGCAAATG CTGGACGAAG 500
   GCCGTGCTGG TGAGAACGTT GGTGTTCTGC TGCCTGGTAT CAAACGTGAA 550
   GAAATCGAAC GTGGTCAGGT TCTGGCGAAG CCAGGCTCAA TCAAGCCACA 600
   CACCAAGTTC GAATCTGAAG TGTACATCCT GTCCAAAGAC GAAGGCGGCC 650
45  GTCATACTCC GTTCTTCAAA GGCTACCGTC CACAGTTCTA CTTCCGTACA 700
   ACTGACGTGA CCGGTACCAT CGAACTGCCA GAAGGCGTAG AGGTGGTAAT 750
   GCCAGGCGAC AACATCAAGA TGGTTGTGAC TCTGATCCAC CCAATCGCGA 800
   TGGACG 806

```

50

2) INFORMATION FOR SEQ ID NO: 55

(i) SEQUENCE CHARACTERISTICS:

```

55  (A) LENGTH: 826 bases
   (B) TYPE: Nucleic acid
   (C) STRANDEDNESS: Double
   (D) TOPOLOGY: Linear

```

60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter gergoviae*
 (B) STRAIN: ATCC 33028

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55

```

CGGCGCGATC CTGGTTGTTG CTGCGACTGA CGGCCCGATG CCGCAGACCC      50
GTGAGCACAT CCTGCTGGGT CGTCAGGTAG GCGTTCCGTA CATCATCGTG      100
10  TTCCTGAACA AGTGCGACAT GGTGATGAC GAAGAGCTGC TGGAACTGGT      150
AGAGATGGAA GTTCGTGAAC TGCTGTCTCA GTACGATTTC CCGGGCGACG      200
ACACCCCGAT CGTTCGCGGT TCTGCGCTGA AAGCGCTGGA AGGCGACGCA      250
GAGTGGGAAG CGAAAATCAT CGAACTGGCT GGCCACCTGG ATACCTAYAT      300
CCCGGAACCA GAGCGTGC GAAGCAAGCG GTTCCTGCTG CCGATCGAAG      350
15  ACGTATTCTC CATTTCCGGT CGTGGTACCG TTGTTACCGG TCGTGTAGAG      400
CGCGGTATCA TCAAGGTTGG TGAAGAAGTT GAAATCGTTG GTATCAAAGA      450
CACCGCGAAA ACCACCTGTA CTGGCGTTGA AATGTTCCGC AACTGCTGG      500
ACGAAGGCCG TGCTGGTGAG AACGTCGGCG TTCTGCTGCG TGGTATCAAG      550
CGTGAAGAAA TCGAACGTGG TCAGGTACTG GCTAAGCCGG GCTCCATCAA      600
20  GCCGCACACC AAGTTCGAAT CTGAAGTGTA CATCCTGTCC AAAGACGAAG      650
GCGGCCGTCA CACTCCGTTT TTCAAAGGCT ACCGTCCGCA GTTCTACTTC      700
CGTACAACCT ACGTGAATGG CACCATCGAA CTGCCGGAAG GCGTAGAGAT      750
GGTAATGCCG GCGACAACA TCAAGATGGT TGTTACCCTG ATCCACCCGA      800
25  TCGCGATGGA CGACGGTCTG CGTTTC      826

```

2) INFORMATION FOR SEQ ID NO: 56

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter hormaechei*
 (B) STRAIN: ATCC 49162

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56

```

GGCGCGATCC TGGTTGTTGC TGCGACTGAC GGCCCTATGC CTCAGACCCG      50
45  TGAGCACATC CTGCTGGGTC GTCAGGTAGG CGTTCCTTAC ATCATCGTGT      100
TCCTGAACAA ATGCGACATG GTTGATGACG AAGAGCTGCT GGAAGTGGTA      150
GAGATGGAAG TTCGTGAACT GCTGTCTCAG TACGATTTCC CAGGCGACGA      200
CACCCCAATC GTTCGTGGTT CCGCGCTGAA AGCGCTGGAA GGCGAMGCAG      250
AGTGGGAAGM GAAAATCATC GARCTGGCTG GCTTCCTGGA TTCTTACATC      300
50  CCAGAACCAG AGCGTGCGAT TGACAAGCCA TTCCTGCTGC CAATCGAAGA      350
CGTATTCTCC ATCTCCGGTC GTGGTACCGT TGTTACCGGT CGTGTWGAGC      400
GCGGTATCAT CAAAGTAGGT GAAGAAGTTG AAATCGTTGG TATCAAAGAG      450
ACTGCGAAGT CTACCTGTAC TGGCGTTGAA ATGTTCCGCA AACTGCTGGA      500
CGAAGGCCGT GCTGGTGAGA ACGTTGGTGT TCTGCTGCGT GGTATCAAAC      550
55  GTGAAGAAAT CGAACGTGGT CAGGTTCTGG CGAAGCCAGG CTCAATCAAG      600
CCACACACCA AGTTCGAATC TGAAGTGTA ATTCTGTCCA AAGACGAAGG      650
CGCCCGTACT ACTCCGTTCT TCAAAGGCTA CCGTCCACAG TTCTACTTCC      700
GTACAACCTGA CGTGACCGGT ACCATCGAAC TGCCAGAAGG CGTAGAGATG      750
GTAATGCCAG GCGACAACAT CAAGATGGTT GTGACGCTGA TCCACCCAAT      800
60  CGCGATGGAC GACGGTCTGC GTTTCGCAA      829

```

2) INFORMATION FOR SEQ ID NO: 57

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter sakazakii*
 (B) STRAIN: ATCC 29544

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57

20	GGCGCTATCC	TGGTTGTTGC	TGCGACTGAC	GGCCCGATGC	CGCAGACCCG	50
	TGAGCACATC	CTGCTGGGTC	GTCAGGTAGG	CGTTCCGTAC	ATCATCGTGT	100
	TCCTGAACAA	ATGCGACATG	GTTGATGACG	AAGAGCTGCT	GGAAGTGGTT	150
	GAGATGGAAG	TGCGCGAGCT	GCTGTCTCAG	TACGACTTCC	CGGGCGACGA	200
	CACCCCGATC	GTTTCGTGGTT	CTGCTCTGAA	AGCGCTGGAA	GGCGACGCTG	250
25	AGTGGGAAGC	GAAAATCATC	GAGCTGGCAG	GTCACCTGGA	TTCCTACATC	300
	CCGGAACCGG	AGCGTGCGAT	TGACAAGCCG	TTCCTGCTGC	CGATCGAAGA	350
	CGTATTCTCC	ATCTCYGGTC	GTGGTACCGT	TGTTACCGGT	CGTGTAGAGC	400
	GCGGTATCAT	CAAGGTTGGT	GAAGAAGTTG	AAATCGTGGG	CATCAAAGAC	450
	ACCGCGAAAT	CCACCTGTAC	CGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	500
30	CGAAGGCCGT	GCGGGCGAGA	ACGTAGGTGT	TCTGCTGCGT	GGTATCAAAC	550
	GTGAAGAAAT	CGAACGTGGT	CAGGTACTGG	CTAAGCCGGG	CTCCATCAAG	600
	CCGCACACCA	AGTTCGAATC	TGAAGTGATC	ATTCTGTCCA	AAGATGAAGG	650
	CGGCCGTCAC	ACTCCGTTCT	TCAAAGGCTA	CCGTCCGCAG	TTCTACTTCC	700
	GTACRACTGA	CGTGACTGGC	ACCATCGAAC	TGCCGGAAGG	CGTTGAGATG	750
35	GTAATGCCGG	GCGACAACAT	CAAAATGGTT	GTTACCCTGA	TCCACCCGAT	800
	CGCGATGGAC	GACGGTCTGC	GTTTCGCAAT	C		831

2) INFORMATION FOR SEQ ID NO: 58

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus casseliflavus*
 (B) STRAIN: ATCC 25788

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58

55	CGGCGCGATC	TTAGTAGTAT	CTGCTGCTGA	TGGTCCTATG	CCTCAAACAC	50
	GTGAACACAT	CTTGTTATCA	CGTAACGTTG	GTGTACCATA	CATCGTTGTT	100
	TTCTTAAACA	AAATGGATAT	GGTTGATGAC	GAAGAATTAC	TAGAATTAGT	150
	TGAAATGGAA	GTTCGTGACT	TATTGTGAGA	ATATGACTTC	CCAGGCGACG	200
60	ATGTTCCCTGT	AATCGCTGGT	TCTGCTTTGA	AAGCTCYTGA	AGGCGATGCT	250


```

TCATACGAAG AAAAAATCAT GGAATTAATG GCTGCAGTTG ACGAATACGT 300
TCCAACCTCCA GAACGTGACA CTGACAAACC ATTCATGATG CCAGTCGAAG 350
ACGTATTCTC AATCACTGGA CGTGGTACTG TTGCTACAGG CCGTGTGTA 400
CGTGGACAAG TTCGCGTTGG TGACGAAGTT GAAATCGTTG GTATTGCTGA 450
5 AGAAACTGCT AAAACAACCT TAAGTGGTGT TGAAATGTTT CGTAAATTGT 500
TAGACTATGC TGAAGCAGGG GATAACATTG GTGCATTGCT ACGTGGTGT 550
GCTCGTGAAG ACATCCAACG TGGACAAGTA TTGGCTAAAG CTGGTACAAT 600
CACACCTCAT ACAAATTTA AAGCTGAAGT TTACGTTTTA ACAAAGAAG 650
AAGGTGGACG TCACACACCA TTCTTCACTA ACTACCGTCC TCAGTTCTAC 700
10 TTCCGTACAA CTGACGTAAC TGGTGTGTT GAATTACCAG AAGGAACTGA 750
AATGGTTATG CCTGGTGATA ACGTAACAAT CGACGTTGAA TTGATCCACC 800
CAATCGCTAT CGAAGACGGA ACTCGTTTCT CAATT 835

```

15

2) INFORMATION FOR SEQ ID NO: 59

(i) SEQUENCE CHARACTERISTICS:

```

20 (A) LENGTH: 826 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

```

    (A) ORGANISM: Enterococcus cecorum
    (B) STRAIN: ATCC 43198

```

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59

```

GGTGCTATCT TAGTAGTATC TGCTGCTGAT GGTCCCTATGC CACAAACTCG 50
TGAACACATT CTTTTATCAC GTAACGTGG TGTTCCATAC ATCGTTGTTT 100
TCTTAAACAA AGTTGATATG GTTGACGACG AAGAATTATT AGAATTAGTT 150
35 GAAATGGAAG TACGTGACTT ATTAACGAA TACGACTTCC CAGGAGACGA 200
TGTTCTCTGTA ATCGCTGGTT CTGCATTAAA AGCTTTAGAA GGCACCCAT 250
CTTACGAAGA AAAAATCTTA GAATTAATGG CTGCAGTTGA CGAATACATC 300
CCAACCTCCAG AACGTGACAA CGATAAACCA TTCATGATGC CAGTCGAAGA 350
CGTATTTTCA ATCACTGGTC GTGGTACTGT TGCTACAGGT CGTGTTGAAC 400
40 GTGGACAAGT ACGTGTGGT GACGAAGTTG AAATAGTTGG TATCCATGAT 450
GAAATTTCTA AAACAACAGT TACTGGTGT GAAATGTTCC GTAAATTATT 500
AGATTACGCT GAAGCTGGAG ACAACATCGG TGCATTATTA CGTGGTGTGG 550
CTCGTGAAGA TATCCAACGT GGTCAAGTAT TAGCTAAACC AGGTTCAATC 600
ACTCCACATA CAAAATTCAC TGCTGAAGTG TACGTTTAA CTAAAGAAGA 650
45 AGGTGGACGT CATACTCCAT TCTTCACTAA CTACCGTCCA CAATTCTACT 700
TCCGTACAAC TGACGTTACA GGTGTAGTTA ACTTACCAGA AGGTACTGAA 750
ATGGTTATGC CTGGTGATAA CGTAACATG GAAGTTGAAT TAATCCACCC 800
AATCGCTATC GAAGACGGAA CTCGTT 826

```

50

2) INFORMATION FOR SEQ ID NO: 60

(i) SEQUENCE CHARACTERISTICS:

```

55 (A) LENGTH: 835 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus dispar*
 (B) STRAIN: ATCC 51266

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60

```

CGGCGCGATC TTGGTAGTAT CTGCTGCTGA TGGTCCTATG CCTCAAACCTC      50
GTGAACACAT CCTATTGTCA CGTAACGTTG GTGTTCCCTTA CATCGTCGTT      100
10 TTCTTGAACA AAATGGACAT GGTGATGAC GAAGAATTAT TAGAATTAGT      150
TGAAATGGAA GTTCGTGACT TATTGTCAGA ATACGACTTC CCAGGCGACG      200
ACACTCCAGT TATCGCAGGT TCAGCTTTGA AAGCCTTAGA AGGCGACGCT      250
TCATATGAAG AAAAAATCTT AGAATTAATG GCTGCAGTTG ACGAATATAT      300
CCCAACTCCA GTTCGTGATA CTGACAAACC ATTCATGATG CCAGTCGAAG      350
15 ATGTATTCTC AATCACTGGT CTGGTACTG TTGCAACTGG TCGTGTGAA      400
CGTGGACAAG TTCGCGTTGG TGACGAAGTT GAAATCGTAG GTATCGCTGA      450
AGAAACTGCT AAAACTACTG TAACAGGTGT TGAAATGTTC CGTAAATTGT      500
TGGATTACGC TGAAGCTGGC GACAACATTG GTGCATTATT ACGTGGTGTG      550
GCTCGTGAAG ATATCCAACG TGGTCAAGTA TTATCAAAAC CAGGTTCAAT      600
20 CACTCCACAT ACAAATTTG CGGCAGAAGT TTACGTTTTA ACTAAAGAAG      650
AAGGTGGACG TCATACTCCA TTCTTCACTA ACTACGCCC ACAATTCTAC      700
TTCCGTACAA CTGACGTAAC AGGTGTTGTT GAATTACCAG AAGGTACTGA      750
AATGGTTATG CCTGGCGATA ACGTTACTAT GGACGTTGAA TTAATCCACC      800
CAATCGCGAT CGAAGACGGT ACTCGTTTCT CAATC      835

```

2) INFORMATION FOR SEQ ID NO: 61

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus durans*
 (B) STRAIN: ATCC 19432

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61

```

CGGAGCTATC TTAGTAGTTT CTGCTGCTGA TGGCCCTATG CCTCAAACCTC      50
45 GTGAACATAT CCTATTATCT CGTCAAGTTG GTGTTCCCTTA CATCGTYGTA      100
TTCTTGAACA AAGTAGATAT GGTTCGATGAC GAAGAATTAC TAGAATTAGT      150
TGAAATGGAA GTTCGTGACT TATTAACAGA ATACGAATTC CCTGGTGACG      200
ATGTTCCCTGT AATCGCTGGT TCAGCTTTGA AAGCTTTAGA AGGCGACGCT      250
TCATACGAAG AAAAAATCCT TGAATTAATG GCTGCAGTTG ACGAATATAT      300
50 CCCAACTCCA GAACGTGACA ACGACAAACC ATTCATGATG CCAGTTGAAG      350
ATGTATTCTC RATCACTGGT CGTGGTACTG TTGCTACAGG TCGTGTGAA      400
CGTGGACAAG TTCGCGTTGG TGACGTTGTA GATATCGTTG GTATCGCAGA      450
AGAAACAGCT CAAACAACAG TTAAGTGGTGT TGAAATGTTC CGTAAATTAT      500
TAGRCTACGC TGAAGCTGGA GACAACATTG GTGCTTTACT ACGTGGTGT      550
55 GCACGTGAAG ACATCCAACG TGGACAAGTT TTAGCTAAAC CAGGTACAAT      600
CACKCTCAT ACAAATTTCT CTGCGAAGT ATACGTGTTG ACTAAAGAAG      650
AAGGTGGACG TCATACTCCA TTCTTCACTA ACTACGCTCC ACAATTCTAC      700
TTCCGTACAA CTGACGTAAC AGGTGTTGTT GAATTACCAG AAGGAACCTGA      750
AATGGTTATG CCTGGCGACA ACGTAACAAT GGAAGTTGAA TTAATCCACC      800
60 CAATCGCTAT CGAAAATGGT ACTAAATTCT CAATC      835

```

2) INFORMATION FOR SEQ ID NO: 62

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 680 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecalis*
 (B) STRAIN: R610

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62

20	AGTAGTTTCT	GCTGCTGATG	GTCCTATGCC	TCAAACACGT	GAACATATCT	50
	TATTATCACG	TAACGTTGGT	GTACCATACA	TCGTTGTATT	CTTAAACAAA	100
	ATGGATATGG	TTGATGACGA	AGAATTATTA	GAATTAGTAG	AAATGGAAGT	150
	TCGTGACTTA	TTATCAGAAT	ACGATTTCCC	AGGCGATGAT	GTTCCAGTTA	200
	TCGCAGGTTT	TGCTTTGAAA	GCTTTAGAAG	GCGACGAGTC	TTATGAAGAA	250
25	AAAATCTTAG	AATTAATGGC	TGCAGTTGAC	GAATATATCC	CAACTCCAGA	300
	ACGTGATACT	GACAAACCAT	TCATGATGCC	AGTCGAAGAC	GTATTCTCAA	350
	TCACTGGACG	TGGTACTGTT	GCTACAGGCC	GTGTTGAACG	TGGTGAAGTT	400
	CGCGTTGGTG	ACGAAGTTGA	AATCGTTGGT	ATTAAAGACG	AAACATCTAA	450
	AACAACGTGT	ACAGGTGTTG	AAATGTTCCG	TAAATTATTA	GACTACGCTG	500
30	AAGCAGGCGA	CAACATCGGT	GCTTTATTAC	GTGGTGTAGC	ACGTGAAGAT	550
	ATCGAACGTG	GACAAGTATT	AGCTAAACCA	GCTACAATCA	CTCCACACAC	600
	AAAATTCAAA	GCTGAAGTAT	ACGTATTATC	AAAAGAAGAA	GGCGGACGTC	650
	ACACTCCATT	CTTCACTAAC	TACCGTCCTC			680

2) INFORMATION FOR SEQ ID NO: 63

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 680 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecalis*
 (B) STRAIN: R487

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63

55	AGTAGTTTCT	GCTGCTGATG	GTCCTATGCC	TCAAACACGT	GAACATATCT	50
	TATTATCACG	TAACGTTGGT	GTACCATACA	TCGTTGTATT	CTTAAACAAA	100
	ATGGATATGG	TTGATGACGA	AGAATTATTA	GAATTAGTAG	AAATGGAAGT	150
	TCGTGACTTA	TTATCAGAAT	ACGATTTCCC	AGGCGATGAT	GTTCCAGTTA	200
	TCGCAGGTTT	TGCTTTGAAA	GCTTTAGAAG	GCGACGAGTC	TTATGAAGAA	250
	AAAATCTTAG	AATTAATGGC	TGCAGTTGAC	GAATATATCC	CAACTCCAGA	300
	ACGTGATACT	GACAAACCAT	TCATGATGCC	AGTCGAAGAC	GTATTCTCAA	350
60	TCACTGGACG	TGGTACTGTT	GCTACAGGCC	GTGTTGAACG	TGGTGAAGTT	400

```

CGCGTTGGTG ACGAAGTTGA AATCGTTGGT ATTAAAGACG AAACATCTAA 450
AACAACTGTT ACAGGTGTTG AAATGTTCCG TAAATTATTA GACTACGCTG 500
AAGCAGGCGA CAACATCGGT GCTTTATTAC GTGGTGTAGC ACGTGAAGAT 550
ATCGAACGTG GACAAGTATT AGCTAAACCA GCTACAATCA CTCCACACAC 600
5 AAAATTCAAA GCTGAAGTAT ACGTATTATC AAAAGAAGAA GCGGACGTC 650
ACACTCCATT CTTCACTAAC TACCGTCCTC 680

```

10 2) INFORMATION FOR SEQ ID NO: 64

(i) SEQUENCE CHARACTERISTICS:

```

15 (A) LENGTH: 685 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

```

    (A) ORGANISM: Enterococcus faecium
    (B) STRAIN: R482

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64

```

25 AGTAGTTTCT GCTGCTGACG GCCCAATGCC TCAAACCTCGT GAACACATCC 50
   TATTGTCTCG TCAAGTTGGT GTTCCTTACA TCGTTGTATT CTTGAACAAA 100
   GTAGACATGG TTGATGACGA AGAATTACTA GAATTAGTTG AAATGGAAGT 150
   TCGTGACCTA TTAACAGAAT ACGAATTCCC TGGTGACGAT GTTCCTGTAG 200
30 TTGCTGGATC AGCTTTGAAA GCTCTAGAAG GCGACGCTTC ATACGAAGAA 250
   AAAATTCTTG AATTAAATGGC TGCAGTTGAC GAATACATCC CAACTCCAGA 300
   ACGTGACAAC GACAAACCAT TCATGATGCC AGTTGAAGAC GTGTTCTCAA 350
   TTACTGGACG TGGTACTGTT GCTACAGGTC GTGTTGAACG TGGACAAGTT 400
   CGCGTTGGTG ACGAAGTTGA AGTTGTTGGT ATTGCTGAAG AAACCTCAAA 450
35 AACAAACAGTT ACTGGTGTTG AAATGTTCCG TAAATTGTTA GACTACGCTG 500
   AAGCTGGAGA CAACATTGGT GCTTTACTAC GTGGTGTGTC ACGTGAAGAC 550
   ATCCAACGTG GACAAGTTT AGCTAAACCA GGTACAATCA CACCTCATAC 600
   AAAATTCTCT GCAGAAGTAT ACGTGTTGAC AAAAGAAGAA GGTGGACGTC 650
40 ATACTCCATT CTTCACTAAC TACCGTCCTC AATTT 685

```

2) INFORMATION FOR SEQ ID NO: 65

(i) SEQUENCE CHARACTERISTICS:

```

45 (A) LENGTH: 825 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

```

55 (A) ORGANISM: Enterococcus flavescens
    (B) STRAIN: ATCC 49996

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65

```

60 CGGCGCGATC TTAGTAGTAT CTGCTGCTGA TGGTCCTAYG CCTCAAACAC 50
   GTGAACACAT CTTGTTATCA CGTAACGTTG GTGTACCATA CATCGTTGTT 100

```

	TTCTTAAACA	AAATGGATAT	GGTTGATGAC	GAAGAATTAC	TAGAATTAGT	150
	TGAAATGGAA	GTTCGTGACT	TATTGTCAGA	ATATGACTTC	CCAGGCGACG	200
	ATGTTCTGT	AATCGCTGGT	TCTGCTTTGA	AAGCTCTTGA	AGGCGATGCT	250
	TCATACGAAG	AAAAAATCAT	GGAATTAATG	GCTGCAGTTG	ACGAATACGT	300
5	TCCAAC TCCA	GAACGTGACA	CTGACAAACC	ATTCATGATG	CCAGTCGAAG	350
	ACGTATTCTC	AATCACTGGA	CGTGGTACTG	TTGCTACAGG	CCGTGTTGAA	400
	CGTGGACAAG	TTCGCGTTGG	TGACGAAGTT	GAAATCGTTG	GTATTGCTGA	450
	AGAAACTGCT	AAAACA ACTG	TA ACTGGTGT	TGAAATGTTC	CGTAAATTGT	500
	TAGACTATGC	TGAAGCAGGG	GATAACATTG	GTGCATTGCT	ACGTGGGGTT	550
10	GCTCGTGAAG	ACATCCAACG	TGGACAAGTA	TTAGCTAAAG	CTGGTACAAT	600
	CACACCTCAT	ACAAAATTTA	AAGCTGAAGT	TTACGTTTTA	ACAAAAGAAG	650
	AAGGTGGACG	TCACACTCCA	TTCTTCACTA	ACTACCGTCC	TCAGTTCTAC	700
	TTCCGTACAA	CTGACGTAAC	TGGTGTGTGT	GAATTACCAG	AAGGAACTGA	750
	AATGGTTATG	CCTGGTGATA	AMGTAACAAT	CGACGTTGAA	TTGATCCACC	800
15	CAATCGCTAT	CGAAGACGGA	ACTCG			825

2) INFORMATION FOR SEQ ID NO: 66

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 636 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus gallinarum*
 (B) STRAIN: R420

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66

35	TCCTATGCCT	CAAAC TCGTG	AACACATCTT	GTTATCACGT	AACGTTGGCG	50
	TACCATACAT	CGTTGTTTTT	TTGAACAAAA	TGGATATGGT	TGATGACGAA	100
	GAATTGCTAG	AATTAGTTGA	AATGGAAGTT	CGTGACCTAT	TGTCTGAGTA	150
	TGACTTCCCA	GGCGACGATG	TTCTTGTAAT	CGCCGTTTCT	GCTTTGAAAG	200
	CTCTTGAAGG	AGATCCTTCA	TACGAAGAAA	AAATCATGGA	ATTGATGGCT	250
40	GCAGTTGACG	AATACGTTCC	AACTCCAGAA	CGTGATACTG	ACAAACCATT	300
	CATGATGCCA	GTCGAAGACG	TATTCTCAAT	CACTGGACGT	GGTACTGTTG	350
	CTACAGGCCG	TGTTGAACGT	GGACAAGTTC	GCGTTGGTGA	TGAAGTAGAA	400
	ATCGTTGGTA	TTGCTGACGA	AACTGCTAAA	ACAACTGTAA	CAGGTGTTGA	450
	AATGTTCCGT	AAATTGTTAG	ACTATGCTGA	AGCAGGGGAT	AACATTGGTG	500
45	CATTGCTACG	TGGGGTTGCT	CGTGAAGACA	TCCAACGTGG	ACAAGTATTG	550
	GCTAAAGCTG	GTACAATCAC	ACCTCATACA	AAATTCAAAG	CTGAAGTTTA	600
	TGTTTTGACA	AAAGAAGAAG	GTGGACGTCA	CACTCC		636

2) INFORMATION FOR SEQ ID NO: 67

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus hirae*
 (B) STRAIN: ATCC 8043

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67

```

CGGAGCTATC TTAGTAGTTT CTGCTGCTGA TGGTCCTATG CCTCAAACCTC 50
GTGAACATAT CCTAYTATCT CGTCAAGTTG GTGTTCCATA CATCGTTGTA 100
TTCTTGAACA AAGTAGATAT GGTTGACGAC GAAGAATTAC TAGAATTAGT 150
10 TGAAATGGAA GTTCGTGACT TATTAACAGA ATACGAATTC CCTGGTGACG 200
ATGTTCCCTGT AGTTGCTGGT YCAGCTTTGA AAGCTTTAGA AGGCGACGCT 250
TCATACGAAG AAAAAATCCT TGAATTGATG GCTGCAGTTG ACGAATATAT 300
CCCAACTCCA GAACGTGACA ACGACAAACC ATTCATGATG CCAGTCGAAG 350
ACGTATTCTC AATCACTGGT CGTGGTACTG TTGCTACAGG TCGTGTTGAA 400
15 CGTGGAACAAG TTCGCGTTGG TGACGTTGTA GATATCGTTG GTATCGCAGA 450
AGAAACAGCT CAAACAACAG TTAAGTGGTGT TGAAATGTTT CGTAAATTAT 500
TAGACTACGC TGAAGCTGGA GACAACATTG GTGCTTTACT ACGTGGTGTT 550
GCACGTGAAG ACATCCAACG TGGACAAGTT TTAGCTAAAC CAGGTACAAT 600
CACACCTCAT ACAAATTTCT CTGCAGAAGT ATACGTGTTG ACAAAGAAG 650
20 AAGGTGGACG TCATACTCCA TTCTTCACTA ACTACCGTCC ACAATTCTAC 700
TTCCGTACRA CTGACGTAAC AGGTGTTGTT GAATTACCAG AAGGAACTGA 750
AATGGTTATG CCTGGCGACA ACGTAACAAT GGAAGTTGAA TTAATCCACC 800
CAATCGCTAT CGAAAACGGT ACTAAATTCT CAATC 835

```

25

2) INFORMATION FOR SEQ ID NO: 68

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus mundtii*
 (B) STRAIN: ATCC 43186

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68

```

CGGAGCAATC TTAGTTGTTT CTGCTGCTGA CGGCCCTATG CCTCAAACCTC 50
GTGAACACAT CCTATTATCT CGTCAAGTTG GTGTACCATA CATCGTTGTA 100
45 TTCTTGAACA AAGTAGATAT GGTTGATGAC GAAGAATTAC TTGAATTAGT 150
TGAAATGGAA GTTCGTGACC TATTAACAGA ATACGAATTC CCTGGTGACG 200
ATGTTCCCTGT AATCGCTGGT TCAGCTTTAA GAGCTTTAGA AGGCGACGCT 250
KCATACGAAG AAAAAATTCT TGAATTGATG GCTGCAGTTG ACGAATATAT 300
CCCAACTCCA GAACGTGATA ACGACAAACC ATTCATGATG CCAGTTGAGG 350
50 ACGTATTCTC AATCACTGGT CGTGGTACTG TTGCTACAGG ACGTGTTGAA 400
CGTGGACAAG YTCGTGTTGG TGACGTTATC GATATCGTTG GTATCGCAGA 450
AGAAACAGCT CAAACAACCTG TAACTGGTGT TGAAATGTTT CGTAAATTAT 500
TAGACTACGC TGAAGCAGGC GATAACATTG GTGCGTTACT ACGTGGTGTT 550
TCACGTGAAG ACATCCAACG TGGTCAAGTT TTAGCTAAAC CAGGTACAAT 600
55 CACACCTCAT ACAAATTTCT CTGCAGAAGT ATACGTGTTG ACTAAAGAAG 650
AAGGTGGACG TCATACTCCA TTCTTCACTA ACTACCGTCC ACAATTCTAC 700
TTCYGTACGA CTGACGTAAC TRGTGTTGTY GAATTACCAG AAGGAACTGA 750
AATGGTTATG CCTGGCGACA ACGTAACAAT GGAAGTTGAA TTAATCCACC 800
60 CAATCGCTAT CGAAAATGGT ACTAAATTCT CAATC 835

```

2) INFORMATION FOR SEQ ID NO: 69

5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 836 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Enterococcus pseudoavium*
 15 (B) STRAIN: ATCC 49372

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69

	CGGAGCTATC	TTAGTAGTAT	CTGCTGCTGA	TGGCCCTATG	CCTCAAACAC	50
20	GTGAACACAT	CTTGTTATCT	CGTAACGTTG	GTGTTTCCTTA	CATCGYTGTA	100
	TTCTTAAACA	AAATGGATAT	GGTTGATGAC	GAAGAATTAC	TAGAATTAGT	150
	TGAAATGGAA	GTTCTGACT	TATTGTCAGA	ATACGATTTC	CCAGGCGACG	200
	ACACTCYAGT	TATCGCTGGT	TCAGCYTTGA	AAGCTTTAGA	AGGCGACCCT	250
	TCATACRAAG	AAAAAATCTT	AGAATTAATG	SCTGCTGTTG	ACGAATACAT	300
25	CCCAACACCA	GTTCGTGATA	CTGACAAACC	ATTCATGATG	CCAGTCGAAG	350
	ACGTATTCTC	AATCACTGGT	CGTGGTACTG	TTGCAACTGG	TCGTGTTGAA	400
	CGTGGACAAG	TTCGCGTTGG	TGACGAAGTT	GAAATCGTAG	GTATCGCTGA	450
	AGAAACTGCT	AAAACAACCTG	TTACAGGTGT	TGAAATGTTT	CGTAAATTGT	500
	TAGACTACGC	TGAAGCAGGC	GATAACATCG	GTGCATTATT	ACGTGGTGTT	550
30	GCACGTGAAG	ACATCCAACG	TGGACAAGTA	TTGGCTAAAC	CAGCTTCAAT	600
	CACTCCACAT	ACAAAATTCT	CTGCAGAAGT	TTACGTTTTA	ACTAAAGAAG	650
	AAGGCGGGCG	TCACACTCCG	TTCTTCACTA	ACTACCGTCC	TCAGTTCTAC	700
	TTCCGTACAA	CTGACGTAAC	TGGTGTTGTT	GATCTACCAG	AAGGTACTGA	750
	AATGGTAATG	CCTGGTGATA	ACGTAACAT	GGAAGTTGAA	TTAATCCACC	800
35	CAATCGCGAT	CGAAGACGGA	ACTCGTTTCT	CTATTC		836

2) INFORMATION FOR SEQ ID NO: 70

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 45 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
 50 (A) ORGANISM: *Enterococcus raffinosus*
 (B) STRAIN: ATCC 49427

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70

55	CGGAGCTRTC	TTAGTAGTAT	CTGCTGCTGA	TGGCCCTATG	CCTCAAACCTC	50
	GTGAACACAT	CTTGTTATCT	CGTAACGTTG	GTGTTTCCTTA	CATCGTTGTA	100
	TTCTTAAACA	AAATGGATAT	GGTTGACGAT	GAAGAATTAC	TAGAATTAGT	150
	TGAAATGGAA	GTTCTGACT	TATTAACCTGA	ATACGACTTC	CCAGGCGACG	200
	ACACTCCAGT	TATCGCAGGT	TCAGCTTTGA	AAGCCTTAGA	AGGCGACGCT	250
60	TCATACGAAG	AAAAAATCTT	AGAATTAATG	GCTGCTGTTG	ATGAATACAT	300

```

      CCCAACACCA GTTCGTGATA CTGACAAACC ATTCATGATG CCAGYGGAAG      350
      ACGTAYTCTC AATCACTGGT CGTGGAAGCTG TTGCAACTGG TCGTGTTGAA      400
      CGTGGACAAG TTCGCGTTGG TGACGAAGTT GAAATCGTAG GTATTGCTGA      450
      AGAAACTGCT AAAACAAGT TACAGGTGT TGAAATGTTT CGTAAATTGT      500
5    TGGATTACGC TGAAGCGGGC GACAACATTG GTGCATTATT ACGTGGTGTT      550
      GCACGTGAAG ACATCCAACG TGGACAAGTA TTGGCTAAAC CAGCTTCAAT      600
      CACTCCACAT ACAAATTCCT CTGCAGAAGT TTACGTTTTA ACTAAAGAAG      650
      AAGGCGGACG TCATACTCCA TTCTTCACTA ACTACCGTCC TCAGTTCTAC      700
      TTCCGTACAA CTGACGTAAC TGGTGTAGTT GATCTACCAG AAGGTACTGA      750
10   AATGGTAATG CCTGGTGATA ACGTAACATG GGAAGTTGAA TTAATCCACC      800
      CAATCGCGAT CGAAGACGGA ACTCGTTTCT CTATT      835

```

15 2) INFORMATION FOR SEQ ID NO: 71

(i) SEQUENCE CHARACTERISTICS:

```

      (A) LENGTH: 835 bases
      (B) TYPE: Nucleic acid
20   (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

```

      (A) ORGANISM: Enterococcus saccharolyticus
      (B) STRAIN: ATCC 43076

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71

```

30   CGGCGCGATC TTAGTAGTAT CTGCTGCTGA TGGTCCTATG CCTCAAACCTC      50
      GTGAACACAT CTTGTTATCT CGTAACGTAG GTGTTCTTA CATCGTTGTA      100
      TTCTTAAACA AAATGGATAT GGTGATGAC GAAGAATTAT TAGAATTAGT      150
      AGAAATGGAA GTTCGTGACT TATTATCAGA ATACGATTTC CCAGGCGATG      200
35   ACACTCCAGT TATTGCAGGT TCTGCTTTGA AAGCTTTAGA AGGCGATCCA      250
      GTTTACGAAG AAAAAATCTT CGAATTAATG GCTGCAGTTG ACGAATATAT      300
      CCCAACTCCA GAACGTGATA CTGAAAACC ATTCATGATG CCAGTTGAGG      350
      ATGTATTCTC AATCACTGGT CGTGGTACTG TTGCTACAGG TCGTGTTGAA      400
      CGTGGACAAG TTCGCGTTGG TGACGTTGTA GAAATCGTTG GTATCGACGA      450
40   AGAAACAGCT CAAACTACTG TAACAGGTGT TGAAATGTTT CGTAAATTAT      500
      TAGACTACGC TGAAGCAGGC GATAACATCG GTGCTTTATT ACGTGGGGTT      550
      GCTCGTGAAG ACATCCAACG TGGACAAGTA TTAGCTAAAC CAGGAACAAT      600
      CACTCCTCAT ACAAATTCG TAGCTGAAGT TTACGTTTTA ACTAAAGAAG      650
      AAGGTGGACG TCATACTCCA TTCTTCACTA ACTACCGTCC TCAATTCTAC      700
45   TTCCGTACAA CTGACGTAAC TGGTGTGTA GAATTACGCG AAGGTACTGA      750
      AATGGTAATG CCTGGTGACA ACGTAACATG CGACGTTGAA TTAATCCACC      800
      CAATCGCTAT CGAAGACGGA ACTCGTTTCT CTATT      835

```

50 2) INFORMATION FOR SEQ ID NO: 72

(i) SEQUENCE CHARACTERISTICS:

```

      (A) LENGTH: 823 bases
55   (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus solitarius*
 (B) STRAIN: ATCC 49428

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72

	GAGCTATCTT	GGTAGTTTCT	GCAGCTGATG	GCCCAATGCC	ACAAACTCGT	50
	GAACATATTT	TGTTGTCACG	TAATGTAGGT	GTACCTTACA	TCGTTGTGTT	100
	CTTGAACAAA	ATGGATATGG	TTGATGACGA	AGAATTACTT	GAGTTAGTTG	150
10	AAATGGAAGT	ACGTGATCTA	TTATCTGAAT	ACGACTTCCC	AGGAGATGAT	200
	ACTCCAGTTA	TTTCCGGTTC	AGCTTTGAAA	GCTTTAGAAG	GCGACGAAGA	250
	ATATGAACAA	AAAATTATGG	ACTTAATGGA	TGCAGTTGAT	GACTIONATTC	300
	CAACTCCTGA	ACGTGACCAT	GACAAACCAT	TCATGATGCC	AATTGAAGAT	350
	GTATTTTCAA	TTACAGGCCG	TGGTACTGTT	GCTACAGGAC	GTGTTGAACG	400
15	CGGGACTATC	AAAGTCGGCG	ATGAAAGTTGA	CATTATTGGT	ATTTCATGAAG	450
	ACGTTAAAAA	GACAACAGTT	ACTGGTGTAG	AAATGTTCCG	TAAATTGTTG	500
	GACTACGCTG	AAGCAGGCGA	TAACATTGGT	ACTTTGTTAC	GTGGTGTGTT	550
	TCGTGATGAT	ATCGAACGTG	GTCAAAGTATT	AGCTAAACCA	GGTTCAATCA	600
	CACCACATAC	AAGATTCTCT	GCTGAAGTTT	ATGTTTTGAC	TAAAGAAGAA	650
20	GGCGGACGTC	ATACTCCATT	CTTCTCAAAC	TATCGTCCTC	AATTCTACTT	700
	CCGTACAAC	GATATCACTG	TGGTCAATTGA	ATTGCCAGAA	GGTACTGAAA	750
	TGGTAATGCC	AGGTGATAAT	GTAACAATGG	ATGTTGAATT	AATCCACCCA	800
	GTCGCTATCG	AAGAAGGAAC	TCG			823

25

2) INFORMATION FOR SEQ ID NO: 73

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus casseliflavus*
 (B) STRAIN: ATCC 25788

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73

	CGGTGCAATC	TTGGTCGTAT	CAGCGACAGA	TGGCCCAATG	CCACAAACAC	50
	GGGAGCATAT	TTTGCTTTCT	CGTCAAGTGG	GTGTGAAACA	TTTGATCGTC	100
45	TTTTTGAATA	AGACGGACCT	TGTCGATGAT	GACGAGTTGA	TCGATTTAGT	150
	TGAAATGGAA	GTCAGAGAA	TGCTGACTGA	ATATGATTTT	CCTGGCGACG	200
	ACATTCCTGT	GATCAAGGGC	TCTGCGTTAA	AAGCCTTGGA	AGGGGACCCA	250
	GATGCTGAAG	CAGCGATCTT	AACGCTGATG	GATACAGTAG	ATGAATATAT	300
	CCCAACGCCA	GAACGTGATA	CTGACAAACC	ATTGTTGTTA	CCGATCGAAG	350
50	ATGTCTTTTC	GATCACAGGA	CGGGGGACCG	TTGCTTCTGG	TCGGATCGAT	400
	CGCGGCATGG	TAAAAGTCGG	GGATGAAGTA	GAAATCGTCG	GAATCAAACC	450
	TGAAACACAA	AAAGCAGTCG	TGACAGGGGT	AGAAATGTTT	CGCAAAACGA	500
	TGGACTTCGG	AGAAGCTGGC	GATAACGTAG	GGGTATTGTT	ACGGGGCATC	550
	ACCCGTGATG	AAATTGAACG	TGGCCAAGTG	TTAGCAAAAC	CAGGTTCTAT	600
55	CACACCGCAT	ACGAAATCCC	AAGCGGAAGT	CTATGTGTTG	ACAAAAGAAG	650
	AAGGCGGTCG	CCATACCCCA	TTCTTTAATA	ATTATCGCCC	ACAATTTTAC	700
	TTCCGTACAA	CGGACGTAAC	TGGGAATATC	GTTTTACCAG	AAGGAACGGA	750
	AATGGTGATG	CCTGGTGACA	ACGTAACGAT	CGATGTGGAA	TTGATCCATC	800
60	CGATCGCTGT	AGAAAATGGA	ACGACCTTCT	CGATT		835

2) INFORMATION FOR SEQ ID NO: 74

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 380 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- 10 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Staphylococcus saprophyticus*
 15 (B) STRAIN: ATCC 15305

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74

	TAACGGGCGT	CTCGATAGAA	AAACACGTGA	AAATCCCAAT	GATTATAAAC	50
20	AATCAATATA	CGATTTTGCT	GAAGCTGTAA	CAAAAGGTAT	TAAGGAACAA	100
	ACAAATAAAA	ATTAATAGGC	AACTTAACCA	GAATCGTTAA	AACTATATGA	150
	AGATTCTGGT	TTTTTAAATT	CAAAAAGTTT	TCTAAAAAAT	TTACTTGCTT	200
	TTTTAAGTAT	AGGTATAAAA	TACGATTGAT	TAAAACAGTA	AAGGAAATGA	250
	ATCATGAAAC	AATTAATAA	GCCTTTATAC	TTTTACCTAT	TACTTTTTAT	300
25	TACAACAACG	CTGATTGGCG	CGTTACTATT	ATATTTGCCA	ATCACAGGTA	350
	AACATCCTAT	TGATTTTGTG	GACGCCCGTT			380

30. 2) INFORMATION FOR SEQ ID NO: 75

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 666 bases
 (B) TYPE: Nucleic acid
 35 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- 40 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Enterococcus flavescens*
 (B) STRAIN: ATCC 49996

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75

45	GCAATCTTGG	TCGTATCAGC	GACAGATGGC	CCAATGCCAC	AAACACGGGA	50
	GCATATTTTG	CTTTCTCGTC	AAGTGGGTGT	GAAACATTTG	ATCGTCTTTT	100
	TGAATAAGAC	GGACCTTGTC	GATGATGACG	AGTTGATCGA	TTTAGTTGAA	150
	ATGGAAGTCA	GAGAATTGCT	GA CTGAATAT	GATTTTCCTG	GCGACGACAT	200
50	TCCTGTGATC	AAGGGCTCTG	CGTTAAAAGC	CTTGGAAGGG	GACCCAGATG	250
	CTGAAGCAGC	GATCTTAACG	CTGATGGATA	CGGTAGATGA	ATATATCCCA	300
	ACGCCAGAAC	GTGATACTGA	CAAACCATTG	TTGTTACCGA	TCGAAGATGT	350
	CTTTTCGATC	ACAGGACGGG	GGACCGTTGC	TTCTGGTCCG	ATCGATCGCG	400
	GCATGGTAAA	AGTCGGGGAT	GAAGTAGAAA	TCGTCGGAAT	CAAACCTGAA	450
55	ACACAAAAAG	CAGTCGTGAC	AGGGGTAGAA	ATGTTCCGCA	AAACGATGGA	500
	CTTCGGAGAA	GCTGGCGATA	ACGTAGGGGT	ATTGTTACGG	GGCATCACCC	550
	GTGATGAAAT	TGAACGTGGC	CAAGTGTTAG	CAAACACAGG	TTCTATCACA	600
	CCGCATACGA	AATTCCAAGC	GGAAGTCTAT	GTGTTGACAA	AAGAAGAAGG	650
60	CGGTCGCCAT	ACCCCA				666

2) INFORMATION FOR SEQ ID NO: 76

5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 751 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

15 (A) ORGANISM: *Enterococcus gallinarum*
 (B) STRAIN: ATCC 49573

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76

	TGGTGC	GATT	TTAGTT	GTAT	CCGCAAC	CAGA	TGGTCCA	ATG	CCTCAA	ACCC	50
20	GGGAAC	ATAT	CTTGCT	TTTC	AGACAAG	TTG	GTGTGAA	ACA	TCTGAT	TGTT	100
	TTCTTGA	ACA	AAATCG	ATT	AGTCGAT	GAC	GAAGAAT	TGA	TTGATT	TTAGT	150
	AGAAATG	GAA	GTAAGAG	AAC	TGCTATCT	GTA	ATATAAT	TTT	CCAGGG	GATG	200
	ACATTCC	TGT	TATCAA	AGGT	TCGGCAT	TAA	AAGCGTT	GGA	AGGAGAC	CCT	250
	GATGCAG	AAG	CTGCCAT	CAT	GGAATTA	ATG	GATACAG	TAG	ACAGCT	TATAT	300
25	CCCAAC	ACCT	GAGCGT	GATA	CAGACAA	ACC	ATTACTC	TTG	CCAGTT	GAA	350
	ATGTCT	TTTT	GATTACT	GGA	CGAGGA	ACAG	TTGCTTC	CGG	ACGGAT	CGAT	400
	CGGGGA	ACAG	TTCGGG	TAGG	CGATGA	AGTA	GAAATCG	TCG	GTATCA	AACC	450
	TGAAAC	CCAA	AAAGCT	GTA	TGACAGG	CGT	CGAAATG	TTC	CGCAAG	ACGA	500
	TGGACT	TTTG	GGAAGC	CGGT	GACAATG	TAG	GTGTCTT	GCT	GAGAGG	GATC	550
30	ACTCGT	GACG	AAATTG	AACG	AGGACA	AGTG	TTGGCTA	AAC	CAGGTT	CGAT	600
	CACACC	ACAT	ACAAAAT	TCC	AAGCAGA	AGT	TTATGT	TATTG	ACGAA	AGAAG	650
	AAGGTG	GTCG	TCATAC	ACCA	TTCTTCA	ACA	ACTATCG	TCC	ACAATT	TTTAT	700
	TTCCGT	TACAA	CGGATG	TGAC	AGGGAAC	ATT	ACATTGC	CCTG	AAGGA	ACAGA	750
35	A										751

2) INFORMATION FOR SEQ ID NO: 77

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 834 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

50 (A) ORGANISM: *Ehrlichia canis*
 (B) STRAIN: Florida

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77

	TGCAGCA	ATA	TTAGTAG	TGT	CTGCAAC	TGA	TGGAGCA	ATG	CCACAA	ACAA	50
55	GAGAAC	ATAT	ATTATT	AGCA	AAGCA	AGTAG	GTGTAAA	AGA	TATAGT	AGTG	100
	TGGATGA	ATA	AGTGTG	ATGT	TGTAGAT	GAT	GAAGAAA	TGT	TGTCAT	TAGT	150
	TGAAATG	GAA	ATAAGG	GAAT	TGTTAT	CAAA	ATATGGG	TAT	CCTGGG	GATG	200
	ATATAG	ATGT	AGTTAG	AGGA	TCTGCAG	TTA	AAGCATT	AGA	AGAAGA	ACA	250
	GGCTCAG	GTG	TGTGG	AGTGA	AAAAATA	ATG	GAATTG	ATGA	ATGCTT	TAGA	300
60	AAAAATA	AAGT	TTACC	AGTAA	GAGAAA	AAGA	TAAGCC	ATTT	TTAATG	TCAA	350

```

TAGAAGATGT GTTTTCAATA CCTGGAAGAG GTACAGTAGT AACAGGAAGA 400
ATAGAAAGAG GAGTAATTAG AGTAGGGGAT AAAATAGAGA TAGTAGGATT 450
GCGTGAGATA CAAAGTACAG TATGTACAGG TGTTGAAATG TTTCATAAAG 500
CATTAGATGC AGGAGAAGCA GGGGATAATG CTGGAATATT GTTAAGAGGG 550
5  ATAAAAAAG AAGATGTAGA AAGAGGGCAA GTATTGAGTG CACCTGGACA 600
GATACATTCA TATAAGAGAT TTAAGGCAGA GGTATATATA TTGAAAAAAG 650
AAGAAGGAGG AAGACATACT CCATTTTTCT CAAATTACCA GCCGCAATTT 700
TATGTTAGAA CAACAGATGT AACAGGGAAT ATAAAGTTAC CAGAAGGAGT 750
AGAAATGGTA ATGCCAGGGG ATAATATAAA TATCGAAGTG AGTTTGGATA 800
10 AGCCTGTTGC TATTGATCAA GGATTGAGAT TTGC 834

```

2) INFORMATION FOR SEQ ID NO: 78

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
 (B) STRAIN: ATCC 23511

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78

```

30  CGGCGCGATC CTGGTAGTTG CTGCGACTGA CGGCCCGATG CCGCAGACTC 50
    GTGAGCACAT CCTGCTGGGT CGTCAGGTAG GCGTTCCGTA CATCATCGTG 100
    TTCCTGAACA AATGCGACAT GGTGTATGAC GAAGAGCTGC TGGAAGTGGT 150
    TGAATGGAA GTTCGTGAAC TTCTGTCTCA GTACGACTTC CCGGGCGACG 200
    ACACTCCGAT CGTTCGTGGT TCTGCTCTGA AAGCGCTGGA AGGCGACGCA 250
35  GAGTGGGAAG CGAAAATCCT GGAAGTGGCT GGCTTCCTGG ATTCTTAYAT 300
    TCCGGAACCA GAGCGTGCGA TTGACAAGCC GTTCCTGCTG CCGATCGAAG 350
    ACGTATTCTC CATCTCCGGT CGTGGTACCG TTGTTACCGG TCGTGTAAG 400
    CGCGGTATCA TCAAAGTTGG TGAAGAAGTT GAAATCGTTG GTATCAAAGA 450
    GACTCAGAAG TCTACCTGTA CTGGCGTTGA AATGTTCCGC AAAGTGCTGG 500
40  ACGAAGGCCG TGCTGGTGAG AACGTAGGTG TTCTGCTGCG TGGTATCAAA 550
    CGTGAAGAAA TCGAACGTGG TCAGGTACTG GCTAAGCCGG GCACCATCAA 600
    GCCGCACACC AAGTTCGAAT CTGAAGTGTA CATTCGTGTC AAAGATGAAG 650
    GCGGCCGTCA TACTCCGTTT TTCAAAGGCT ACCGTCCGCA GTTCTACTTC 700
    CGTACTACTG ACGTGACTGG TACCATCGAA CTGCCGGAAG GCGTAGAGAT 750
45  GGTAATGCCG GGCGACAACA TCAAAATGGT TGTTACCCTG ATCCACCCGA 800
    TCGCGATGGA CGACGGT 817

```

2) INFORMATION FOR SEQ ID NO: 79

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Escherichia fergusonii*
 (B) STRAIN: ATCC 35469

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79

```

5  CGATCCTGGT AGTTGCTGCG ACTGACGGCC CGATGCCGCA GACTCGTGAG      50
   CACATCCTGC TGGGTCGTCA GGTAGGCGTT CCGTACATCA TCGTGTTTCCT    100
   GAACAAGTGC GACATGGTTG ATGACGAAGA GCTGCTGGAA CTGGTTGAAA      150
   TGGAAGTTCG TGAACCTCTG TCTCAGTACG ACTTCCCAGG CGACGACACT      200
10  CCGATCGTTC GTGGTTCTGC TCTGAAAGCG CTGGAAGGCG ACGCAGAGTG      250
   GGAAGCGAAA ATCCTGGAAC TGGCTGGCTT CCTGGATTCT TACATTCCGG      300
   AACCAGAGCG TGCATTTGAC AAGCCGTTCC TGCTGCCGAT CGAAGACGTG      350
   TTCTCCATCT CCGGTCGTGG TACCGTTGTT ACCGGTCGTG TAGAACGCGG      400
   TATCATCAAA GTTGGTGAAG AAGTTGAAAT CGTTGGTATC AAAGAGACTC      450
15  AGAAGTCTAC CTGTACTGGC GTTGAAATGT TCCGCAAAC GCTGGACGAA      500
   GGCCGTGCTG GTGAGAACGT AGGTGTTCTG CTGCGTGGTA TCAAACGTGA      550
   AGAAATCGAA CGTGGTCAGG TACTGGCTAA GCCGGGCACC ATCAAGCCGC      600
   ACACCAAGTT CGAATCTGAA GTGTACATTC TGTCCAAAGA TGAAGGCGGT      650
   CGTCATACTC CGTTCTTCAA AGGCTACCGT CCGCAGTTCT ACTTCCGTAC      700
20  TACTGACGTG ACTGGTACCA TCGAACTGCC GGAAGGCGTA GAGATGGTAA      750
   TGCCGGGCGA CAACATCAAA ATGGTTGTTA CCCTGATCCA CCGATCGCG      800
   ATGGACGACG GTCTGCGTTT CGCAA                                825
  
```

25 2) INFORMATION FOR SEQ ID NO: 80

(i) SEQUENCE CHARACTERISTICS:

```

30  (A) LENGTH: 829 bases
   (B) TYPE: Nucleic acid
   (C) STRANDEDNESS: Double
   (D) TOPOLOGY: Linear
  
```

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

```

35  (A) ORGANISM: Escherichia hermannii
   (B) STRAIN: ATCC 33650
  
```

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80

```

   GGCGCGATCC TGGTTGTTGC TGCGACTGAC GGCCCGATGC CGCAGACCCG      50
   TGAGCACATC CTGCTGGGTC GTCAGGTAGG CGTTCCGTAC ATCATCGTGT      100
   TCCTGAACAA ATGCGACATG GTTGATGACG AAGAGCTGCT GGAAGTGGTT      150
45  GAGATGGAAG TTCGCGAACT GCTGTCCCAG TACGATTTCC CGGGCGACGA      200
   CACCCCGATC GTTCGTGGTT CCGCGCTGAA AGCGCTGGAA GGCGAAGCAG      250
   AGTGGGAAGA GAAAATCATC GAACTGGCTG GCTACCTGGA TTCCTATATC      300
   CCGGAACCAG AGCGTGCGAT TGACAAGCCG TTCCTGCTGC CTATCGAAGA      350
   CGTATTCTCC ATCTCCGGCC GTGGTACCGT TGTTACCGGT CGTGTAAGAGC      400
50  GCGGTATCAT CAAAGTGGGT GAAGAAGTTG AAATCGTGGG TATCAAAGAT      450
   ACTGCGAAAT CAACCTGTAC CGGCGTTGAA ATGTTCCGCA AACTGCTGGA      500
   CGAAGGCCGT GCGGGCGAGA ACGTGGGTGT TCTGCTGCGT GGTATCAAAC      550
   GTGAAGAAAT CGAACGTGGT CAGGTACTGG CTAAGCCGGG TTCCATCAAG      600
   CCKCACACCA AGTTCGAATC TGAAGTGTAC ATTCTGTCCA AAGACGAAGG      650
55  CGGCCGTAC ACTCCGTTCT TCAAAGGCTA CCGTCCGAG TTCTACTTCC      700
   GTACAACCTGA CGTGACTGGC ACCATCGAAC TGCCGGAAGG CGTTGAGATG      750
   GTAATGCCGG GCGACAACAT CAAAATGGTT GTTACCCTGA TCCACCCGAT      800
   CGCGATGGAC GACGGTCTGC GTTTCGCAA                                829
  
```

60

2) INFORMATION FOR SEQ ID NO: 81

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 816 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia vulneris*
 (B) STRAIN: ATCC 33821

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81

CGGCGCGATC	CTGGTTGTTG	CTGCGACTGA	CGGCCCGATG	CCGCAGACCC	50
GTGAGCACAT	CCTGCTGGGT	CGTCAGGTAG	GCGTTCCGTA	CATCATCGTG	100
TTCCTGAACA	AATGCGACAT	GGTTGATGAC	GAAGAGCTGC	TGGAAGTGGT	150
TGAGATGGAA	GTGCGTGAAC	TTCTGTCCCA	GTACGACTTC	CCGGGCGACG	200
ACACCCCGAT	CATTTCGTGT	TCTGCGCTGA	AAGCGCTGGA	AGGCGAAGCT	250
GAGTGGGAAG	AGAAAATCGT	TGAGCTGGCT	GGCTACCTGG	ATTCCTACAT	300
CCCGGAACCA	GAGCGTGC GA	TTGACAAGCC	GTTCCTGCTG	CCGATCGAAG	350
ACGTATTCTC	CATCTCCGGT	CGTGGTACCG	TTGTTACCGG	TCGTGTAGAG	400
CGCGGTATCA	TCAARGTKGG	TGAAGAAGTT	GAAATCGTGG	GTATCAAAGA	450
TACTGCGAAA	TCTACCTGTA	CCGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
ACGAAGGTCG	TGCAGGCGAG	AACTGCGGCG	TTCTGCTGCG	TGGTATCAAG	550
CGTGAAGAGA	TCCAGCGTGG	CCAGGTTCCTG	GCTAAGCCGG	GCTCAATCAA	600
GCCGCACACC	AAGTTCGAAT	CCGAAGTGTA	CATCCTGTCC	AAAGACGAAG	650
GCGGCCGTCA	CACTCCGTTT	TTCAAAGGCT	ACCGTCCGCA	GTTCTACTTC	700
CGTACAACATG	ACGTGACTGG	CACCATCGAA	CTGCCGGAAG	GCGTAGAGAT	750
GGTAATGCCG	GGCGACAACA	TCAAAATGGT	TGTTACCCTG	ATCCATCCGA	800
TCGCGATGGA	CGACGG				816

2) INFORMATION FOR SEQ ID NO: 82

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Eubacterium lentum*
 (B) STRAIN: ATCC 43055

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82

CGGCGCCTCC	TCGTTATCGC	CGCCACCGAC	GGCCCGATGG	CCCAGACCCG	50
CGAGCACATC	CTGCTCGCCC	GTCAGGTCGG	CGTGCCCTAC	ATCGTGGTCT	100
TCCTGAACAA	GTGCGACATG	GTCGACGACG	AGGAGCTCCT	CGAGCTCGTC	150
GAGATGGAAG	TTGCGGAGCT	GCTCGACTCT	TACGAGTTCC	CGGGCGACGA	200
CACCCCGATC	ATCCGCGGCT	CCGCTTTGAA	GGCCCTCGAG	GGCGACAAAG	250
AGTGGCAGGA	GAAGGTCTGG	GAGCTCATGG	ACGCCGTCGA	CTCCTACATC	300
CCGACGCCGG	AGCGCATGGT	CGACAAGCCG	TTCCTGATGG	CCGTCGAGGA	350

```

CACGATGACC ATCACCGGCC GCGGCACCGT TGCCACCGGT CGTGTGGAGC 400
GTGGTACGCT GCATGTCAAC GACCCGCTGG AGATCGTCGG TATCAAGGAG 450
ACCCAGAACA CGGTCTGCAC CCGTATCGAG ATGTTCCGCA AGCTGCTCGA 500
CGAGGCTCAG GCCGGCGACA ACATCGGCTG CCTGCTCCGC GGTGTCAAGC 550
5 GCGAGGAGAT CGTTCGCGGC CAGGTTCTCT GCAAGCCCGG TAGCGTGACC 600
CCGCACACCG AGTTCGAGGG TCAGGTCTAC ATCCTGACGA AGGAAGAGGG 650
CGGCCGCCAC ACGCCGTTCT TCGACGGCTA CCGTCCGCAG TTCTACTTCC 700
GCACGACGGA CGTGACGGGT GTTGCCCAACC TTCCCGAGGG CACCGAGATG 750
GTCATGCCGG GCGACAACGT GGAGATCAAG GCGGAGCTCA TTCACCCGAT 800
10 CGCCAGGAAG AGGGCTGCGT TCGCTAAC 828

```

2) INFORMATION FOR SEQ ID NO: 83

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 20 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 25 (A) ORGANISM: *Eubacterium nodatum*
 (B) STRAIN: ATCC 33099

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83

```

30 GGAGCAATTC TGGTTTGTGC AGCAACKGAC GGACCAATGC CTCAGACAAG 50
  AGAACATATC CTTTGTGCAA GGCAGGTAGG AGTGCCATAT ATCATCGTAT 100
  TCCTGAATAA ATGTGACATG GTGGATGAYG AAGAGCTTCT GGAAGTTGTA 150
  GAGATGGAAG TAAGAGAACT TCTCAGTGAG TATGAATTCC CGGGAGATGA 200
  TACCCCGATA GTAAGAGGTT CAGCCCTGAA GGCAGTGGAA GAACCAATG 250
35 GAGAATGGGC AGACAAGATT GTAGAGCTGA TGGAGGAAGT AGATAAATAC 300
  ATTCCTGAAC CAAAGAGAGA TAACGACAAA CCGTTCCTGA TGCCTGTAGA 350
  GGACGTATTC TCAATAACAG GAAGAGGAAC AGTAGCGACA GGAAGRGTG 400
  AAAGAGGAAT CCTGAAGGTC GGTGATGAAG TAGAAATCGT GGAATGAGC 450
  GAAGAGAGAA GAAAGGTAGT AGTAACGGGA GTTGAAATGT TCAGAAAGCT 500
40 TCTGGATGAA GCAGAGACAG GAGACAACAT CGGAGCACTG CTGAGAGGAG 550
  TTCAGAGAAC RGAGATCCAG AGAGGTCAGG TATTGGCRGC ACCTGGAACG 600
  ATCAACCCAC ATACAAAGTT CAAGGGTCAG GTATATGTAC TGAAGAAGGA 650
  AGAAGGAGGA AGGCATACGC CGTTCCTCAA YGGATACAGW CCACAGTTCT 700
  ACTTCAGAAC AACAGACGTA ACAGGAGATT TGCAGCTGCC GGAAGGARCA 750
45 GAGATGTGCA TGCCGGGAGA TAATGTGGTA ATGAACRTCA GCCTGATCAC 800
  TCCGATTGCT ATAGAAGAGG GWCTGAGATT TGCCA 835

```

50 2) INFORMATION FOR SEQ ID NO: 84

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 826 bases
 (B) TYPE: Nucleic acid
 55 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60 (vi) ORIGINAL SOURCE:

DEMANDES OU BREVETS VOLUMINEUX

LA PRÉSENTE PARTIE DE CETTE DEMANDE OU CE BREVET
COMPREND PLUS D'UN TOME.

CECI EST LE TOME 1 DE 4

NOTE: Pour les tomes additionels, veuillez contacter le Bureau canadien des brevets

JUMBO APPLICATIONS/PATENTS

THIS SECTION OF THE APPLICATION/PATENT CONTAINS MORE
THAN ONE VOLUME

THIS IS VOLUME 1 OF 4

NOTE: For additional volumes-please contact the Canadian Patent Office

DEMANDES OU BREVETS VOLUMINEUX

LA PRÉSENTE PARTIE DE CETTE DEMANDE OU CE BREVET
COMPREND PLUS D'UN TOME.

CECI EST LE TOME 2 DE 4

NOTE: Pour les tomes additionnels, veuillez contacter le Bureau canadien des brevets

JUMBO APPLICATIONS/PATENTS

THIS SECTION OF THE APPLICATION/PATENT CONTAINS MORE
THAN ONE VOLUME

THIS IS VOLUME 2 OF 4

NOTE: For additional volumes-please contact the Canadian Patent Office

(A) ORGANISM: *Ewingella americana*
 (B) STRAIN: ATCC 33852

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84

```

5      GCGATCCTGG TTGTTGCTGC AACTGATGGC CCTATGCCAC AGACTCGTGA      50
      GCACATCCTG TTGGGTCGYC AGGTTGGCGT TCCATTTCATG ATCGTATTCA      100
      TGAACAAATG CGACATGGTT GATGACGAAG AGCTGCTGGA ACTGGTAGAA      150
      ATGGAAGTTC GYGAACCTCT GTCTGCTTAC GATTTCCCAG GCGACGACAT      200
10     CCCAGTTGTT AAAGGTTTCAG CGCTGAAAGC ACTGGAAGGC GAAGCAGAGT      250
      GGAAGCTAA GATCATCGAG CTGGCTGGCC ACCTGGATAG CTACATCCCA      300
      GAACCAGAGC GTGCGATTGA CAAGCCATTC CTGCTGCCAA TCGAAGACGT      350
      ATTCTCCATC TCCGGTTCGT GTACCGTTGT TACCGGTCGT GTAGAGCGCG      400
      GTATCATCAA AGTTGGCGAA GAAGTTGAAA TCGTTGGTAT CAAGGACACT      450
15     GTTAAGTCTA CTTGTACTGG CGTTGAAATG TTCCGCAAAC TGCTGGACGA      500
      AGGCCGTGCT GGTGAGAACG TTGGTGTCTT GCTGCGTGGT ATCAAGCGTG      550
      AAGACATCGA ACGTGGTCAG GTTCTGGCTA AACCAGGTTT AATCAAACCA      600
      CACACCACWT TYGACTCAGA AGTTTATATC CTGAGCAAAG ATGAAGGCGG      650
      CCGTCATACT CCGTTCTTCA AAGGTACCG TCCACAGTTC TACTTCCGTA      700
20     CAACTGACGT GACCGGTACC ATCGAACTGC CAGAAGGCGT AGAGATGGTA      750
      ATGCCAGGTG ACAACATCAA CATGRTAGTT ACCCTGATCC ACCCAATCGC      800
      GATGGATGAC GGTCTGCGTT TCGCAA      826
  
```

25

2) INFORMATION FOR SEQ ID NO: 85

(i) SEQUENCE CHARACTERISTICS:

```

30     (A) LENGTH: 828 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear
  
```

(ii) MOLECULE TYPE: Genomic DNA

35

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Francisella tularensis*
 (B) STRAIN: LVS

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85

```

      TGGTGCTATT CTAGTATGTT CTGCTGCGGA TGGTCCTATG CCACAAACTC      50
      GTGAGCACAT TCTGCTTTCT CGTCAAGTTG GTGTACCAA AATCGTTGTT      100
      TTCTTAAACA AGTG TGACAT GGTTGATGAT GAAGAGTTAT TAGAGCTAGT      150
45     TGAGATGGAA GTTCGTGAGC TTTTAGATCA GTATGAGTTC CCAGGTGATG      200
      ACACTCCAGT TATTATGGGT TCAGCTCTTA GAGCTATTGA AGGTGACGAA      250
      GCTTACGTTG AGAAAATTGT TGAGCTAGTT CAAGCTATGG ATGACTATAT      300
      TCCTGCTCCT GAGCGTGATA CTGAGAAGCC ATTTATTCTT CCGATCGAAG      350
      ATGTATTCTC AATTTTCAGGT CGTGGTACTG TTGTAAGTGG TCGTATTGAG      400
50     CGCGGTGTAG TTAACGTTGG TGATGAAGTT GAAGTTGTTG GTATTTCGTCC      450
      AACTCAAAAA ACTACAGTAA CTGGTGTGGA AATGTTCCGT AAGCTTTTAG      500
      ATAGAGGGGA AGCTGGTGAT AACGTTGGTA TCCTAGTTCG TGGACTTAAG      550
      AGAGATGATG TTGAGCGTGG ACAAGTATTA TGTAAGCCAG GTTCAATTAA      600
      GCCACATACT AAGTTTGAAG CTGAGGTTTA TGTATTATCT AAAGAAGAGG      650
55     GTGGTAGACA TACTCCATTC TTCAAGGGAT ATAGACCACA ATTCTACTTC      700
      CGTACTACAG ACATTACTGG AGCTGTTGAG CTTCCAGAGG GTGTAGAAAT      750
      GGTATGCCT GGTGATAACG TTAAGATGAC TATCACTCTA ATTAACCCAA      800
      TCGCTAGGAT GAAGGGTTAC GTTTTGCA      828
  
```

60

2) INFORMATION FOR SEQ ID NO: 86

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Fusobacterium nucleatum* subsp. *polymorphum*
 (B) STRAIN: ATCC 10953

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86

CGGTGCTATC	ATCGTAGKTG	CTGCTACTGA	TGGTCCGATG	CCTCARACTC	50
GTGAGCAYAT	CYTGCTGGCT	CGTCAGGTAA	ACGTWCKKAG	ACTGGTTGTA	100
TTCATGAACA	AGTGYGACAT	GGTAGACGAC	GCTGAAATGY	TGGAACCTCGT	150
TGAAATGGAA	ATGCGTGAAC	TGCTTTCAGC	YTACGAATTC	GAYGGYGACA	200
ACACTCCKTT	CATTCAGGGT	TCTGCTCTTG	GTGCRTTGAA	YGGCGTTGAA	250
AAGTGGGAAG	AGAAGGTTAT	GGANCTGATG	GATGCTTGCG	ACACTTGGAT	300
TCCTTTGCCT	CCGCGTGATA	TTGAYAAACC	GTTCTTGATG	CCGGTTGAAG	350
ACGTATTCTC	AATCACTGGT	CGTGGTACTG	TAGCTACTGG	TCGTATCGAA	400
GCTGGTGTTA	TCCATGTAGG	TGACGAAGTT	GAAATCCTCG	GTTTGGGTGA	450
AGACAAGAAG	TCTGTTGTAA	CTGGTGTTGA	AATGTTCCGC	AAGTTGCTGG	500
ATCAAGGTGA	AGCTGGTGAC	AACGTAGGTY	TGTTGCTCCG	TGGTATCGAC	550
AAGAACGAAA	TCAAACGTGG	TATGGTTCTT	TGTAAGCCCG	GTCAGATTAA	600
ACCTCACTCT	AAGTTCAAAG	CTTCTATCTA	CGTTTTGAAG	AAAGAAGAAG	650
GTGGTCGTCA	CACTCCGTTT	CACAACAAAT	ACCGTCCTCA	GTTCTATCTG	700
CGTACTATGG	ACTGTACAGG	TGAAATCWCT	CTTCCGGAAG	GAAGTGAAT	750
GGTAATGCCT	GGTGATAACG	TAGAAATCAC	TGTAGAACTG	ATCTACCCGG	800
TAGCATTGAA	CGTAGGTTTG	CGTTTCGCT			829

2) INFORMATION FOR SEQ ID NO: 87

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Gemella haemolysans*
 (B) STRAIN: ATCC 10379

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87

CTATCTTAGT	AATCGCTGCT	ACAGATGGAC	CAATGGCTCA	AACTCGTGAG	50
CACATCCTAT	TATCTCGTAA	CGTTGGAGTA	CCAAAAATCG	TTGTATTCTT	100
AAACAAATGT	GATATGGTTG	ATGACGAAGA	GTTATTAGAA	TTAGTTGAAA	150
TGGAAGTTCG	TGAAGTATTA	TCTGAATACG	GATTCGACGG	AGATGAAGTA	200
CCAGTAATCA	AAGGTTCTGC	TCTTAAAGCT	CTTGAAGGAG	ATGCAGATGC	250
AGAAAAAGCT	ATCATCGAAT	TAATGGAAAC	AGTTGACGAA	TACATCCCAA	300
CTCCAGAACG	TGATAACGCT	AAACCATTCA	TGATGCCAGT	TGAGGACGTA	350

```

TTCTCAATCA CAGGTCGTGG TACAGTTGCT ACTGGACGTG TTGAACGTGG 400
ACAAGTTAAA GTTGGAGACG TAGTAGAAAT CGTTGGATTA ACTGAAGAAC 450
CAGCTTCAAC TACTGTAACA GGTGTTGAAA TGTTCGTAA ATTATTAGAT 500
TACGCTGAAG CAGGAGATAA CATCGGTGCA TTATTACGTG GTGTTGCTCG 550
5 TGAAGACATC GAACGTGGAC AAGTTTtagc AGCTCCTAAA ACAATCACTC 600
CACACACTCA ATTCGTAGCT GACGTGTACG TATTATCTAA AGAAGAAGGT 650
GGACGTCACA CTCCATTCTT CACAAACTAC CGTCCTCAAT TCTACTTCCG 700
TACTACTGAC GTAACGGTG TAGTTACTTT ACCAGAAGGT ACTGAAATGG 750
TAATGCCTGG GGATAACGTA TCAATCAACG TAGAACTTAT TTCTCCAATC 800
10 GCGATCGAAG AAGGAACTCG TTTCTCAA 828

```

2) INFORMATION FOR SEQ ID NO: 88

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 823 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Gemella morbillorum*
 (B) STRAIN: ATCC 27824

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88

```

30 TCTTAGTAAT CGCTGCTACA GATGGTCCTA TGGCTCAAAC TCGTGAACAC 50
ATCCTATTAT CTCGTAACGT TGGAGTACCT AAAATTGTTG TATTCTTAAA 100
CAAATGTGAT ATGGTTGATG ACGAAGAGTT ATTAGAATTA GTAGAAATGG 150
AAGTTCGTGA ACTATTATCT GAATACGGAT TTGATGGAGA TGAAC TACCA 200
GTAATCAAAG GTTCAGCTCT TAAAGCTCTT GAAGGAGATG CAGATGCTGA 250
35 AAAAGCTATC ATCGAATTAA TGGAAACAGT TGACGAGTAC ATCCCAACTC 300
CAGAACGTGA TAACGCTAAA CCATT TATGA TGCCAGTTGA GGACGTGTTC 350
TCAATCACAG GTCGTGGTAC AGTTGCTACT GGACGTGTTG AACGTGGACA 400
AGTTAAAGTT GGTGACGTAG TAGAAATCGT TGGATTAACT GAAGAACCAG 450
CTTCAACTAC TGTAACAGGT GTTGAAATGT TCCGTAAATT ATTAGATTAC 500
40 GCTGAAGCAG GAGATAACAT CGGTGCATTA TTACGTGGTG TTGCTCGTGA 550
AGATATCGAA CGTGGACAAG TTTTAGCAGC TCCTAAAACA ATCACTCCAC 600
ATACTCAATT CGTAGCTGAT GTGTACGTAT TATCTAAAGA AGAAGGTGGA 650
CGTCACACTC CATTCTTCAC AAAC TACC GT CCACAATTCT ACTTCCGTAC 700
TACTGACGTA ACTGGTGTAG TTA CTTTACC AGAAGGTACT GAAATGGTAA 750
45 TGCCTGGGGA CAACGTATCA ATCAACGTAG AACTTATTTC TCCAATCGCT 800
ATCGAAGAAG GAACTCGTTT CTC 823

```

50 2) INFORMATION FOR SEQ ID NO: 89

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Haemophilus actinomycetemcomitans*
 (B) STRAIN: ATCC 33384

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89

```

5  GCTATCTTAG TAGTAGCAGC AACCGACGGT CCTATGCCAC AAACCTCGTGA      50
   GCACATCTTA TTAGGTCGCC AAGTAGGTGT TCCTTACATC ATCGTATTCT      100
   TAAACAAATG CGACATGGTA GATGACGAAG AGTTATTAGA ATTAGTTGAA      150
   ATGGAAGTTC GTGAACTTCT TTCTCAATAT GACTTCCCGG GCGATGACAC      200
10  CCCAATCGTA CGCGGTTCTG CATTAAAAGC GCTTGAAGGC GATGCCGCAT      250
   GGGGAAGAAA AATCCTTGAA TTAGCAAACC ATTTAGATAC TTACATCCCG      300
   GAACCTGAGC GTGCTATCGA CCAACCGTTC CTTCTTCCAA TTGAAGATGT      350
   GTTCTCTATC TCCGGTTCGT GTACCGTAGT AACGGGTCGT GTTGAGCGCG      400
   GTATCATCCG TACCGGTGAT GAAGTTGAAA TCGTGGGTAT CAAACCGACT      450
15  GCAAAAACCA CCGTAACCGG TGTTGAAATG TTCCGTAAAT TACTTGACGA      500
   AGGTCGTGCG GGTGAAAACA TCGGTGCATT ATTGCGTGGT ACTAAACGTG      550
   AAGAAATCGA ACGTGGTCAG GTATTGGCGA AACCGGGGTC AATCACCCCG      600
   CACACTGACT TCGAATCTGA AGTGATACGTA TTGTCCAAAG AAGAAGGTGG      650
   TCGTCATACT CCATTCTTCA AAGGTTACCG TCCACAATTC TATTTCCGTA      700
20  CAACTGACGT AACC GG TACT ATCGAGTTAC CTGAAGGCGT GGAAATGGTT      750
   ATGCCTGGCG ATAACATCAA AATGACCGTA TCCTTAATTC ACCCAATTGC      800
   GATGGACCAA GGTTTACGTT TCGCTATCG      829

```

25 2) INFORMATION FOR SEQ ID NO: 90

(i) SEQUENCE CHARACTERISTICS:

```

30  (A) LENGTH: 833 bases
   (B) TYPE: Nucleic acid
   (C) STRANDEDNESS: Double
   (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Haemophilus aphrophilus*
 (B) STRAIN: ATCC 33389

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90

```

   TGGTGCTATC TTAGTAGTAG CAGCAACTGA TGGTCCTATG CCACAAACTC      50
   GTGAGCACAT CTTATTAGGT CGCCAAGTAG GTGTTCTTCA CATCATCGTA      100
   TTCTTAAACA AATGCGACAT GGTAGATGAC GAAGAGTTAT TAGAATTAGT      150
45  TGAAATGGAA GTTCGTGAAC TTCTTTCTCA ATATGACTTC CCGGGTGATG      200
   ATACACCAAT CGTACGTGGT TCTGCATTAC AAGCGTTAAA CGGCGTTGCA      250
   GAATGGGAAG AAAAAATCCT TGAATTAGCA AACC ACTTAG AACTTACAT      300
   TCCTGAGCCA CAACGTGCTA TCGACCAACC GTTCCTTCTT CCAATTGAAG      350
   ACGTGTTCTC TATCTCCGGT CGTGGTACTG TAGTAACAGG TCGTGTTGAG      400
50  CGTGGTATCA TCCGTACCGG TGATGAAGTT GAAATCGTAG GTATCAAACC      450
   GACTGCGAAA ACTACCGTAA CCGGTGTTGA AATGTTCCGT AAATTACTTG      500
   ACGAAGGTCG TGCAGGTGAA AACATCGGTG CATTATTACG TGGCACTAAA      550
   CGTGAAGAAA TCGAACGTGG TCAAGTATTG GCTAAACCGG GCTCAATCAC      600
   TCCGCACACT GATTTCGAAT CTGAAGTGTA CGTATTATCC AAAGAAGAAG      650
55  GTGGTCGTCT TACTCCATTC TTCAAAGGTT ACCGTCCACA ATTCTATTTC      700
   CGTACCAACTG ACGTAACCGG TACTATCGAG TTACCGGAAG GCGTGAAAT      750
   GGTATGCCTT GGCGATAACA TCAAAATGAC TGTATCCTTA ATCCACCCAA      800
   TCGCGATGGA CCAAGGTTTA CGTTTCGCTA TCG      833

```

2) INFORMATION FOR SEQ ID NO: 91

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 815 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Haemophilus ducreyi*
 (B) STRAIN: DSM 8925

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91

	CGGCGCTATC	TTAGTTGTAG	CAGCAACTGA	TGGTCCTATG	CCTCAAACCTC	50
	GTGAACACAT	CTTATTAGGC	CGCCAAGTTG	GTGTTCCCTA	CATCATCGTA	100
20	TTCTTAAATA	AATGCGATAT	GGTAGATGAT	GAAGAATTAT	TAGAATTAGT	150
	TGAAATGGAA	GTTTCGTGAAC	TTCTTTCTCA	ATATGATTTC	CCAGGTGACG	200
	ATACTCCTAT	CGTTCGTGGT	TCAGCATTAC	AAGCATTAAA	TGGTGTGCCT	250
	GAGTGGGAAG	AAAAAATCAT	TGAATTAGCA	CAACACTTAG	ATTCTTATAT	300
	CCCTGAGCCT	GAGCGTGCGA	TTGATAAACC	TTTCTTATTA	CCAATCGAAG	350
25	ACGTATTCTC	AATTTTCAGGT	CGTGGTACAG	TAGTAACCGG	TCGTGTTGAG	400
	CGTGGTATCA	TCAAATCAGG	TGAAGAAGTT	GAAATCGTAG	GGATTAAAGA	450
	AACGACAAAA	ACAACAGTAA	CCGGTGTGTA	GATGTTCCGT	AAACTATTAG	500
	ACGAAGGTCG	TGCGGGTGAA	AACGTAGGTG	CCTTATTACG	TGGTACTAAA	550
	CGTGAAGAAA	TCGAACGTGG	TCAAGTATTA	GCGAAACCAG	GTACAATTAC	600
30	ACCACACACT	GATTTTGAAT	CAGAAGTTTA	TGTATTATCA	AAAGAAGAAG	650
	GTGGTCGTCA	TACTCCATTTC	TTCAAAGGTT	ATCGTCCTCA	GTTCTACTTC	700
	CGYACAACGG	ACGTAACAGG	AACGATTGAA	TTACCTGAAG	ATGTTGAGAT	750
	GGTAATGCCT	GGTGATAATA	TCAAGATGAC	AGTAAGCTTA	ATTCACCCTA	800
35	TCGCGATGGA	CGAAG				815

2) INFORMATION FOR SEQ ID NO: 92

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 830 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Haemophilus haemolyticus*
 (B) STRAIN: ATCC 33390

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92

	TGGTGCTATC	TTAGTAGTAG	CAGCAACTGA	TGGTCCAATG	CCACAAACTC	50
55	GTGAGCACAT	CTTATTAGGT	CGCCAAGTAG	GTGTTCCATA	CATCATCGTA	100
	TTCTTAAACA	AATGCGACAT	GGTAGATGAC	GAAGAGTTAT	TAGAATTAGT	150
	AGAAATGGAA	GTTTCGTGAAC	TTCTTTCTCA	ATATGACTTC	CCAGGTGACG	200
	ATACACCAAT	CGTACGTGGT	TCTGCATTAC	AAGCATTAAA	TGGCGTAGCA	250
	GAATGGGAAG	AAAAAATCCT	TGAGTTAGCA	AACCACTTAG	ATACTTACAT	300
60	CCCAGAACCA	GAGCGTGCAA	TTGACCAACC	GTTCTTCTT	CCAATCGAAG	350

```

5  ATGTGTTCTC AATCTCAGGT CGTGGTACAG TAGTAACTGG TCGTGTAGAA 400
   CGTGGTATCA TCCGTACTGG TGATGAAGTA GAAATCGTAG GTATCAAAGA 450
   TACAGCAAAA ACTACTGTAA CGGGTGTTGA AATGTTCCGT AAATTACTTG 500
   ACGAAGGTCG TGCAGGTGAA AACATCGGTG CATTATTACG TGGTACCAA 550
   CGTGAAGAAA TCGAACGTGG TCAAGTATTA GCGAAACCAG GTTCAATCAC 600
   GCCACACACT GACTTCGAAT CAGAAGTTTA TGTATTATCA AAAGAAGAAG 650
   GTGGTCGTCA TACTCCATTC TTCAAAGGTT ACCGTCCACA ATTCTATTTT 700
   CGTACAAC TG ACGTAACTGG TACTATCGAG TTACCAGAAG GCGTAGAAAT 750
   GGTAATGCCA GGCGATAACA TCAAGATGAC AGTAAGCTTA ATCCACCCAA 800
10 TCGCGATGGA CCAAGGTTTA CGTTTCGCAA 830

```

2) INFORMATION FOR SEQ ID NO: 93

15

(i) SEQUENCE CHARACTERISTICS:

```

   (A) LENGTH: 824 bases
   (B) TYPE: Nucleic acid
   (C) STRANDEDNESS: Double
20  (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

```

25  (A) ORGANISM: Haemophilus parahaemolyticus
   (B) STRAIN: ATCC 10014

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93

```

30  TCTTAGTAGT AGCAGCAACA GACGGTCCAA TGCCACAAAC TCGTGAGCAC 50
   ATCTTATTAG GTCGCCAAGT AGGTGTTCCA TACATCATCG TATTCTTAA 100
   CAAATGCGAT ATGGTTGACG ATGAAGAATT ATTAGAATTA GTTGAAATGG 150
   AAGTGCGTGA ACTTCTTTCA CAATATGACT TCCCAGGTGA TGACACGCCA 200
   GTAGTACGTG GTTCAGCGTT ACAAGCGTTA AACGGCGTAG CAGAGTGGGA 250
35  AGAAAAAATT CTTGAATTAG CAAACCACTT AGATACATAC ATCCAGAGC 300
   CAGAGCGTGC GATTGATAAA CCATTCTTAT TACCAATCGA AGACGTATTC 350
   TCAATCTCAG GTCGTGGTAC AGTAGTAACA GGTTCGTGTTG AGCGTGGTAT 400
   CATCAAAGCG GGTGAAGAAG TTGAAATCGT AGGTATCAA GACACTGCGA 450
   AAACAACAGT AACTGGCGTG GAAATGTTCC GTAAATTATT AGACGAAGGT 500
40  CGTGCGGGTG AAAACGTTGG TGCATTATTA CGTGGTACAA AACGTGAAGA 550
   AATCGAACGT GGTCAAGTGT TAGCGAAACC AGGTACAATT ACACCACACA 600
   CAGACTTCGA ATCAGAAGTG TACGTATTAT CAAAAGAAGA AGGTGGTCGT 650
   CACACTCCAT TCTTCAAAGG TTACCGTCCA CAATTCTACT TCCGTACAAC 700
   TGACGTAAC TGGTACTATTG AATTACCAGA AGGCGTAGAA ATGGTAATGC 750
45  CAGGCGATAA CATCAAATG ACAGTATCAT TAATCCACCC AATCGCGATG 800
   GACGAAGGTT TACGTTTTCG GATT 824

```

50 2) INFORMATION FOR SEQ ID NO: 94

(i) SEQUENCE CHARACTERISTICS:

```

   (A) LENGTH: 833 bases
   (B) TYPE: Nucleic acid
55  (C) STRANDEDNESS: Double
   (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

60 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Haemophilus parainfluenzae*
 (B) STRAIN: ATCC 7901

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94

```

5      TGGTGCCTATC TTAGTAGTAG CAGCAACTGA TGGTCCTATG CCACAAACTC      50
      GTGAGCACAT CTTATTAGGT CGCCAAGTAG GTGTTTCCTTA CATCATCGTG      100
      TTCTTAAACA AATGCGACAT GGTAGATGAC GAAGAGTTAT TAGAATTAGT      150
      TGAAATGGAA GTTCGTGAAC TTCTTTCTCA ATATGACTTC CCGGGTGACG      200
10     ATACACCAAT CGTACGTGGT TCTGCATTAC AAGCGTTAAA CGGCGTWGCA      250
      GAATGGGAAG AAAAAATCCT TGAATTAGCT AGCCACTTAG ATTCTTACAT      300
      TCCTGAGCCT CAACGTGCTA TCGACCAACC GTTCCTTCTT CCAATCGAAG      350
      CGTGTTCTC TATCTCCGGT CGTGGTACAG TAGTAACAGG TCGTGTGAG      400
      CGTGGTATCA TCCGTACCGG TGATGAAGTT GAAATCGTAG GTATCAAACC      450
15     GACTGCGAAA ACTACCGTAA CCGGTGTTGA AATGTTCCGT AAATTACTTG      500
      ACGAAGGTCG TGCAGGTGAA AACATCGGTG CATTATTACG TGGTACYAAA      550
      CGTGAAGAAA TCGAACGTGG TCAAGTATTG GCTAAACCGG GTTCAATCAC      600
      TCCACACACT GATTTCGAAT CTGAAGTGTA CGTATTATCC AAAGAAGAAG      650
      GTGGTCGTCA TACTCCATTC TTCAAAGGTT ACCGTCCACA ATTCTATTTT      700
20     CGTACAAC TGACGTAAACCGG TACTATCGAA TTACCGGAAG GCGTGGAAT      750
      GGTATGCCT GGTGATAACA TCAAATGAC TGTATCCTTA ATCCACCCAA      800
      TCGCGATGGA CCAAGGTTTA CGTTTCGCTA TCG      833
  
```

25 2) INFORMATION FOR SEQ ID NO: 95

(i) SEQUENCE CHARACTERISTICS:

```

30     (A) LENGTH: 824 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear
  
```

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

```

      (A) ORGANISM: Haemophilus paraphrophilus
      (B) STRAIN: ATCC 29241
  
```

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95

```

      TGGTGCCTATC TTAGTAGTAG CAGCAACTGA TGGTCCTATG CCACAAACTC      50
      GTGAGCACAT CTTATTAGGT CGCCAAGTAG GTGTTTCCTTA CATCATCGTA      100
      TTCTTAAACA AATGCGACAT GGTAGATGAC GAAGAGTTAT TAGAATTAGT      150
45     TGAAATGGAA GTTCGTGAAC TTCTTTCTCA ATATGACTTC CCGGGTGACG      200
      ATACGCCAAT CGTACGTGGT TCTGCATTAC AAGCGTTAAA CGGCGTTGCA      250
      GAATGGGAAG AAAAAATCCT TGAATTAGCA AACCATTGG ATACTTACAT      300
      TCCTGAGCCA CAACGTGCTA TCGACCAACC GTTCCTTCTT CCAATCGAAG      350
      ACGTGTTCTC TATCTCCGGT CGTGGTACAG TAGTAACAGG TCGTGTGAG      400
50     CGTGGTATCA TCCGTACCGG TGATGAAGTT GAAATCGTAG GTATCAAACC      450
      GACTGCGAAA ACTACCGTAA CCGGTGTTGA AATGTTCCGT AAATTACTTG      500
      ACGAAGGTCG TGCAGGTGAA AACATCGGTG CATTATTACG TGGTACCAAA      550
      CGTGAAGAAA TCGAACGTGG TCAAGTATTG GCTAAACCGG GTTCAATCAC      600
      TCCACACACT GATTTCGAAT CTGAAGTGTA CGTATTATCC AAAGAAGAAG      650
55     GTGGTCGTCA TACTCCATTC TTCAAAGGTT ACCGTCCACA ATTCTATTTT      700
      CGTACAAC TGACGTAAACCGG TACTATCGAG TTACCGGAAG GTGTGGAAT      750
      GGTAAATGCCT GGCGATAACA TCAAATGAC CGTATCCTTA ATCCACCCAA      800
      TCGCGATGGA CCAAGGTTTA CGTT      824
  
```


2) INFORMATION FOR SEQ ID NO: 96

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 818 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Haemophilus segnis*
 (B) STRAIN: ATCC 33393

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96

```

GCTATCTTAG TAGTAGCAGC AACTGATGGT CCTATGCCAC AACTCGTGA      50
GCACATCTTA TTAGGTCGCC AAGTAGGTGT TCCTTACATC ATCGTATTCT      100
20 TAAACAAATG CGACATGGTA GATGACGAAG AGTTATTAGA ATTAGTTGAA      150
ATGGAAGTTC GTGAACTTCT TTCTCAATAT GACTTCCCAG GTGATGATAC      200
TCCAATCATT CGTGGTTCTG CATTACAAGC GTTAAACGGC GTAGCAGAAT      250
GGGAAGAAAA AATCCTTGAA TTAGCTCAAG CATTAGATAC TTACATTCCT      300
GAACCTGAGC GTGCAATCGA CCAACCGTTC CTTCTTCCAA TTGAAGACGT      350
25 GTTCTCAATC TCTGGTCGTG GTACTGTAGT AACAGGTCGT GTAGAGCGTG      400
GTATCATCCG TACCGGTGAT GAAGTTGAAA TCGTTGGTAT CAAACCAACT      450
GCGAAAACAA CCGTAACCGG TGTTGAAATG TTCCGTAAAT TACTTGACGA      500
AGGTCGTGCA GGTGAAAACA TCGGTGCATT ATTACGTGGT ACTAAACGTG      550
AAGAAATCGA ACGTGGTCAA GTATTAGCGA AACC GG GTTC AATCACTCCA      600
30 CACACTGACT TCGAATCTGA AGTG TACGTA TTATCTAAAG AAGAAGGTGG      650
TCGTCATACT CCATTCTTCA AAGGTTACCG TCCACAATTC TATTTCCGTA      700
CAACTGACGT AACC GG TACT ATCGAGTTAC CGGAAGGCGT GGAAATGGTT      750
ATGCCTGGCG ATAACATCAA AATGACCGTA TCCTTAATCC ACCCAATCGC      800
GATGGACCAA GGT TTACG      818
35

```

2) INFORMATION FOR SEQ ID NO: 97

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 763 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Hafnia alvei*
 (B) STRAIN: ATCC 13337

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97

```

CGGCGCTATC CTGGTTGTTG CTGCGACTGA CGGCCCTATG CCTCAGACTC      50
55 GTGAGCACAT CCTGCTGGGT CGTCAGGTTG GCGTTCCTTW CATCATCGTR      100
TTCCTGAACA AATGCGACAT GGTTGATGAT GAAGAGCTGC TGGAAC TGGT      150
AGAAATGGAA GTTCGTGAAC TTCTGTCTCA GTACGACTTC CCWGGYGATG      200
ATACTCCAAT CATCCGTGGT TCTGCTCTGA AAGCGCTGGA AGGYGMACCT      250
GAGTGGGAAG CTAAGATCGT AGAACTGGCT GAAACTCTGG ATTCTTACAT      300
60 YCCACARCCA GAACGTGCTA TCGAYAAGCC ATTCCTGCTG CCAATCGAAG      350

```

	ACGTATTCTC	TATCTCTGGC	CGTGGTACWG	TTGTTACCGG	TCGTGTAGAG	400
	CGCGGTATCG	TTAAAGTTGG	TGAAGAAATT	GARATCGTTG	GTATCAAAGA	450
	TACCGTTAAA	TCAACTTGTA	CCGGCGTTGA	AATGTTCCGT	AAACTGCTGG	500
	ACGAAGGTCG	TGCAGGCGAG	AACGTTGGTG	TTCTGCTGCG	TGGTATCAAG	550
5	CCTGAAGACA	TCGAACGTGG	TCAGGTTCTG	GCTAAACCAG	GYTCYATCAA	600
	GCCACACACC	AAGTTCGAAT	CAGAAGTTTA	TATTCTGAGC	AAAGATGAAG	650
	GCGGYCGTCA	TACTCCGTTT	TTCAAAGGCT	ACCGTCCACA	GTTCTACTTC	700
	CGTACAACTG	ACGTGACCGG	TACCATCGAA	TTGCCAGAAG	GCGTGGAAAT	750
	GGTAATGCCA	GGC				763

10

2) INFORMATION FOR SEQ ID NO: 98

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

25 (A) ORGANISM: *Kingella kingae*
 (B) STRAIN: ATCC 23330

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98

	CGGCGCAATC	TTGGTATGTT	CAGCAGCTGA	CGGTCCTATG	CCACAAACTC	50
30	GCGAACACAT	CTTGTTGGCT	CGCCAAGTAG	GTGTACCTTA	TATCATCGTA	100
	TTCATGAACA	AATGCGACAT	GGTCGATGAT	GCTGAGTTGT	TGGAATTGGT	150
	TGAAATGGAA	ATCCGTGACT	TGTTGTCTAG	CTACGATTTT	CCAGGCGACG	200
	ATTGCCCAAT	CGTTCAAGGT	TCTGCATTGC	GYGCATTGGA	AGGCGACGCT	250
	GCATACAAAG	AAAAAATCTT	TGAATTGGCT	GCTGCTTTGG	ATAGCTACAT	300
35	TCCTACTCCA	GAACGTGCTG	TTGATAAACC	ATTCTTGTTG	CCAATCGAAG	350
	ATGTATTCTC	TATCTCTGGT	CGTGGTACAG	TAGTTACTGG	TCGTGTAGAG	400
	CGCGGTATCA	TCAAAGTAGG	CGAAGAGATT	GAAATCGTTG	GTTTGAAAGA	450
	CACGCAAAAA	ACCACTTGTA	CTGGCGTGGA	AATGTTCCGC	AAATTGTTGG	500
	ACGAAGGTCA	AGCTGGTGAT	AACGTTGGTG	TATTATTGCG	TGGTACGAAG	550
40	CGTGAAGACG	TTGAACGTGG	TCAGGTATTG	GCTAAACCAG	GTTCTATCAC	600
	TCCGCACACT	AAATTTGAAG	CTGAAGTGTA	TGTGTTGAGC	AAAGAAGAAG	650
	GTGGCCGTC	TACGCCATTC	TTTCGCTAAT	ACCGCCAC	ATTCTACTTC	700
	CGTACGACTG	ACGTAACTGG	TGCAGTTACT	TTGTCTGAGG	GTGTGGAAAT	750
	GGTTATGCCA	GGCGAAAACG	TGAAAATCAC	TGTTGAGTTG	ATTGCACCTA	800
45	TCGCTAGGAA	AACGGTTTGC	GTTTTGCG			828

2) INFORMATION FOR SEQ ID NO: 99

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

60 (A) ORGANISM: *Klebsiella ornithinolytica*

(B) STRAIN: ATCC 31898

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99

5	GGCGCGATCC	TGGTTGTTGC	TGCGACTGAC	GGCCCGATGC	CGCAGACTCG	50
	TGAGCACATC	CTGCTGGGTC	GTCAGGTAGG	CGTTCCGTAC	ATCATCGTGT	100
	TCCTGAACAA	ATGCGACATG	GTTGATGACG	AAGAGCTGCT	GGAGCTGGTT	150
	GAAATGGAAG	TCCGTGAGCT	GCTGTCTCAG	TACGACTTCC	CGGGCGACGA	200
	CACGCCGATC	GTTTCGTGGTT	CCGCTCTGAA	AGCGCTGGAA	GGCGAAGCAG	250
10	ACTGGGAAGC	GAAAATCATC	GAAGTGGCTG	GCTACCTGGA	TTCTTACATC	300
	CCGGAACCAG	AGCGTGCGAT	TGACAAGCCG	TTCCTGCTGC	CGATCGAAGA	350
	CGTATTCTCC	ATCTCCGGTC	GTGGTACCGT	TGTTACCGGT	CGTGTAGAGC	400
	GCGGTATCAT	CAAAGTGGGC	GAAGAAAGTTG	AAATCGTTGG	TATCAAAGAG	450
	ACTGCGAAGT	CTACCTGTAC	TGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	500
15	CGAAGGCCGT	GCTGGTGAGA	ACGTTGGTGT	TCTGCTGCGT	GGTATCAAAC	550
	GTGAAGAAAT	CGAACGTGGT	CAGGTACTGG	CTAAGCCGGG	CTCTATCAAG	600
	CCGCACACCA	AGTTCGAATC	TGAAGTGTA	ATTCTGTCCA	AAGACGAAGG	650
	CGGCCGTCT	ACTCCGTTCT	TCAAAGGCTA	CCGTCCGCAG	TTCTACTTCC	700
	GTACAACTGA	CGTGACTGGC	ACCATCGAAC	TGCCGGAAGG	CGTAGAGATG	750
20	GTCATGCCGG	GCGACAACAT	CAAAATGGTT	GTTACCCTGA	TTCACCCGAT	800
	CGCGATGGAC	GATGGTCTGC	GTTTCGCA			826

25 2) INFORMATION FOR SEQ ID NO: 100

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 749 bases
	(B)	TYPE: Nucleic acid
30	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

(A)	ORGANISM: <i>Klebsiella oxytoca</i>
(B)	STRAIN: ATCC 33496

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100

40	GATGCCGCAG	ACTCGTGAGC	ACATCCTGCT	GGGTCGTCAG	GTAGGCGTTC	50
	CGTACATCAT	CGTGTTCTCTG	AACAAGTGCG	ACATGGTTGA	TGACGAAGAG	100
	CTGCTGGAAC	TGGTTGAAAT	GGAAGTTCGT	GAAGTCTGT	CTCAGTACGA	150
	TTTCCCGGGC	GACGACACTC	CGATCGTTTCG	TGGTTCGCT	CTGAAAGCGC	200
45	TGGAAGGCGA	CGCWGAGTGG	GAACKKAAA	TCATCGAACT	GGCTGGCTTC	250
	CTGGATTCTT	ACATTCGGGA	ACCAGAGCGT	GCGATTGACA	AGCCGTTCTCT	300
	GCTGCCGATC	GAAGACGTAT	TCTCCATCTC	CGGTCGTGGT	ACCGTTGTTA	350
	CCGGTCGTGT	AGAGCGCGGT	ATCATCAAAG	TTGGCGAAGA	AGTTGAAATY	400
	GTTGGTATYA	AAGACACTGC	TAAGTCTACC	TGTACTGGCG	TTGAAATGTT	450
50	CCGCAAACTG	CTGGACGAAG	GCCGYGCTGG	TGAGAACGTT	GGTGTCTCTGC	500
	TGCGTGGTAT	CAAACGTGAA	GAAATCGAAC	GTGGTCAGGT	ACTGGCTAAG	550
	CCGGGCTCTA	TCAAGCCGCA	CACCAAGTTC	GAATCTGAAG	TTTATATCCT	600
	GTCCAAAGAC	GAAGGCGGCC	GTCACACTCC	GTTCTTCAA	GGCTACCGTC	650
	CGCAGTTCTA	CTTCCGTACA	ACTGACGTGA	CTGGCACCAT	CGAACTGCCG	700
55	GAAGGCGTAG	AGATGGTTAT	GCCGGGCGAC	AACATCAAAA	TGGTTGTTA	749

2) INFORMATION FOR SEQ ID NO: 101

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 830 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella planticola*
 (B) STRAIN: ATCC 33531

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101

```

15  TGGCGCGATC CTGGTTGTTG CTGCGACTGA CGGCCCGATG CCGCAGACTC      50
    GTGAGCACAT CCTGCTGGGT CGTCAGGTAG GCGTTCCGTA CATCATCGTG      100
    TTCCTGAACA AATGCGACAT GGTTGATGAC GAAGAGCTGC TGGAAGTGGT      150
    TGAAATGGAA GTTCGTGAGC TGCTGTCTCA GTACGACTTC CCGGGCGACG      200
    AACTCCGAT  CGTTCGTGGT TCCGCTCTGA AAGCGCTGGA AGGCGAAGCA      250
20  GACTGGGAAG CGAAAATCAT CGAACTGGCT GGCTACCTGG ATTCTTACAT      300
    CCCGGAACCA GAGCGTGCGA TTGACAAGCC GTTCCTGCTG CCTATCGAAG      350
    ACGTATTCTC CATCTCCGGT CGTGGTACCG TTGTTACCGG TCGTGTAAG      400
    CGCGGTATCA TCAAAGTGGG CGAAGAAGTT GAAATCGTTG GTATCAAAGA      450
    TACTGCTAAR TCWACCTGTA CYGGCGTTGA AATGTTCCGC AAAGTGTG      500
25  ACGAAGGCCG TGCTGGTGAG AACGTTGGTG TTCTGCTGCG TGGTATCAA      550
    CGTGAAGAAA TCGAACGTGG TCAGGTACTG GCTAAGCCGG GCTCTATCAA      600
    GCCGCACACC AAGTTCGAAT CTGAAGTGTA CATTCGTGCC AAAGACGAAG      650
    GCGGCCGTCA TACTCCGTTT TTCAAAGGCT ACCGTCCGCA GTTCTACTTC      700
    CGTACAACATG ACGTGACTGG CACCATCGAA CTGCCGGAAG GCGTAGAGAT      750
30  GGTAAATGCCG GCGGACAACA TCAAATGGT TGTACCCTG ATTCAACCRA      800
    TCGCGATGGA CGACGGTCTG CGTTTCGCAA      830
  
```

35 2) INFORMATION FOR SEQ ID NO: 102

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 806 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae* subsp. *ozaenae*
 (B) STRAIN: ATCC 11296

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102

```

50  CCTGGTTGTT GCTGCGACTG ACGGCCCGAT GCCGCAGACT CGTGAGCACA      50
    TCCTGCTGGG TCGTCAGGTA GCGTTCGGT ACATCATCGT GTTCCTGAAC      100
    AAATGCGACA TGGTTGATGA CGAAGAGCTG CTGGAAGTGG TTGAGATGGA      150
    AGTTCGTGAA CTGCTGTCTC AGTACGATTT CCCGGGCGAC GACACCCCGA      200
55  TCGTTCGTGG TTCTGCTCTG AAAGCGCTGG AAGGCGACGC AGAGTGGGAA      250
    GCGAAAATCA TCGAACTGGC TGGCCACCTG GATACCTATA TCCCGBAACC      300
    AGAGCGTGCG ATTGACAAGC CGTTCCTGCT GCCGATCGAA GACGTATTCT      350
    CCATCTCCGG TCGTGGTACC GTTGTACCG GTCGTGTAGA GCGCGGTATC      400
    ATCAAAGTAG GTGAAGAAGT TGAAATCGTT GGTATCAAAG AAACCGCGAA      450
60  AACCACCTGT ACTGGCGTTG AAATGTTCCG CAACTGCTG GACGAAGGCC      500
  
```

```

GTGCTGGTGA GAACGTAGGT GTTCTGCTGC GTGGTATCAA ACGTGAAGAA 550
ATCGAACGTG GTCAGGTACT GGCTAAGCCG GGCACCATCA ACCCGCACAC 600
CAAGTTCGAA TCTGAAGTGT ACATCCTGTC CAAAGACGAA GGCGGCCGTC 650
ATACTCCGTT CTTCAAAGGC TACCGTCCGC AGTTCCTACTT CCGTACTACT 700
5 GACGTGACTG GCACCATCGA ACTGCCGGAA GCGGTAGAGA TGGTAATGCC 750
GGGCGACAAC ATCAAATGG TTGTTACCCT GATCCACCCG ATCGCGATGG 800
ACGACG 806

```

10

2) INFORMATION FOR SEQ ID NO: 103

(i) SEQUENCE CHARACTERISTICS:

```

15 (A) LENGTH: 743 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

```

(A) ORGANISM: Klebsiella pneumoniae subsp. pneumoniae
(B) STRAIN: ATCC 13883

```

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103

```

GCAGACTCGT GAGCACATCC TGCTGGGTCG TCAGGTAGGC GTTCCGTACA 50
TCATCGTGTT CCTGAACAAA TGCGACATGG TTGATGACGA AGAGCTGCTG 100
GAACTGGTTG AGATGGAAGT TCGTGAAGTCTGCTCTCAGT ACGATTTCCTC 150
30 GGGCGACGAC ACTCCGATCG TTCGTGGTTC TGCTCTGAAA GCGCTGGAAG 200
GCGACGCAGA GTGGGAAGCG AAAATCATCG AACTGGGCTGG CCACCTGGAT 250
ACCTATATCC CGGAACCAGA GCGTGCGATT GACAAGCCGT TCCTGCTGCC 300
GATCGAAGAC GTATTCTCCA TCTCCGGTCG TGGTACCGTT GTTACCGGTC 350
GTGTAGAGCG CCGTATCATC AAAGTAGGTG AAGAAGTTGA AATCGTTGGT 400
35 ATCAAAGAAA CCGCGAAAAC CACCTGTACT GGC GTTGAAA TGTTCCGCAA 450
ACTGCTGGAC GAAGGCCGTG CTGGTGAGAA CGTAGGTGTT CTGCTGCGTG 500
GTATCAAACG TGAAGAAATC GAACGTGGTC AGGTACTGGC TAAGCCGGGC 550
ACCATCAACC CGCACACCAA GTTCGAATCT GAAGTGTAAC TCCTGTCCAA 600
AGACGAAGGC GGCCGTCACA CTCCGTTCTT CAAAGGCTAC CGTCCGCAGT 650
40 TCTACTTCCG TACTACTGAC GTGACTGGCA CCATCGAACT GCCGGAAGGC 700
GTAGAGATGG TAATGCCGGG CGACAACATC AAAATGGTTG TTA 743

```

45 2) INFORMATION FOR SEQ ID NO: 104

(i) SEQUENCE CHARACTERISTICS:

```

50 (A) LENGTH: 819 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

55 (vi) ORIGINAL SOURCE:

```

(A) ORGANISM: Klebsiella pneumoniae subsp. rhinoscleromatis
(B) STRAIN: ATCC 13884

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104

60

```

5  TGGTTGTTGC TGC GACTGAC GGCCCGATGC CGCAGACTCG TGAGCACATC 50
   CTGCTGGGTC GTCAGGTAGG CGTTCCGTAC ATCATCGTGT TCCTGAACAA 100
   ATGCGACATG GTTGATGACG AAGAGCTGCT GGAAGCTGGT GAGATGGAAG 150
   TTCGTGAACT RCTGTCTCAG TACGATTTCC CGGGCGACGA CACCCCGATC 200
   GTTCGTGGTT CTGCTCTGAA AGCGCTGGAA GGCACGCAG AGTGGGAAGC 250
   GAAAATCATC GAACTGGCTG GCCACCTGGA TACCTATATC CCGGAACCAG 300
   AGCGTGCGAT TGACAAGCCG TTCCTGCTGC CGATCGAAGA CGTATTCTCC 350
   ATCTCCGGTC GTGGTACCGT TGTTACCGGT CGTGTAGAGC GCGGTATCAT 400
   CAAAGTAGGT GAAGAAGTTG AAATCGTTGG TATCAAAGAA ACCGCGAAAA 450
10 CCACCTGTAC TGGCGTTGAA ATGTTCCGCA AACTGCTGGA CGAAGGCCGT 500
   GCTGGTGAGA ACGTAGGTGT TCTGCTGCGT GGTATCAAAC GTGAAGAAAT 550
   CGAACGTGGT CAGGTACTGG CTAAGCCGGG CACCATCAAC CCGCACACCA 600
   AGTTCGAATC TGAAGTGTA ATCCTGTCCA AAGACGAAGG CGGCCGTAC 650
   ACTCCGTTCT TCAAAGGCTA CCGTCCGCAG TTCTACTTCC GTACTACTGA 700
15 CGTGACTGGC ACCATCGAAC TGCCGGAAGG CGTAGAGATG GTAATGCCGG 750
   GCGACAACAT CAAAATGGTT GTTACCCTGA TCCATCCGAT CGCGATGGAC 800
   GACGGTCTGC GTTTCGCAA 819

```

20

2) INFORMATION FOR SEQ ID NO: 105

(i) SEQUENCE CHARACTERISTICS:

```

25 (A) LENGTH: 832 bases
   (B) TYPE: Nucleic acid
   (C) STRANDEDNESS: Double
   (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

30

(vi) ORIGINAL SOURCE:

```

   (A) ORGANISM: Kluyvera ascorbata
   (B) STRAIN: ATCC 33433

```

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105

```

   CGGCGCGATC CTGGTTGTTG CTGCGACTGA TGGCCCTATG CCACAGACTC 50
   GTGAGCACAT CCTGCTGGGT CGTCAGGTAG GCGTTCCTTA CATCATCGTG 100
   TTCCTGAACA AATGYGACAT GGTGATGAC GAAGAGCTGC TGGAAGTGGT 150
40 TGAAATGGAA GTTCGTGAAC TTCTGTCTCA GTACGATTTC CCAGGCGACG 200
   ATACTCCAAT CATCCGTGGT TCTGCTCTGA AAGCGCTGGA AGGCGATGCA 250
   GAGTGGAAG CGAAAATCAT CGAACTGGCT GGCTTCCTGG ATTCTTACAT 300
   CCCAGAACCA GAACGTGCTA TCGATAAGCC GTTCCTGCTG CCAATCGAAG 350
   ACGTATTCTC CATCTCCGGT CGTGGTACCG TTGTTACCGG TCGGTAGAG 400
45 CGCGGTATCA TCAAAGTTGG YGAAGAAGTT GAAATCGTTG GTATCAAAGA 450
   CACCGCTAAG TCTACCTGTA CCGGCGTTGA AATGTTCCGC AACTGCTGG 500
   ACGAAGGCCG TGCTGGTGAG AACGTTGGTG TTCTGCTGCG TGGTATCAA 550
   CGTGAAGAAA TCGAACGTGG TCAGGTTCTG GCTAAGCCAG GCTCTATCAA 600
   GCCGCACACC AAGTTCGAAT CTGAAGTGTA CATCTGTGCC AAAGACGAAG 650
50 GCGGCCGTCA TACTCCGTTT TTCAAAGGCT ACCGTCCACA GTTCTACTTC 700
   CGTACTACTG ACGTGACCGG TACCATCGAA CTGCCAGAAG GCGTTGAGAT 750
   GGTAATGCCA GCGACAACA TCAAGATGGT TGTGACTCTG ATCCACCCAA 800
   TCGCGATGGA CGACGGCCTG CGTTTCGCAA CC 832

```

55

2) INFORMATION FOR SEQ ID NO: 106

(i) SEQUENCE CHARACTERISTICS:

```

60 (A) LENGTH: 830 bases

```

(B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Kluyvera cryocrescens*
 (B) STRAIN: ATCC 33435

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106

	TGGCGCGATC	CTGGTTGTTG	CTGCAACTGA	TGGCCCTATG	CCACAGACTC	50
	GTGAGCACAT	CCTGCTGGGT	CGTCAGGTAG	GCGTTCCTTA	CATCATCGTG	100
15	TTCCCTGAACA	AATGTGACAT	GGTTGATGAC	GAAGAGCTGC	TGGAAGTGGT	150
	TGAAATGGAA	GTTCTGTAAC	TTCTGTCTCA	GTACGATTTC	CCAGGCGACG	200
	ACACTCCTAT	CGTTCGTGGT	TCCGCGCTGA	AAGCGCTGGA	AGGCGACGCT	250
	GAGTGGGAAG	CAAAAATCAT	CGAACTGGCT	GGCTTCCTGG	ATTCTTACAT	300
	CCCAGAACCA	GAGCGTGCGA	TTGATAAGCC	GTTCTGCTG	CCAATCGAAG	350
20	ACGTATTCTC	CATCTCCGGT	CGTGGTACCG	TTGTTACCGG	TCGTGTAGAG	400
	CGCGGTATCA	TCAAAGTTGG	TGAAGAAGTT	GAAATCGTGG	GTATCAAAGA	450
	CACGTGCTAAG	TCTACCTGTA	CCGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
	ACGAAGGCCG	TGCTGGTGAG	AACGTTGGTG	TTCTGCTGCG	TGGTATCAAA	550
	CGTGAAGAAA	TCGAACGTGG	TCAGGTTCTG	GCTAAGCCAG	GCTCCATCAA	600
25	GCCGCACACC	AAATTCGAAT	CTGAAGTTTA	CATCCTGTCC	AAAGACGAAG	650
	GCGGCCGTCA	TACTCCGTTT	TTCAAAGGCT	ACCGTCCACA	GTTCTACTTC	700
	CGTACTACTG	ACGTGACTGG	TACCATCGAA	CTGCCAGAAG	GCGTAGAGAT	750
	GGTAATGCCG	GGCGACAACA	TCAAATGGT	TGTTACCCTG	ATCCACCCAA	800
30	TCGCGATGGA	CGACGGTCTG	CGTTTCGCAA			830

2) INFORMATION FOR SEQ ID NO: 107

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 826 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Kluyvera georgiana*
 (B) STRAIN: ATCC 51603

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107

	CGCGATCCTG	GTTGTTGCTG	CGACTGACGG	CCCGATGCCG	CAGACTCGTG	50
50	AGCACATCCT	GCTGGGTCGT	CAGGTTGGCG	TTCCGTACAT	CATCGTGTTT	100
	CTGAACAAAT	GCGACATGGT	TGATGACGAA	GAGCTGCTGG	AACTGGTTGA	150
	AATGGAAGTT	CGTGAAC TTC	TGTCTCAGTA	CGACTTCCCG	GGCGACGACA	200
	CGCCGATCGT	TCGTGGTTCT	GCTCTGAAAG	CGCTGGAAGG	CGACGCTGAG	250
	TGGGAAGCGA	AAATCATCGA	ACTGGCGGGC	TTCCTGGATT	CTTACATCCC	300
55	GGAACCAAG	CGTGCGATTG	ACAAGCCGTT	CCTGCTGCCG	ATCGAAGACG	350
	TATTCTCCAT	CTCCGGTCGT	GGTACC GTT	TTACCGGTG	TGTAGAACGC	400
	GGTATCATCA	AAGTTGGCGA	AGAAGTTGAA	ATCGTTGGTA	TCAAAGACAC	450
	CGCTAAGTCT	ACCTGTACTG	GCGTTGAAAT	GTTCCGCAA	CTGCTGGACG	500
	AAGGCCGTGC	TGGTGAGAAC	GTTGGTGTTC	TGCTGCGTGG	TATCAAACGT	550
60	GAAGAAATCG	AACGTGGTCA	GGTACTGGCT	AAGCCGGGTT	CTATCAAGCC	600

```

GCACACCAAG TTCGAATCTG AAGTGTACAT TCTGTCCAAA GACGAAGGCG 650
GCCGTCATAC TCCGTTCTTC AAAGGCTACC GTCCGCAGTT CTACTTCCGT 700
ACTACTGACG TGACTGGCAC CATCGAAGTG CCGGAAGGCG TTGAGATGGT 750
AATGCCGGGC GACAACATCA AAATGGTTGT TACCCTGATC CACCCGATCG 800
5 CGAAGGACGA AGGTCTGCGT TTCGCA 826

```

2) INFORMATION FOR SEQ ID NO: 108

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 803 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lactobacillus casei* subsp. *casei*
 (B) STRAIN: ATCC 393

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108

```

25 GCTGCTGATG GCCCAATGCC ACAAACCTCGT GAACATATCT TACTTTCACG 50
TCAAGTTGGT GTTCCATACA TCGTTGTATT CATGAACAAA TGTGACATGG 100
TTGACGATGA AGAATTACTA GAATTAGTTG AAATGGAAAT TCGTGATCTA 150
TTAACTGAAT ATGAATTCCC TGGCGATGAC ATTCTGTAA TCAAAGGTTTC 200
AGCTCTTAAA GCACTTCAAG GTGAAGCTGA CTGGGAAGCT AAAATTGACG 250
30 AGTTAATGGA AGCTGTAGAT TCTTACATTC CAACTCCAGA ACGTGATACT 300
GACAAACCAT TCATGATGCC AGTTGAGGAT GTATTCTCAA TCACTGGTCG 350
TGGAACAGTT GCAACTGGAC GTGTTGAACG TGGACAAGTT AAAGTTGGTG 400
ACGAAGTAGA AGTTATCGGT ATTGAAGAAG AGAGCAAAAA AGTAGTAGTA 450
ACTGGAGTAG AAATGTTCCG TAAATYACTA GATTACGCTG AAGCTGGCGA 500
35 CAACATTGGC GCACTTCTAC GTGGTGTTCG TCGTGAAGAT ATCCAACGTG 550
GTCAAGTATT AGCTAAACCA GGTTCGATTA CTCCACACAC TAACTTCAAA 600
GCTGAAACTT ATGTTTAAAC TAAAGAAGAA GGTGGACGTC ACACTCCATT 650
CTTCAACAAC TACCGCCAC AATCTATTT CCGTACTACT GACGTAACGT 700
GTATTGTTAC ACTTCCAGAA GGTACTGAAA TGGTAATGCC TGGTGATAAC 750
40 ATTGAGCTTG CAGTTGANCT AATTGCACCA ATCGCTATCG AAGACGGTAC 800
TAA 803

```

2) INFORMATION FOR SEQ ID NO: 109

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lactococcus lactis* subsp. *lactis*
 (B) STRAIN: ATCC 19435

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109


```

CGGTGCAATC CTCGTTGTTG CTGCAACTGA TGGACCAATG CCACAAACTC      50
GTGAACACAT CTTGCTTTCA CGTCAAGTTG GTGTTAAATA CCTTATCGTC      100
TTCCTTAACA AGGCTGACCT TGTGATGAT GAAGAATTGA TGGAACTCGT      150
TGAAATGGAA GTTCGTGACC TCTTGAGCGA ATACGACTTC CCAGGTGACG      200
5  ATATTCCTGT AATCGCTGGT TCAGCACTTG GTGCTTTGAA CGGTGAACCA      250
CAATGGGTTG CTAAAGTTGA AGAATTGATG GACATCGTTG ATGAATACAT      300
CCCAACTCCA GAACGCGACA CTGACAAACC ACTCCTTCTT CCAGTCGAAG      350
ACGTATTCTC TATCACTGGT CGTGGTACAG TTGCTTCAGG ACGTATCGAA      400
CGTGGTACTG TTAAAGTTGG TGACGAAGTT GAAATCGTTG GTATCAAAGA      450
10 AGAAACTAAA AAAGCTGTTG TTAAGTGGTAT CGAAATGTTC CGTAAAACAC      500
TTACTGAAGG TCTTGCTGGT GATAACGTCG GTGCACTTCT CCGTGGTATC      550
CAACGTGACG AAATCGAAGC TGGTCAAGTT ATTGCTAAAC CAGGTTCAAT      600
CACTCCACAC AAAGTTTTCG AAGGTGAAGT TTACGTATTG AGCAAAGAAG      650
AAGGCGGACG TCACACTCCA TTCTTCGACA ACTACCGTCC TCAATTCTAC      700
15 TTCCACACAA CTGACGTTAC TGGTTCAGTT AACTTCCAG AAGGAACTGA      750
AATGGTAATG CCTGGTGACA ACGTGCATAT CGACGTTGAA TTGATCCACC      800
CAGTTGCGAT CGAACAAGGT ACTAC                                     825

```

20

2) INFORMATION FOR SEQ ID NO: 110

(i) SEQUENCE CHARACTERISTICS:

```

25 (A) LENGTH: 824 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

30

(vi) ORIGINAL SOURCE:-----

```

    (A) ORGANISM: Leclercia adecarboxylata
    (B) STRAIN: ATCC 23216

```

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110

```

GGCGCGATCC TGGTTGTTGC TGCAGCTGAC GGCCCAATGC CTCAGACCCG      50
TGAGCACATC CTGCTGGGTC GTCAGGTAGG CGTTCCTTTC ATCATCGTGT      100
TCCTGAACAA ATGCGACATG GTTGATGACG AAGAGCTGCT GGAAGTGGTT      150
40 GAGATGGAAG TTCGTGAACT YCTGTCCCAG TACGACTTCC CGGGCGACGA      200
CACCCCAATC GTTCGTGGTT CTGCGCTGAA AGCGCTGGAA GGCGAAGCAG      250
AGTGGGAAGA GAAAATCATC GARCTGGCTG GCTACCTGGA TTCTTACATC      300
CCAGAGCCAG AGCGTGCGAT TGACAAGCCG TTCCTGCTGC CTATCGAAGA      350
CGTATTCTCC ATCTCCGGTC GTGGTACCGT TGTTACCGGT CGTGTAGAGC      400
45 GCGGTATCAT CAARGTTGGC GAAGAAGTTG AAATCGTTGG TATCAAGGAC      450
ACTGCTAAGT CTACCTGTAC CGGCGTTGAA ATGTTCCGCA AACTGCTGGA      500
CGAAGGCCGT GCCGGTGAGA ACGTTGGTGT TCTGCTGCGT GGTATCAAAC      550
GTGAAGAAAT CGAACGTGGT CAGGTTCTGG CTAAGCCAGG CTCYATCAAG      600
CCGCACACCA AGTTCGAATC TGAAGTGATC ATCCTGTCYA AAGACGAAGG      650
50 CGGCCGTCAT ACTCCGTTCT TCAAAGGCTA CCGTCCACAG TTCTACTTCC      700
GTACKACTGA CGTGACCGGT ACCATCGARC TGCCAGAAGG CGTTGAGATG      750
GTAATGCCAG GCGACAACAT CAAAATGGTT GTTACCCTGA TCCACCCAAT      800
CGCAATGGAC GATGGTCTGC GTTC                                     824

```

55

2) INFORMATION FOR SEQ ID NO: 111

(i) SEQUENCE CHARACTERISTICS:

```

60 (A) LENGTH: 838 bases

```

(B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Legionella micdadei*
 (B) STRAIN: ATCC 33218

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111

	CGGAGCGATA	TTAGTAGTAT	CAGCAGCGGA	TGGCCCAATG	CCTCAAACGA	50
	GAGAGCACAT	ACTYTTATCC	CGSCAGGTAG	GTGTTCCCTA	TATAGTAGTG	100
15	TTCTTAAACA	AAGCTGACAT	GGTGGATGAT	GCGGAGTTAT	TAGAATTAGT	150
	TGAAATGGAA	GTACGCGAYT	TGTTGAGCAG	CTATGAATTT	CCAGGAGATG	200
	AGATCCCGAT	TGTAGTTGGT	TCAGCATTAA	AAGCATTGGA	AGGCGATACG	250
	AGTGATATAG	GTGTACCAGC	GATTGAGAAG	TTAGTTGAGA	CGATGGATTG	300
	TTATATACCT	GAGCCGGTAA	GAAACATCGA	TAAAAGTTTC	TTGTTACCGA	350
20	TCGAAGACGT	GTTCTCAATA	TCTGGACGAG	GAACAGTAGT	AACAGGACGT	400
	ATCGAAAGCG	GGATCATCAA	AGTTGGTGAG	GAAGTCGAGA	TTGTTGGTAT	450
	ACGTGACACT	CAAAAGACGA	CATGCACAGG	CGTTGAAATG	TTCCGTAAAT	500
	TACTTGACGA	AGGTCGAGCT	GGAGACAACG	TTGGTATATT	GCTACGTGGT	550
	ACGAAGCGGG	ATGAAGTTGA	ACGCGGACAA	GTATTAGCTA	AGCCGGGAAG	600
25	CATTAAACCG	CATACTAAAT	TTGAAGCTGA	AGTGTATGTG	TTGTCAAAG	650
	ATGAAGGTGG	ACGTCATACC	CCATTCTTTA	ACGGATATCG	GCCTCAATTT	700
	TACTTCAGGA	CCACAGACGT	AACTGGTTCT	TGTGATTTAC	CTGARGGTAT	750
	AGAAATGGTA	ATGCCAGGTG	ATAACGTCAA	GCTGATTGTT	AGCTTACACT	800
30	CACCGATTGC	TATGGACGAA	GGTTTGCGTT	TTGCAATC		838

2) INFORMATION FOR SEQ ID NO: 112

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 838 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Legionella pneumophila* subsp. *pneumophila*
 (B) STRAIN: ATCC 33152

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112

	CGGAGCGATA	CTGGTTGTAT	CAGCAGCTGA	TGGTCCTATG	CCACAAACGA	50
50	GGGAACACAT	TCTATTGTCT	CGCCAGGTAG	GTGTTCCATA	TATTGTTGTG	100
	TTCATGAACA	AAGCGGATAT	GGTTGATGAC	CCTGAGTTAT	TAGAGTTAGT	150
	GGAAATGGAA	GTGCGAGATT	TATTAAGCAG	TTACGATTTT	CCAGGGGATG	200
	ACATACCTAT	TGTTGTTGGT	TCAGCTTTGA	AAGCATGGA	AGGTGAAGAC	250
	AGTGATATAG	GCGTTAAGGC	TATTGAGAAA	TTGGTTGAAA	CAATGGATTG	300
55	ATACATTCCT	GAGCCAGTTA	GAAACATAGA	CAAGCCATTT	TTGTTGCCGA	350
	TTGAAGACGT	ATTTTCAATT	TCTGGACGCG	GAACAGTGGT	AACTGGTCGT	400
	GTAAGAGAGTG	GAATTGTTAA	AGTTGGTGAG	GAAGTTGAAA	TTGTTGGAAT	450
	AAGAGACACC	CAAAAGACGA	CTTGACGGG	TGTTGAGATG	TTCCGTAAAT	500
	TACTTGATGA	AGGTCGAGCT	GGTGATAACG	TTGGTGTGTT	ATTACGAGGT	550
60	ACGAAGCGAG	ATGAAGTGGA	GCGTGGACAG	GTATTGGCGA	AGCCAGGAAC	600

	CATCAAGCCA	CACACCAAGT	TTGAAGCAGA	AGTGTATGTA	TTATCCAAGG	650
	AAGAAGGCGG	ACGTCACACT	CCATTCTTTA	ATGGATACCG	TCCACAATTC	700
	TATTTCAGAA	CCACTGACGT	GACAGGTACT	TGTGACTTGC	CATCAGGAGT	750
	TGAAATGGTA	ATGCCTGGAG	ATAATGTGCA	ATTAGTTGTT	AGCTTGCATG	800
5	CTCCGATTGC	GATGGATGAA	GGTTTAAGAT	TCGCAATT		838

2) INFORMATION FOR SEQ ID NO: 113

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leminorella grimontii*
- (B) STRAIN: ATCC 33999

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113

25	GTGCAATCCT	GGTAGTAGCA	GCGACTGACG	GCCCGATGCC	TCAGACTCGC	50
	GAGCACATCC	TGCTGGGTCG	TCAGGTAGGC	GTTCCGTACA	TCATCGTATT	100
	CCTGAACAAG	TGCGATATGG	TTGATGACGA	AGAGCTGCTG	GAGCTGGTTG	150
	ARATGGAAGT	TCGCGAACTG	CTGTCTCAGT	ACGACTTCCC	GGGCGACGAC	200
	ACTCCGGTAG	TCCGCGGTTT	AGCGCTGAAA	GCGCTGGAAG	GCGAAGCCGA	250
30	GTGGGAARCG	AAAATCATCG	AGCTGGCAGG	CCMTCTGGAT	ACTTATATCC	300
	CAGAACCTGA	GCGTGCGATT	GACAAGCCGT	TCCTGCTGCC	KATCGAAGAC	350
	GTATTCTCTA	TCTCCGGCCG	TGGTACCGTT	GTTACCGGTC	GTGTAGAGCG	400
	CGGCATCATC	AAAGTCGGTG	AAGAAGTGGA	AATCGTCGGT	ATCAAAGATA	450
	CCACCAAGAG	CACCTGTACC	GGCGTTGAAA	TGTTCCGTAA	GCTGCTGGAC	500
35	GAAGGCCCGT	CGGGCGAGAA	CGTGGGCGTT	CTGCTGCGCG	GTACCAAGCG	550
	TGACGAAATC	GAACGTGGTC	AAGTTCTGGC	CAAGCCGGGC	ACCATCACTC	600
	CTCACACCCA	GTTCGTGTCA	GAAGTGTATA	TCCTGAGCAA	GGATGAAGGC	650
	GGCCGTCATA	CTCCGTTCTT	CAAAGGCTAC	CGTCCTCAGT	TCTACTTCCG	700
	TACGACTGAC	GTGACAGGCA	CCATCGAACT	GCCGGAAGGC	GTAGAGATGG	750
40	TAATGCCAGG	CGACAACATT	CAGATGACCG	TAAGTCTGAT	TGCGCCGATC	800
	GCAATGGACG	AAGGTCTGCG	CTTCGCAA			828

2) INFORMATION FOR SEQ ID NO: 114

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 826 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leminorella richardii*
- (B) STRAIN: ATCC 33998

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114

```

5  GCTATCCTGG TTGTTGCTGC GACTGACGGC CCAATGCCTC AGACTCGTGA 50
   GCACATCCTG CTGGGTCGCC AGGTAGGCGT TCCTTACATC ATCGTGTTCC 100
   TGAACAAGTG CGACATGGTT GATGACGAAG AGCTGCTGGA ACTGGTAGAA 150
   ATGGAAGTTC GTGAACTTCT GTCTCAATAC GACTTCCCGG GCGACGATAC 200
   GCCGGTTGTT CGCGGTTTCT CGCTGAAAGC GCTGGAAGGT GACGCYGAGT 250
   GGGGAARCGAA AATCATTGAA CTGGCGGAAT CCTTRGATAC TTAYATTCCA 300
   GAGCCAGAGC GTGCGATTGA CAAGCCGTTT CTGCTGCCTA TCGAAGACGT 350
   TTTCTCTATC TCTGGCCGTG GTACTGTAGT CACCGGTCGT GTAGAGCGCG 400
   GCATCATCAA AGTTGGTGAA GAAGTGGAAA TCGTGGGAAT CAAAGACACC 450
10  ACCAAGACCA CCTGTACTGG CGTTGAAATG TTCCGTAAGC TGCTGGACGA 500
   AGGCCGTGCA GGTGAGAACG TTGGTGTTCT GCTGCGYGGT ACTAAGCGTG 550
   ACGAAATCGA ACGTGGTCAG GTACTGGCTA AGCCAGGCAC CATCACTCCT 600
   CACACAGAAAT TCGTGTCAGA AGTGTATATC CTGAGCAAGG ATGAAGGCGG 650
   YCGTCATACT CCGTTCTTCA AAGGCTACCG TCCTCAGTTC TACTTCCGTA 700
15  CGACTGACGT GACCGGCACC ATCGAACTGC CAGAAGGCGT AGAGATGGTA 750
   ATGCCAGGCG ATAACATCCA GATGGTAGTT ACGCTGATTG CCCCAATCGC 800
   GATGGACGAA GGTCTGCGCT TCGCAA 826

```

20

2) INFORMATION FOR SEQ ID NO: 115

(i) SEQUENCE CHARACTERISTICS:

```

25  (A) LENGTH: 843 bases
     (B) TYPE: Nucleic acid
     (C) STRANDEDNESS: Double
     (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

30

(vi) ORIGINAL SOURCE:

```

-- (A) --ORGANISM: Leptospira interrogans
   (B) STRAIN: ATCC 23581

```

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115

```

   TCGGGCGATT CTTGTAGTAT CCGCAACTGA CGGACCTATG CCACAAACAA 50
   AAGAACATAT CTTTCTTGCT CGTCAGGTAG GTGTTCCATA TGTAATTGTA 100
   TTCATTAACA AAGCAGATAT GCTTGCTGCT GACGAAAGAG CAGAAATGAT 150
40  CGAAATGGTT GAGATGGACG TTCGTGAACT TCTCAATAAG TATAGCTTCC 200
   CAGGAGATAC AACTCCTATC GTTCATGGTT CTGCGGTAAA AGCACTTGAG 250
   GGCGATGAAT CTGAAATTGG GATGCCTGCA ATTCTCAAAT TGATGGAAGC 300
   TCTGGATACT TTCGTTCCAA ATCCAAAACG TGTAATCGAC AAACCTTTCC 350
   TTATGCCAGT AGAAGACGTT TTCTCGATCA CTGGTCGTGG AACTGTTGCA 400
45  ACTGGAAGAG TGGAACAAGG TGTTTTGAAA GTGAACGACG AAGTTGAAAT 450
   TATCGGTATC CGCCCAACAA CAAAACTGT TGTACCAGGT ATCGAAATGT 500
   TCAGAAACT TCTCGATCAA GCGGAAGCTG GCGACAACAT CGGCGCTCTT 550
   CTTCGTGGAA CTAAAAAAGA AGAAATCGAA AGAGGGCAAG TTCTTGCGAA 600
   GCCAGTTTCT ATCACTCCTC AAAAAAGTT TGCCGCTGAG GTGTATGTAT 650
50  TAACTAAGGA TGAAGGCGGA CGTCATACTC CGTTTATCAA TAACTACCGT 700
   CCTCAGTTTT ACTTTAGAAC AACTGACGTA ACCGGAGTTT GTAACCTTCC 750
   TAATGGTGTC GAAATGGTTA TGCCTGGTGA TAACGTTTCT TTGACGGTTG 800
   AATTGATTAG CCCGATCGCA ATGGACAAGG GTCTTAAGTT CGC 843

```

55

2) INFORMATION FOR SEQ ID NO: 116

(i) SEQUENCE CHARACTERISTICS:

```

60  (A) LENGTH: 832 bases

```

(B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5 (ii)MOLECULE TYPE: Genomic DNA

(vi)ORIGINAL SOURCE:

(A) ORGANISM: *Megamonas hypermegale*
 (B) STRAIN: ATCC 25560

10

(xi)SEQUENCE DESCRIPTION: SEQ ID NO: 116

	CGGTGCTATC	CTCGTTGTTA	GTGCTGCTGA	TGGTCCTATG	CCTCAGACTC	50
	GTGAACACAT	CCTTCTCGCT	CGTCAGGTTG	GTGTTCCAGC	TATCGTTGTA	100
15	TTCCTCAACA	AAGCTGACCA	GGTTGATGAC	CCTGAACTTC	TCGAACTTGT	150
	TGAAATGGAA	GTTCGTGAAC	TTCTTTCCAG	CTATGACTTC	CCAGGCGATG	200
	ACGTTCCAGT	AATCACTGGT	TCCGCTCTTC	AGGCTCTCGA	AGGCGACGAA	250
	GAAGCTAAAA	AGAAAATTCT	TGAATTAATG	GATGCTGTTG	ATGATTACAT	300
	CCCAACTCCA	ACACGTGACA	CTGATAAACC	TTTCTTAATG	CCAGTTGAAG	350
20	ACGTATTCAC	AATTACTGGT	CGTGGTACTG	TTGCTACAGG	CCGTGTTGAA	400
	CGTGGCGAAC	TTAAACTTGG	TGACAGCGTT	GAAATCGTTG	GTCTTTCCGA	450
	TGAAAAGAAA	TCCACTACTG	TAACTGGTAT	CGAAATGTTC	CGCAAAATGC	500
	TTGATAGCGC	TGTTGCTGGT	GATAACATCG	GTGCACTTCT	TCGTGGTATT	550
	GACCGTAAAG	AAATCGAACG	TGGTCAAGTT	CTTGCTAAAC	CTGGCACAAAT	600
25	TCATCCACAC	AAAAAATTCA	AAGCTCAGGT	TTACGTATTA	ACTAAAGAAG	650
	AAGGTGGACG	TCATACTCCA	TTCTTCTCCA	ACTATCGTCC	ACAGTTCTAT	700
	TTCCGTACTA	CTGACGTTAC	TGGTGTGTA	ACTCTTCCAG	AAGGTACTGA	750
	AATGGTTATG	CCTGGCGATA	ACATTGAAAT	GAGCATCGAA	CTCATCACTC	800
30	CAATCGCTAT	TGAAAAGGT	CTTCGCTTCG	CT		832

2) INFORMATION FOR SEQ ID NO: 117

35 (i)SEQUENCE CHARACTERISTICS:

(A) LENGTH: 820 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii)MOLECULE TYPE: Genomic DNA

(vi)ORIGINAL SOURCE:

(A) ORGANISM: *Mitsuokella multacida*
 (B) STRAIN: ATCC 27723

45

(xi)SEQUENCE DESCRIPTION: SEQ ID NO: 117

	TGGTGCTATC	CTCGTCGTTT	CCGCTGCTGA	TGGCCCCGATG	CCGCAGACGC	50
50	GTGAGCACAT	CCTGCTCGCT	CGCCAGGTCG	GTGTTCCGGC	AATCGTTGTC	100
	TTCCTCAACA	AGGTTGACCA	GGTTGACGAT	CCGGAGCTCC	TCGAGCTCGT	150
	CGAGATGGAA	GTTCGCGAGC	TGCTCTCCAG	CTACGACTTC	CCGGGCGATG	200
	ACATCCCTGT	AATCGCTGGT	TCCGCTCTGA	AGGCCCTCGA	AGGCGACGAA	250
	GAGCAGAAGA	AGAACATCCT	CAAGCTCATG	GAAGCTGTCT	ATGAGTACAT	300
55	CCCGACGCCG	GTCCGCGACA	ACGCTAAGCC	GTTCCTGATG	CCGGTCGAGG	350
	ATGCTTTTAC	GATCACGGGC	CGTGGTACGG	TTGCAACGGG	CCGCGTTGAG	400
	CGTGGTGAGC	TCAAGATGAA	CGATACGGTT	GAGATCGTTG	GTCTGCAGGA	450
	CGAGCCGCGT	CAGACGGTTG	TCACGGGCAT	CGAGATGTTC	CGCAAGATGC	500
	TTGATTTTCG	TGAGGCTGGC	GATAACATCG	GTGCTCTGCT	CCGTGGTATC	550
60	GACCGCAAGG	AGATCGAGCG	TGGCCAGGTT	CTCGCAAAGC	CGGGCACGAT	600

5 TCATCCGCAC ACGAAGTTCA AGGCTCAGGT CTATGTCCTG ACGAAAGAAG 650
 AAGGCGGCCG TCATACGCCG TTCTTCACGA ACTATCGCCC GCAGTTCTAC 700
 TTCCGCACGA CGGACGTAAC TGGCGTAGTC AAATGCGCGG AAGGCACGGA 750
 GATGGTTATG CCTGGCGATA ACGTCGAGAT GGAAGTTGAG CTCATCACCC 800
 CGATCGCTAT CGAGAAGGGC 820

2) INFORMATION FOR SEQ ID NO: 118

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mobiluncus curtisii* subsp. *holmesii*
 (B) STRAIN: ATCC 35242

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118

25 CGGCGCTATC CTCGTGGTGG CTGCTACTGA CGGTCCGATG GCTCAGACCA 50
 AGGAACACAT CCTGTTGGCT AAGCAGGTTG GCGTGCCCTC CATCCTGGTC 100
 GCTCTGAACA AGTGCGATTC TTCCGATGTG GACGAAGACA TGCTCGAAAT 150
 CGTCGAGGAC GAAATCCGCG ATGACCTGGA GAAGCAGGGC TTCGATCGTG 200
 ACTGCCCCGAT TATCCACGTT TCCGCTCTGA AGGCCCTGGA AGGCGACCCC 250
 30 GAGTGGACCA AGAAGATTGA AGAGCTCATG GAAGCGGTCTG ATACCTACAT 300
 TCCTGAGCCT GTTCGTGACC TCGACAAGCC GTTCTTGATG CCTATCGAAG 350
 ACGTCTTCAC CATTACTGGT CGCGGTACCG TAGTGACCGG TCGTGTGGAA 400
 CGCGGCAAGC TACCGTTGAA CGCCGAAGTG GAAATCGTAG GTATTTCGTCC 450
 TACGCAAAAG ACCACCGTTA CCGGTATCGA AATGTTCCAC AAGTCCATGG 500
 35 ACGAAGCCTA CGCCGGCGAG AACTGTGGTC TGTGCTGCG TGGCACCAAG 550
 CGTGAGGACG TTGAGCGCGG TCAGGTGTGTC TGCATTCTCTG GCTCCGTGAC 600
 CCCGCACACC AAGTTCGAGG GCAAGGTCTA CATCTTGAAG AAGGACGAAG 650
 GTGGACGTCA CAAGTCGTTT TACGACGGCT ACCGCCCCGCA GTTCTTCTTC 700
 CGCACCACCG ACGTGACCGG TGTATTTCAC CTGCCCCGAAG GCACCGAAAT 750
 40 GGTATGCCT GGCACACCA CCGAAATTAG CGTTGAGCTG ATTCAGCCTA 800
 TCGCTATGGA GGAAGGTCTC GGCTTCGCTA T 831

45 2) INFORMATION FOR SEQ ID NO: 119

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Moellerella wisconsensis*
 (B) STRAIN: ATCC 35017

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119

```

GGTGCAATTC TGGTTGTTGC TGCAACTGAT GGCCCTATGC CACAGACTCG      50
TGAGCACATC CTGTTAGGTC GTCAGGTTGG CGTTCCATAC ATCATCGTTT      100
TCCTGAACAA ATGTGACATG GTAGACGACG AAGAGCTGTT AGAACTGGTT      150
GAAATGGAAG TCCGTGAGCT GCTGTCTCAG TACGATTTCC CAGGCGATGA      200
5  CACTCCAGTA ATCCGTGGTT CAGCGCTGAA AGCTCTGGAA GGCGAAGCTG      250
AGTGGGAAGC TAAAATCATT GAACTGGCAG AAGCACTGGA TTCTTATATC      300
CCAGAGCCAG AGCGTGACAT TGATAAGCCA TTCTGTGTAC CAATCGAAGA      350
CGTATTCTCA ATTTTCAGGCC GTGGTACAGT TGTTACTGGT CGTGTGAGC      400
GTGGTATCGT TAAAGTCGGT GAAGAAGTTG AAATCGTTGG TATCAAAGAT      450
10 ACCGTGAAAA CAACATGTAC TGGCGTTGAA ATGTTCCGTA AACTGCTGGA      500
CGAAGGCCGT GCTGGTGAGA ACGTTGGTGT TCTGCTGCGT GGTACTAAAC      550
GTGATGATAT CGAACGTGGT CAAGTATTGG CTAAACCAGG TTCAATCACT      600
CCGCATACAA CTTTCGAATC AGAAGTTTAC ATCCTGAGCA AAGATGAAGG      650
TGGCCGTCAT ACTCCATTCT TCAAAGGTTA CCGTCCACAG TTCTACTTCC      700
15 GTACAACTGA CGTAACCGGT ACTATCGAAC TGCCAGAAGG CGTTGAGATG      750
GTAATGCCAG GTGATAACAT CAAAATGATC GTTACTCTGA TCCACCCAAT      800
TGCAATGGAT GCAGGTCTGC GTTTT      825

```

20

2) INFORMATION FOR SEQ ID NO:120

(i) SEQUENCE CHARACTERISTICS:

```

25 (A) LENGTH: 827 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

30

(vi) ORIGINAL SOURCE:

```

    (A) ORGANISM: Branhamella catarrhalis
    (B) STRAIN: ATCC 43628

```

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120

```

TGGTGCTATC TTGGTTGTTT CTGCAACTGA TGGTCCTATG CCACAAACTC      50
GTGAGCATAT CCTACTATCT CGTCAGGTTG GTGTACCATA CATCATGGTA      100
TTCATGAACA AGTGCGATAT GGTTGATGAT GAAGAGCTAC TAGAATTGGT      150
40 TGAATGGAAG GTTCGTGAAC TTCTATCTGA CTATGATTTT CCTGGTGATG      200
ATACCCCAAT CATCAAAGGT TCAGCACTAG AAGCATTGAA TGGTTCTGAT      250
GGTAAATATG GCGAGCCTGC AGTTCTAGAA CTGCTAGACA CACTAGACAG      300
CTATATCCCA GAGCCTGAGC GTGATATCGA TAAGTCATTC TTGATGCCAA      350
TTGAAGATGT CTTCTCGATC TCAGGTCGTG GTACAGTTGT GACTGGTCGT      400
45 GTTGAATCAG GTATTATTAA AGTTGGTGAT GAAATTGAAA TCATCGGTAT      450
CAAACCAACT GCTAAAACCA CCTGTACTGG TGTGAAATG TTCCGTAAAC      500
TGTTAGACGA AGGTCGTGCA GGTGAGAACT GTGGTATCTT GTTGCGTGGT      550
ACTAAGCGTG AAGAAGTTCA ACGCGGTCAA GTACTTGCAA AACCAGGTTT      600
AATCACCCCA CATACTAAGT TTGATGCTGA AGTTTATGTA CTGTCAAAAG      650
50 AAGAAGGTGG TCGTCACACC CCATTCTTAA ATGGCTATCG CCCACAGTTC      700
TACTTCCGTA CCACAGATGT GACTGGTGCC ATCACTCTAC AAGAAGGTAC      750
CGAAATGGTT ATGCCTGGTG ACAATGTTGA GATGAGTGTT GAGCTTATCC      800
ACCCAATCGC CAGGATAAAG GTCTACG      827

```

55

2) INFORMATION FOR SEQ ID NO: 121

(i) SEQUENCE CHARACTERISTICS:

```

60 (A) LENGTH: 806 bases

```

(B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5 (ii)MOLECULE TYPE: Genomic DNA

(vi)ORIGINAL SOURCE:

(A) ORGANISM: *Morganella morganii* subsp. *morganii*
 (B) STRAIN: ATCC 25830

10 (xi)SEQUENCE DESCRIPTION: SEQ ID NO: 121

	CGGCGCTATC	CTGGTTGTTG	CTGCAACTGA	TGGCCCTATG	CCACAGACCC	50
	GTGAGCACAT	CCTGTTAGGT	CGTCAGGTTG	GCGTTCCTTA	CATCATCGTA	100
15	TTCCTGAACA	AATGTGACAT	GGTTGATGAT	GAAGAGCTGC	TGGAAGTGGT	150
	TGAAATGGAA	GTTTCGTGAAC	TTCTGTCTCA	GTACGATTTT	CCTGGCGACG	200
	ACACGCCAAT	CGTTCGCGGT	TCAGCGCTGA	AAGCACTGGA	AGGCGAGCCA	250
	GAGTGGGAAG	CTAARATCGT	TGAACCTGGCA	GGTTTCCTGG	ATTCTTACAT	300
	CCCTGAGCCA	GAGCGTGCAA	TTGACAAGCC	GTTCTGCTG	CCAATCGAAG	350
20	ACGTATTCTC	AATCTCCGGC	CGTGGTACCG	TTGTTACCGG	TCGTGTTGAG	400
	CGCGGTATCA	TCAAGGTTGG	TGAGGAAGTT	GAAATCGTGG	GTATCAAAGA	450
	TACTGCGAAA	ACCACCTGTA	CCGGTGTTGA	AATGTTCCGC	AAACTGCTGG	500
	ACGAAGGCCG	TGCMGGTGAG	AACGTCGGTG	TTCTGCTGCG	TGGTACCAAG	550
	CGTGAAGAAA	TGAACGTGG	TCAGGTTCTG	GCTAAACCAG	GTTCAATCAA	600
25	ACCACAYACC	AAATTTGAAT	CAGAAGTTTA	TATTCTGAGC	AAAGATGAAG	650
	GTGGTCGTCA	TACTCCATT	TTCAAAGGYT	ACCGTCCACA	GTTCTACTTC	700
	CGTACCACAG	ACGTAACAGG	TACTATCGAA	CTGCCGGAAG	GCGTTGAAAT	750
	GGTAATGCCG	GGCGACAACA	TCAAATGAT	CGTCACCCTG	ATCCACCCAA	800
	TCGCAA					806

30

2)INFORMATION FOR SEQ ID NO: 122

35 (i)SEQUENCE CHARACTERISTICS:

(A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii)MOLECULE TYPE: Genomic DNA

(vi)ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*
 (B) STRAIN: TB 299

45

(xi)SEQUENCE DESCRIPTION: SEQ ID NO: 122

	GGTGCATCC	TGGTGGTCGC	CGCCACCGAC	GGCCCGATGC	CCCAGACCCG	50
50	CGAGCACGTT	CTGCTGGCGC	GTCAAGTGGG	TGTGCCCTAC	ATCCTGGTAG	100
	CGCTGAACAA	GGCCGACGCA	GTGGACGACG	AGGAGCTGCT	CGAACTCGTC	150
	GAGATGGAGG	TCCGCGAGCT	GCTGGCTGCC	CAGGAATTCG	ACGAGGACGC	200
	CCCGGTTGTG	CGGGTCTCGG	CGCTCAAGGC	GCTCGAGGGT	GACGCGAAGT	250
	GGGTTGCCTC	TGTCGAGGAA	CTGATGAACG	CGGTCGACGA	GTCGATTCCG	300
55	GACCCGGTCC	GCGAGACCGA	CAAGCCGTTT	CTGATGCCCG	TCGAGGACGT	350
	CTTCACCATT	ACCGGCCGCG	GAACCGTGGT	CACCGGACGT	GTGGAGCGCG	400
	GCGTGATCAA	CGTGAACGAG	GAAGTTGAGA	TCGTCGGCAT	TCGCCCATCG	450
	ACCACCAAGA	CCACCGTCAC	CGGTGTGGAG	ATGTTCCGCA	AGCTGCTCGA	500
	CCAGGGCCAG	GCGGGCGACA	ACGTTGGTTT	GCTGCTGCGG	GGCGTCAAGC	550
60	GCGAGGACGT	CGAGCGTGCG	CAGGTTGTCA	CCAAGCCCGG	CACCACCACG	600

	CCGCACACCG	AGTTCGAAGG	CCAGGTCTAC	ATCCTGTCCA	AGGACGAGGG	650
	CGGCCGGCAC	ACGCCGTTCT	TCAACAACATA	CCGTCCGCAG	TTCTACTTCC	700
	GCACCACCGA	CGTGACCGGT	GTGGTGACAC	TGCCGGAGGG	CACCGAGATG	750
	GTGATGCCCG	GTGACAACAC	CAACATCTCG	GTGAAGTTGA	TCCAGCCCGT	800
5	CGCCATGGAC	GAAGGTCTGC	GTTTC			825

2) INFORMATION FOR SEQ ID NO: 123

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 806 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria cinerea*
 (B) STRAIN: ATCC 14685

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123

25	CGGTGCGATC	TTGGTATGTT	CCGCAGCTGA	CGGTCCTATG	CCGCAAACTC	50
	GCGAACACAT	CCTGTTGGCC	CGCCAAGTAG	GTGTACCTTA	CATCATCGTG	100
	TTCATGAACA	AATGCGACAT	GGTTGACGAT	GCCGAGCTGT	TGGAGCTGGT	150
	TGAAATGGAA	ATCCGTGACT	TGCTGTCAAG	CTACGACTTC	CCAGGTGACG	200
	ACTGCCCGAT	CGTACAAGGT	TCTGCACTGA	AAGCCTTGGA	AGGCGACGCA	250
30	GCTTACGAAG	AAAAAATCTT	CGAATTGGCT	GCTGCATTGG	ACAGCTACAT	300
	CCCAACACCT	GAGCGTGCAG	TGGACAAACC	TTTCTTGTTG	CCTATCGAAG	350
	ACGTATTCTC	TATTTCCGGT	CGCGGTACAG	TAGTAACCGG	TCGTGTAGAG	400
	CGCGGTATCA	TCCACGTTGG	TGACGAGATC	GAAATCGTAG	GTCTGAAAGA	450
	AACTCAAAAA	ACCACTTGTA	CCGGTGTGTA	AATGTTCCGC	AAACTGCTGG	500
35	ACGAAGGTCA	AGCTGGTGAC	AACGTAGGTG	TATTGCTGCG	TGGTACTAAA	550
	CGTGAAGACG	TAGAGCGTGG	TCAAGTATTG	GCTAAACCGG	GTACTATCAC	600
	TCCTCACACC	AAGTTCAAAG	CAGAAGTATA	CGTACTGAGC	AAAGAAGAGG	650
	GTGGTCGTCA	CACTCCGTTT	TTCGCTAACT	ACCGTCCACA	ATTCTACTTC	700
	CGTACTACCG	ACGTAACCGG	CGCGGTTACT	TTGGAAGAAG	GTGTAGAAAT	750
40	GGTAATGCCG	GGTGAGAACG	TAACCATTAC	TGTAGAACTG	ATTGCGCCTA	800
	TCGCTA					806

45 2) INFORMATION FOR SEQ ID NO: 124

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria elongata* subsp. *elongata*
 (B) STRAIN: ATCC 25295

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124

5 CGGCGCAATC TTGGTATGTT CCGCTGCTGA CCGTCCTATG CCGCAAACCTC 50
 GCGAACACAT CCTGTTGGCC CGCCAAGTAG GCGTACCTTA CATCATCGTG 100
 TTCATGAATA AATGCGACAT GGTGAYGAT GCCGAACGTC TGGAACCTGGT 150
 TGAAATGGAA ATCCGTGACT TGCTGTCAAG CTACGACTTC CCAGGCGACG 200
 ACTGCCCGAT CGTACAAGGT TCCGCACTGA AAGCCTTGGA AGGCGACGCA 250
 GCTTACGAAG AAAAAATCTT CGAACTGGCT GCTGCATTGG ACAGCTACAT 300
 CCCGACACCT GAGCGTGCCG TGGACAAACC GTTCCTGTTG CCTATCGAAG 350
 ACGTATTCTC TATCTCCGGC CGTGGTACAG TAGTAACCGG TCGTGTAGAG 400
 CGCGGTATCA TCCACGTCGG TGACGAGATC GAAATCGTAG GTCTGAAAGA 450
 10 AACCCTAAAA ACCACTTGTA CCGGTGTTGA AATGTTCCGC AAACCTGCTGG 500
 ACGAAGGTCA AGCAGGTGAC AACGTAGGCG TATTGCTGCG CCGTACCAA 550
 CGTGAAGAAG TGGAACGCGG TCAAGTATTG GCTAAACCGG GTACCATCAC 600
 TCCTCACACC AAATTCAAAG CAGAAGTTTA CGTATTGAGC AAAGAAGAGG 650
 GTGGTTCGTC TACTCCGTTT TTCGCTAACT ACCGTCCACA ATTCTACTTC 700
 15 CGTACTACCG ACGTAACCGG TCGCGTTACT TTGGAAGAAG GTGTAGAAAT 750
 GGTATGCCT GGTGAGAACG TGGCCATCAC TGTAGAACTG ATTGCACCTA 800
 TCGCTATGGA AGAAGGTCTG CG 820

20

2) INFORMATION FOR SEQ ID NO: 125

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 820 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria flavescens*
 (B) STRAIN: ATCC 13120

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125

40 CGGCGCGACT TGGTATGTTT CGCAGCTGAC GGTCTATGTC CGCAAACCCG 50
 CGAACACATC CTGTTGGCTC GCCAAGTAGG TGTACCTTAC ATCATCGTAT 100
 TCATGAACAA ATGCGACATG GTAGACGATG CCGAGCTGTT GGAACCTGGT 150
 GAAATGGAAA TTCGTGACTT GTTGTCAGC TACGACTTCC CAGGCGACGA 200
 CTGCCCCAATC GTACAAGGTT CTGCACTGAA AGCTTTGGAA GGTGATGCTG 250
 CTTACGAAGA AAAAAATCTT GAATTGGCTG CTGCCTTGA CAGCTACATC 300
 CCAACACCTG AGCGTGCTGT GGACAAACCT TTCTTGTTGC CTATCGAAGA 350
 CGTATTCTCT ATCTCTGGTC GTGGTACAGT AGTAACCGGT CGCGTAGAGC 400
 45 GCGGTATCAT CCACGTTGGT GACGAGATCG AAATCGTAGG TCTGAAAGAA 450
 ACTCAAAAAA CCACTTGATC CGGCGTTGAA ATGTTCCGCA AACTGCTGGA 500
 CGAAGGTCAA GCAGGTGACA ACGTAGGCGT ATTGCTGCGT GGTACTAAAC 550
 GTGAAGACGT AGAGCGTGGT CAAGTATTGG CTAAACCAGG TACCATCACT 600
 CCTCACACCA AATTCAAAGC AGAAGTATAC GTAGTGAGCA AAGAAGAGGG 650
 50 TGGTTCGTAC ACTCCATTTT TCGCTAACTA CCGTCCACAA TTCTACTTCC 700
 GTACTACCGA CGTAACCTGGT GCAGTTACTT TGGAAGAAGG CGTAGAAATG 750
 GTAATGCCAG GTGAGAACGT AACCATTACT GTAGAACTGA TTGCGCCAAT 800
 CGCTATGGAA GAAGTCTGCG 820

55

2) INFORMATION FOR SEQ ID NO: 126

(i) SEQUENCE CHARACTERISTICS:

- 60 (A) LENGTH: 830 bases

(B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5 (ii)MOLECULE TYPE: Genomic DNA

(vi)ORIGINAL SOURCE:

(A) ORGANISM: *Neisseria gonorrhoeae*
 (B) STRAIN: ATCC 49226

10 (xi)SEQUENCE DESCRIPTION: SEQ ID NO: 126

	GGTGCAATCC	TGGTATGTTT	TGCTGCCGAC	GGCCCTATGC	CGCAAACCCG	50
	CGAACACATC	CTGCTGGCCC	GTCAAGTAGG	CGTACCTTAC	ATCATCGTGT	100
15	TCATGAACAA	ATGCGACATG	GTCGACGATG	CCGAGCTGTT	GGAAGTGGTT	150
	GAAATGGAAA	TCCGCGACCT	GCTGTCCAGC	TACGACTTCC	CCGGCGACGA	200
	CTGCCCCGATC	GTACAAGGTT	CCGCACTGAA	AGCCTTGGA	GGCGATGCCG	250
	CTTACGAAGA	AAAAATCTTC	GAAGTGGCTA	CCGCATTGGA	CAGCTACATC	300
	CCGACTCCCG	AGCGTGCCGT	GGACAAACCA	TTCTTGCTGC	CTATCGAAGA	350
20	CGTGTCTCTC	ATTTCGGGCC	GCGGTACCGT	AGTCACCGGC	CGTGTAGAGC	400
	GAGGTATCAT	CCACGTTGGT	GACGAGATTG	AAATCGTCGG	TCTGAAAGAA	450
	ACCCAAAAAA	CCACCTGTAC	CGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	500
	CGAAGGTCAG	GCGGGCGACA	ACGTAGGCGT	ATTGCTGCGC	GGTACCAAAC	550
	GTGAAGACGT	AGAACGCGGT	CAGGTATTGG	CCAAACCGGG	TACTATCACT	600
25	CCTCACACCA	AGTTCAAAGC	AGAAGTGATC	GTATTGAGCA	AAGAAGAGGG	650
	CGGCCGCCAT	ACCCCGTTTT	TCGCCAACTA	CCGTCCCCAA	TTCTACTTCC	700
	GTACCACTGA	CGTAACCGGC	GCGGTTACTT	TGGAAAAAGG	TGTGGAAATG	750
	GTAATGCCGG	GTGAGAACGT	AACCATTACT	GTAGAACTGA	TTGCGCCTAT	800
30	CGCTATGGAA	GAAGGTCTGC	GCTTTGCGAT			830

2) INFORMATION FOR SEQ ID NO: 127

35 (i)SEQUENCE CHARACTERISTICS:

(A) LENGTH: 816 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40 (ii)MOLECULE TYPE: Genomic DNA

(vi)ORIGINAL SOURCE:

45 (A) ORGANISM: *Neisseria lactamica*
 (B) STRAIN: ATCC 23970

(xi)SEQUENCE DESCRIPTION: SEQ ID NO: 127

	CGGCGCAATC	TTGGTATGTT	CCGCCGCCGA	CGGCCCTATG	CGGCAAACCC	50
50	GCGAACACAT	TCTGTTGGCC	CGCCAAGTAG	GTGTACCTTA	CATCATCGTA	100
	TTCATGAACA	AATGCGATAT	GGTCGACGAT	GCCGAGCTGT	TGGAAGTGGT	150
	TGAAATGGAA	ATCCGCGACC	TGCTGTCAAG	CTACGACTTC	CCAGGCGACG	200
	ACTGCCCAAT	CGTACAAGGT	TCCGCACTGA	AAGCTTTGGA	AGGCGATGCC	250
	GCTTACGAAG	AAAAATCTT	CGAACTGGCT	GCCGCATTGG	ACAGCTACAT	300
55	CCCGACTCCC	GAGCGTGCCG	TGGACAAACC	TTTCCTGCTG	CCTATCGAAG	350
	ACGTATTCTC	CATCTCCGGC	CGCGGTACGG	TAGTAACCGG	CCGTGTAGAG	400
	CGCGGTGTCA	TCCACGTTGG	CGACGAGATC	GAAATCGTCG	GTCTGAAAGA	450
	AACCCAAAAA	ACCACCTGTA	CCGGTGTCTGA	GATGTTCCGC	AAACTGCTGG	500
	ACGAAGGTCA	GGCAGGCGAC	AACGTAGGCG	TATTGCTGCG	CGGTACCAA	550
60	CGTGAAGAAG	TGGAACGCGG	TCAGGTATTA	GCCAAACCGG	GTACCATCAC	600

	TCCGCACACC	AAGTTCAAAG	CAGAAGTGTA	TGTATTGAGC	AAAGAAGAGG	650
	GCGGTCGTCA	CACTCCGTTC	TTCGCCAACT	ACCGTCCGCA	ATTCTACTTC	700
	CGTACCACCG	ACGTAACCGG	CGCGGTTACT	TTGGAAGAAG	GCGTGGAAT	750
	GGTAATGCCC	GGTGAGAACG	TAACCATTAC	TGTAGAACTG	ATTGCGCCTA	800
5	TCGCTATGGA	AGAAGG				816

2) INFORMATION FOR SEQ ID NO: 128

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria meningitidis*
 (B) STRAIN: ATCC 13077

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128

25	CGGTGCAATC	CTGGTATGTT	CCGCAGCCGA	CGGTCCTATG	CCGCAAACCC	50
	GCGAACACAT	CCTGCTGGCC	CGTCAAGTAG	GCGTACCTTA	CATCATCGTG	100
	TTCATGAACA	AATGCGACAT	GGTCGACGAT	GCCGAGCTGT	TGGAAGTGGT	150
	TGAAATGGAA	ATCCGCGACC	TGCTGTCCAG	CTACGACTTC	CCCGGCGACG	200
	ACTGCCCGAT	CGTACAAGGT	TCCGCACTGA	AAGCCTTGGA	AGGCGATGCC	250
30	GCTTACGAAG	AAAAAATCTT	CGAATTGGCT	GCTGCATTGG	ACAGCTACAT	300
	CCCGACTCCC	GAGCGTGCCG	TGGACAAACC	TTTCTTGTTG	CCTATCGAAG	350
	ACGTATTCTC	TATTTCCGGT	CGTGGTACAG	TAGTAACCGG	TCGTGTAGAG	400
	CGCGGTATCA	TCCACGTCGG	TGACGAGATC	GAAATCGTCG	GTCTGAAAGA	450
	AACTCAAAAA	ACCACTTGTA	CCGGTGTTGA	AATGTTCCGC	AAACTGCTGG	500
35	ACGAAGGTCA	AGCAGGCGAC	AACGTAGGCG	TATTGCTGCG	CGGTACCAAA	550
	CGTGAAGACG	TAGAGCGTGG	TCAAGTATTG	GCTAAACCGG	GTACAATCAC	600
	TCCTCACACC	AAGTTCAAAG	CAGAAGTATA	CGTACTGAGC	AAAGAAGAGG	650
	GCGGCCGCCA	TACCCCGTTC	TTGCCTCACT	ACCGTCCCCA	ATTCTACTTC	700
	CGTACCACCG	ACGTAACCGG	CGCGGTTACT	TTGGAAGAAG	GTGTGGAAAT	750
40	GGTAATGCCG	GGCGAGAACG	TAACCATCAC	CGTAGAACTG	ATTGCGCCTA	800
	TCGCTATGGA	AGAAGGTTTG	CGCTTTGCGA	T		831

45 2) INFORMATION FOR SEQ ID NO: 129

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 815 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria mucosa*
 (B) STRAIN: ATCC 19696

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129

	CGGCGCAATC	TTGGTATGTT	CTGCTGCTGAC	GGTCCTATGC	CGCAAACCCG	50
	GYGAACACAT	CCTGTTGGCC	CGTCAAGTAG	GYGTACCTTA	CATCATCGTG	100
	TTCATGAACA	AATGCGACAT	GGTTGACGAT	GCCGAAYTGT	TGGAAGTGGT	150
	TGAAATGGAA	ATCCGTGACT	TGCTGTCAAG	CTACGACTTC	CCTGGYGACG	200
5	ACTGCCCCGAT	TGTACAAGGT	TCTGCACTGA	AAGCCTTGGA	AGGCGATGCC	250
	GCTTACGAAG	AAAAAATCTT	CGAACTGGCT	GCCGCATTGG	ACAGCTACAT	300
	CCCGACTCCC	GAGCGTGCCG	TAGACAAACC	GTTCCTGTTG	CCTATCGAAG	350
	ACGTATTCTC	CATCTCCGGT	CGTGGTACAG	TAGTAACCGG	CCGTGTAGAG	400
	CGCGGTGTTA	TCCACGTTGG	TGACGAGATC	GAAATCGTAG	GTCTGAAAGA	450
10	AACCCAAAAA	ACCACATGTA	CCGGTGTGTA	AATGTTCCGC	AAACTGCTGG	500
	ACGAAGGTCA	AGCCGGTGAC	AACGTAGGCG	TATTGCTGCG	CGGTACCAAA	550
	CGTGAAGAAG	TGGAACGCGG	TCAAGTATTG	GCTAAACCGG	GTACCATCAC	600
	TCCGCACACC	AAATTCAAAG	CAGAAGTGTA	CGTATTGAGC	AAAGAAGAGG	650
	GTGGTCGTCA	TACTCCGTTT	TTCGCTAACT	ACCGTCCTCA	ATTCTACTTC	700
15	CGTACTACCG	ACGTAACCGG	TGCGGTTACT	TTGGAAGAAG	GTGTAGAAAT	750
	GGTTATGCCT	GGTGAGAAYG	TAGCCATYAC	TGTAGAAGT	ATTGCGCCTA	800
	TYGCTATGGA	AGAAG				815

20

2) INFORMATION FOR SEQ ID NO: 130

(i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 829 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria sicca*
- (B) STRAIN: ATCC 9913

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130

	GGCGCAATCT	TGGTATGTTT	CGCTGCTGAC	GGTCCTATGC	CGCAAACCCG	50
	CGAACACATC	CTGTTGGCCC	GCCAAGTAGG	CGTACCTTAC	ATCATCGTGT	100
	TCATGAACAA	ATGCGACATG	GTTGACGATG	CCGAGCTGTT	GGAAGTGGTT	150
40	GAAATGGAAA	TCCGTGACTT	GCTGTCAAGC	TACGACTTCC	CTGGTGACGA	200
	CTGCCCCGATC	GTACAAGGTT	CTGCACTGAA	AGCCTTGGA	GGCGACGCCG	250
	CTTACGAAGA	AAAAATCTTC	GAAGTGGCTG	CTGCATTGGA	CAGCTACATC	300
	CCGACTCCTG	AGCGTGCCGT	GGACAAACCG	TTCCTGTTGC	CTATTGAAGA	350
	CGTATTCTCC	ATCTCCGGTC	GCGGTACCGT	AGTAACCGGC	CGTGTAGAGC	400
45	GCGGTGTTAT	CCACGTTGGT	GACGAGATTG	AAATCGTAGG	TCTGAAAGAA	450
	ACCCAAAAAA	CCACTTGTA	CGGTGTTGAA	ATGTTCCGCA	AACTGCTGGA	500
	CGAAGGTCAA	GCCGGTGACA	ACGTAGGCGT	ATTGCTGCGC	GGTACCAAAC	550
	GTGAAGAAGT	GGAACGCGGT	CAAGTATTGG	CTAAACCGGG	TACCATCACT	600
	CCTCACACTA	AATTCAAAGC	AGAAGTTTAC	GTATTGAGTA	AAGAAGAGGG	650
50	TGGTCGTCAT	ACTCCGTTCT	TCGCTAACTA	CCGTCCTCAA	TTCTACTTCC	700
	GTACTACCGA	CGTAACCGGC	GCGGTTACTT	TGGAAGAAGG	TGTAGAAATG	750
	GTTATGCCTG	GTGAGAACGT	AGCCATCACT	GTAGAAGTGA	TTGCACCGAT	800
	CGCTATGGAA	GAAGTCTGCT	GCTTTGCGA			829

55

2) INFORMATION FOR SEQ ID NO: 131

(i) SEQUENCE CHARACTERISTICS:

60

- (A) LENGTH: 814 bases

(B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Neisseria subflava*
 (B) STRAIN: ATCC 14221

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131

	CGGCGCGACT	TGGTATGTTT	CGCAGCTGAT	GGTCCTATGC	CTCAAACCTCG	50
	CGAACACATC	CTGTTGGCTC	GCCAAGTAGG	TGTACCTTAC	ATCATCGTAT	100
15	TCATGAACAA	ATGCGACATG	GTTGACGATG	CCGAGCTGTT	GGAACCTGGT	150
	GAAATGGAAA	TCCGTGACCT	GTTGTCAAGC	TACGACTTCC	CAGGCGACGA	200
	CTGCCCCAATC	GTACAAGGTT	CTGCACTGAA	AGCTTTGGAA	GGTGACGCTG	250
	GTTACGAAGA	GAAAATCTTC	GAATTGGCTG	CTGCTCTGGA	CAGCTACATC	300
	CCAACACCTG	AGCGTGCTGT	GGACAAACCT	TTCTTGTTGC	CTATCGAAGA	350
20	CGTATTCTCT	ATCTCTGGCC	GTGGTACAGT	AGTAACTGGT	CGTGTAGAGC	400
	GCGGTATCAT	CCACGTTGGT	GACGAGATCG	AAATCGTAGG	TCTGAAAGAA	450
	ACCCAAAAAA	CCACTTGTA	CGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	500
	CGAAGGTCAA	GCTGGTGACA	ACGTAGGCGT	ATTGCTGCGT	GGTACCAAAC	550
	GTGAAGACGT	AGAGCGTGGT	CAAGTATTGG	CTAAACCAGG	TACCATTACT	600
25	CCTCACACCA	AATTCAAAGC	AGAAGTATAC	GTACTGAGCA	AAGAAGAGGG	650
	TGGTCGTCAC	ACTCCATTCT	TCGCTAACTA	CCGTCCACAA	TTCTACTTCC	700
	GTACTACTGA	CGTAACTGGT	GCAGTTACTT	TGGAAGAAGG	CGTAGAAATG	750
	GTAATGCCAG	GTGAGAACGT	AACCATTACT	GTAGAACTGA	TTGCGCCTAT	800
	CGCTATGGAA	GAAG				814

30

2) INFORMATION FOR SEQ ID NO: 132

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 818 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Neisseria weaveri*
 (B) STRAIN: ATCC 51223

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132

	GCCATCTTGG	TATGTTCTGC	TGCTGACGGT	CCTATGCCGC	AAACCCGTGA	50
50	GCACATCCTG	TTGGCTCGTC	AAGTAGGTGT	ACCCTACATC	ATCGTATTCA	100
	TGAACAAATG	CGATATGGTT	GATGATGCAG	AGCTGCTGGA	ATTGGTAGAA	150
	ATGGAAATCC	GTGATCTGCT	GAGCAGCTAC	GATTTCCCTG	GCGATGATTG	200
	YCCAATCGTG	CAAGGTTCTG	CTTTGAAAGC	TTTGGAAGGT	GATGCCGCTT	250
	ACGAAGAAAA	AATCTTTGAA	TTAGCTGCTG	CATTGGATAG	CTATATTCCA	300
55	ACWCCTGAGC	GYGCTGTTGA	TAAACCATTG	CTGTTGCCGA	TTGAAGATGT	350
	ATTCTCAATT	TCAGGTCGTG	GTACAGTAGT	AACTGGTCGT	GTAAGACGCG	400
	GTATTATTCA	CGTAGGCGAT	GAAATTGAAA	TTGTAGGTTT	GAAAGARACY	450
	CAAAAACTA	CTTGTACCGG	CGTTGAAATG	TTCCGTAAAT	TGCTGGATSA	500
	AGGTCAGGCT	GGTGATAACG	TAGGCGTATT	GTTGCGTGGT	ACCAAACGTG	550
60	AAGACGTTGA	GCGTGGTCAA	GTATTGGCTA	AGCCTGGTWC	TATTACTCCG	600

CAYACCAAAT TCAAAGCAGA RGTKTATGTW TTGAGYAAGG AAGAAGGCGG 650
 TCGTCATACT CCGTTCTTCG CTAACATATCG TCCGCAATTC TATTTCCGTA 700
 CTACAGACGT TACCGGTGCK GTRACTTTAG AAGAAGGTGT GGAAATGGTA 750
 ATGCCTGGTG AGAAYGTTGC CATTACTGTW GARYTGATYG CTCCGATTGC 800
 5 KATGGAAGAA GGYTGCGT 818

2) INFORMATION FOR SEQ ID NO: 133

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 836 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Ochrobactrum anthropi*
 (B) STRAIN: ATCC 49188

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133

25 CGGCGCAATT CTGGTTGTTT CGGCCGCTGA CGGCCCGATG CCGCAGACCC 50
 GTGAGCACAT CCTGCTCGCT CGTCAGGTTG GCGTTCCGGC AATCGTCGTG 100
 TTCCTGAACA AGTGCGACCA GGTGACGAT GCAGAACTGC TCGAACTGGT 150
 TGAAGTGGAA GTTCGCGAAC TTCTGTCGAA ATACGATTTC CCGGGCGACG 200
 AAGTTCCGAT CATCAAGGGC TCGGCTCTTG CTGCTCTGGA AGATTCTTCG 250
 30 AAGGAACTGG GCGAAGACGC CGTTCGTTTCG CTGATGGCCG CTGTTGACGA 300
 CTACATTCCG ACCCCGGAAC GTCCGATCGA CCAGCCGTTT CTGATGCCGA 350
 TCGAAGACGT TTTCTCGATC TCGGGCCGTG GTACGGTTGT GACGGGTCGC 400
 GTTGAGCGCG GTATCGTCAA GGTGTTGAA GAAGTTGAAA TCGTCGGCAT 450
 CAAGGCGACG GCGAAGACGA CGGTAACCGG CGTTGAAATG TTCCGCAAGC 500
 35 TGCTCGAYCA GGGCCAGGCT GCGACAACA TCGGCGCTCT GATCCGCGGC 550
 GTTGGCCGTG AAGACGTTGA ACGCGGCCAG GTTCTCTGCA AGCCGGGTTT 600
 TGTGAAGCCG CACACCAAGT TCAAGGCAGA AGCCTACATT CTGACCAAGG 650
 ACGAAGGTGG CCGTCATACG CCGTTCTTTA CGAACTACCG TCCGCAGTTC 700
 TACTTCCGCA CGACGGACGT GACCGGTGTT GTCACGCTGC CGGAAGGCAC 750
 40 GGAAATGGTT ATGCCTGGCG ACAACGTCGC TATGGACGTC ACCCTGATCG 800
 TGCCGATCGC CATGGAAGAG AAGCTCCGCT TCGCTA 836

2) INFORMATION FOR SEQ ID NO: 134

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 805 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pantoea agglomerans*
 (B) STRAIN: ATCC 27155

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134

CCTGGTTGTT GCTGCGACTG ATGGCCCAAT GCCACAGACC CGTGAGCACA 50
 TCCTGCTGGG TCGTCAGGTT GGCCTTCCTT ACATCATCGT GTTCCTGAAC 100
 AAGTGTGACA TGGTTGATGA TGAAGAGCTG CTGGAAGTGG TAGAGATGGA 150
 AGTACGTGAC CTGCTGTCAC AGTACGACTT CCCAGGCGAT GACACCCCGA 200
 5 TCGTTCGTGG TTCTGCTCTG AAAGCGCTGG AAGGCGTTCC TGAGTGGGAA 250
 GCAAAAATCG TTGAGCTGGC TGAACACCTG GACAACTACA TCCCGGATCC 300
 AGTCCGTGCG ATCGACATGC CGTTCCTGCT GCCAATCGAA GACGTATTCT 350
 CAATCTCTGG CCGTGGTACC GTTGTTACCG GTCGTGTTGA GCGCGGCATC 400
 GTTAAAGTCG GCGACGAAGT TGAATCGTG GGTATCAAAG ATACTGCGAA 450
 10 ATCAACCTGT ACCGGTGTGG AGATGTTCCG TAAGCTGCTG GACCAGGGTC 500
 AGGCAGGCGA AAACGTGTGGT GTTCTGCTGC GCGGTATCAA GCGTGAAGAC 550
 ATCCAGCGTG GCCAGGTTCT GGCTAAGCCA GGCTCAATCA AGCCGCACAC 600
 CCAGTTCGAG TCAGAAGTTT ACGTTCTGTC TAAAGACGAA GGTGGCCGCC 650
 ATACTCCGTT CTTCAAAGGC TATCGTCCAC AGTTCTACTT CCGTACAAC 700
 15 GATGTAACCG GTTCAGTAGA GCTGCCAGAA GGCCTTGAGA TGGTCATGCC 750
 AGGCGACAAC ATCAAAATGG TTGTTACCCT GATCCACCCA ATCGCAATGG 800
 ACGAA 805

20

2) INFORMATION FOR SEQ ID NO: 135

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30

(vi) ORIGINAL SOURCE: _____

- (A) ORGANISM: *Pantoea dispersa*
 (B) STRAIN: ATCC 14589

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135

CGCGATCCTG GTTGTGCTG CACTGATGG CCAATGCCT CAGACCCGTG 50
 AGCACATCCT GCTGGGCCGT CAGGTTGGCG TTCCTTACAT CATCGTGTTT 100
 CTGAACAAGT GTGACATGGT TGATGACGAA GAGCTGCTGG AACTGGTTGA 150
 40 GATGGAAGTT CGCGATCTGC TGTCTCAGTA CACTTCCCA GGCGACGATA 200
 CCCCAATCGT ACGCGTTTCT GCGCTGAAAG CGCTGGAAGG CGACGCTGAG 250
 TGGGAAGCGA AAGTCGTTGA GCTGGCTGGT CACCTGGATA CTTACATTCC 300
 AGATCCAGTA CGTGCTATCG ATCTGCCGTT CTTGCTGCCA ATCGAAGACG 350
 TATTCTCAAT CTCTGGCCGT GGTACCGTTG TTACCGGTCG TGTGAGCGC 400
 45 GGCATCGTGA AAGTGGCGA CGAAGTAGAA ATCGTTGGTA TCAAAGCGAC 450
 TGCCAAGTCT ACCTGTACCG GTGTTGAAAT GTTCCGCAA CTGCTGGACC 500
 AGGGTCAGGC AGGCGAGAAC TGTGGTGTTC TGCTGCGCGG TATCAAGCGT 550
 GAAGAGATCC AGCGTGGTCA GGTTCCTGGCT AAGCCAGGCA CCATCAAGCC 600
 ACACACCAAG TTCGTATCAG AAGTGTACGT ACTGTCTAAA GACGAAGGCG 650
 50 GCCGTCATAC TCCGTTCTTC AAAGGCTACC GTCCACAGTT CTAATTCCGT 700
 ACYACTGATG TGACCGGCAM CATMGAAGT CCAGAAGGCG TTGAGATGGT 750
 AATGCCAGGC GACAACATCA AAATGRCCGT TGAGCTGATC CACCCAATCG 800
 CGATGGACCA GGGTCTGCGT TTCGC 825

55

2) INFORMATION FOR SEQ ID NO: 136

(i) SEQUENCE CHARACTERISTICS:

- 60 (A) LENGTH: 762 bases

285

(B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5 (ii)MOLECULE TYPE: Genomic DNA

(vi)ORIGINAL SOURCE:

(A) ORGANISM: *Pasteurella multocida*
 (B) STRAIN: NCTC 10322

10 (xi)SEQUENCE DESCRIPTION: SEQ ID NO: 136

	CACAAACACG	TGAGCACATC	CTTTTAGGTC	GCCAAGTAGG	CGTTCCTTAC	50
	ATCATCGTAT	TCTTAAACAA	ATGCGACATG	GTGGATGATG	AAGAATTATT	100
15	AGAATTAGTT	GAAATGGAAG	TGCGTGAAC	TCTTTCTCAA	TATGATTTCC	150
	CAGGTGATGA	TACACCAATC	GTACGTGGTT	CAGCGTTACA	AGCGTTAAAC	200
	GGYGTAGCTG	AGTGGAAGA	GAAAATTCTT	GAGTTAGCCA	ACCACTTAGA	250
	TACTTACATT	CCAGAGCCAC	AACGTGCAAT	CGACCAACCG	TTCCTTCTTC	300
	CGATTGAAGA	CGTGTTCTCA	ATTTCTGGTC	GTGGTACAGT	AGTAACAGGT	350
20	CGTGTTGAGC	GTGGTATCAT	CCGTACAGGT	GAAGAGGTTG	AAATTGTTGG	400
	TATTAAAGCG	ACAACGAAGA	CCACAGTAAC	AGGTGTTGAG	ATGTTCCGTA	450
	AATTATTAGA	CGAAGGTCGT	GCGGGTGAGA	ACGTTGGTGC	TTTATTACGT	500
	GGTACTAARC	GTGAAGAAAT	CGAACGTGGT	CAAGTGTTAG	CGAAACCGGG	550
	TTCAATYACG	CCACACACTG	ATTTTGAATC	AGAAGTTTAC	GTGTTATCAA	600
25	AAGAAGAAGG	TGGTCGTCAT	ACACCATTCT	TCAAAGGTTA	CCGTCCACAG	650
	TTCTACTTCC	GTACAACGGA	CGTAACAGGT	ACAATCGAAT	TACCGGAAGG	700
	TGTTGAGATG	GTGATGCCTG	GTGATAACAT	CAAGATGACT	GTAAGTTTGA	750
	TTCACCCAAT	CG				762

30

2) INFORMATION FOR SEQ ID NO: 137

(i)SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 832 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40 (ii)MOLECULE TYPE: Genomic DNA

(vi)ORIGINAL SOURCE:

(A) ORGANISM: *Peptostreptococcus anaerobius*
 (B) STRAIN: ATCC 27337

45 (xi)SEQUENCE DESCRIPTION: SEQ ID NO: 137

	TGGAGCTATC	TTAGTTGTAT	CAGCAGCGGA	TGGACCAATG	CCACAAACAA	50
	GAGAACACAT	CTTATTATCA	AGACAAGTAG	GAGTACCATA	TATCGTAGTA	100
50	TATTTGAATA	AAGCAGATAT	GGTAGAAGAT	GAAGAATTAT	TAGAATTAGT	150
	AGAAATGGAA	GTAAGAGAAT	TACTATCTGA	ATATGGATTG	CCAGGAGATG	200
	AAATTCCAAT	CATAACAGGA	TCATCCTTAG	GAGCATTAAT	TGGAGAACAA	250
	AAATGGATAG	ATCAAATCAT	GGCATTGATG	AAAGCCGTAG	ATGAATATAT	300
	TCCAACACCG	GAAAGAGCAG	TAGATCAACC	ATTCTTGATG	CCAATCGAAG	350
55	ACGTATTTAC	AATTACAGGA	AGAGGAAGTG	TAGTAACAGG	AAGAGTTGAA	400
	AGAGGAGTTG	TAAAAGTWGG	AGAAGAAGTT	GAAATCGTAG	GAATCAAAGC	450
	GACAACAAAG	ACAACCTGTA	CYGGAGTAGA	AATGTTCCGA	AAATTATTGG	500
	ATCAAGGACA	AGCAGGAGAT	AACATCGGAG	CTTTATTTRAG	AGGAACCAAG	550
	AAAGAAGATG	TAGAAAGAGG	ACAAGTATTG	GCAAAACCAG	GAACAATTCA	600
60	TCCTCATACA	AACTTCAGTG	GAGAAGTATA	TGTATTGACA	AAAGAAGAAG	650

GAGGAAGACA	TACTCCATTC	TTCTCAGGAT	ACAGACCACA	ATTTTACTTT	700
AGAACCACAG	ATATTACAGG	AGCAGTAACA	TTACCAGAAG	GAGTAGAAAT	750
GGTAATGCCR	GGAGATAATA	TCACAATGAC	AGTAGAATTG	ATTCACCCAA	800
TTGCAATGGA	AACAGGATTA	CGATTTGCAA	TT		832

5

2) INFORMATION FOR SEQ ID NO: 138

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 823 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Peptostreptococcus asaccharolyticus*
 (B) STRAIN: LSPQ 2639

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138

25	TAGTATGTTT	AGCAGCAGAY	GGTCCAATGC	CACAAACAAG	AGAACACATT	50
	CTACTAGCAA	GACAAGTTGG	TGTACCAAAG	ATAGTAGTAT	TCCTAAACAA	100
	AGAAGACCAA	GTAGACGATC	CAGAACTAAT	TGAATTAGTA	GAGATGGAAA	150
	TCAGAGACCT	ACTATCAGAA	TATGACTTCG	AYGGAGACAA	CACACCAATC	200
	GTAGTAGGAT	CAGCATTAAA	AGCCCTAGAC	GATCCAGACG	GAGAATGGGG	250
	AGACAAAATC	GTAAACTAA	TGGAAGMAGT	AGACGAATAC	ATCCCAACAC	300
30	CAGTAAGAGA	TACAGAACAC	CCATTCCTAA	TGCCAATCGA	AGACRTATTC	350
	TCAATYACAG	GAAGAGGAAC	AGTAGCAACA	GGAAGAGTAG	AACAAGGTGT	400
	AGTAAAAGTA	GGMGACACAG	TAGAACTAGT	AGGCTTAACA	GACGAAAGCA	450
	GACAAAGTAGT	AGTAACAGGT	GTAAGAAATGT	TTAGAAAACA	ACTAGACCTA	500
	GCAGAAGCMG	GAGACAACAT	TGGAGCCCTA	CTAAGAGGAG	TACAAAGAGA	550
35	AGAAATCCAA	AGAGGACAAG	TACTAGCAGC	ACCAGGAACA	ATCAAACCAC	600
	ACACAAAATT	TGAAGCAGAA	GTATACGTAC	TAACAAAAGA	AGAAGGTGGA	650
	AGACACACAC	CATTCTTTAA	CGGATACAGA	CCACAATTCT	ACTTCAGAAC	700
	AACAGACGTA	ACAGGAGACA	TCCAAC TAGC	AGACGGAGTA	GAAATGGTAA	750
	TGCCAGGAGA	CAACTCAACA	TTTACAGTAA	CACTAATCAC	ACCAATCGCA	800
40	ATGGACGAAG	GACTAAGATT	CGC			823

2) INFORMATION FOR SEQ ID NO: 139

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 832 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Peptostreptococcus prevotii*
 (B) STRAIN: ATCC 9321

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139

60	CTATCATCGT	AGTATCTGCA	GCAGACGGTC	CAATGCCCAA	ACAGAGAGAA	50
----	------------	------------	------------	------------	------------	----

```

CACATCCTAC TAGCAAGACA AGTAGGCGTT CCAAAAATCG CAGTATTCCT 100
AAACAAAGAA GACCAAGTAG ACGATCCAGA ACTAATCGAA TTAGTAGAAA 150
TGGAAATCAG AGACCTACTT TCAGAAATACG ACTTCGATGG AGACAACGCT 200
CCAGTAGTAG TAGGATCTGC TCTTAAATCA CTAGAAGAAG GCGGAGAAGG 250
5 CCCATGGTCA GACAAAATCC TTGACCTAAT GGCACAAGTA GACGAATACT 300
TCGACATCCC AGAAAGAGAC AACGACCAAC CATTCCTAAT GCCAGTAGAA 350
GACGTAATGA CAATCTCAGG ACGTGGAACA GTAGCAACAG GAAGAGTTGA 400
AAGAGGAACA CTAAAAGTTG GTGATACAGT AGAAATCGTA GGACTAACAG 450
AAGATACAAA AGAAACAGTA GTAACCTGGAG TAGAAATGTT CCACAAATCM 500
10 CTAGACCAAG CAGAATCTGG AGATAACGTA GGACTACTAC TAAGAGGAGT 550
AACAAAGAGAT CAAATCTCAA GAGGACAAGT ACTAGCAAAA CCAGGWTCAG 600
TAAACCCACA CACAGAATTC GAAGGTCAAG TATACGTACT AACAAAAGAA 650
GAAGGTGGAC GTCACACACC ATTCTTCAGT GGATATAGAC CACAATTCTT 700
CTTTAGAACA ACAGACGTAA CAGGAGACAT CGAACTAGAA GAAGGCGTAG 750
15 AAATGGTAAT GCCAGGAGAC AACGCAACAT TCAAAATCAC ACTCCAAAAA 800
CCAATCGCTC TAGAAGAAGG ACTAAGATTC GC 832

```

20 2) INFORMATION FOR SEQ ID NO: 140

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 831 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Porphyromonas asaccharolytica*
 (B) STRAIN: ATCC 25260

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140

```

35 CGGTGCTATC ATCGTAGTTG CTGCAACTGA TGGTCCTATG CCTCAGACGC 50
GTGAGCACAT CCTACTAGCA CGTCAGGTCA ACGTACCTCG TCTAGTTGTC 100
TTTATGAACA AGTGCGACCT TGTTGATGAC GAGGAGATGC TCGAGCTCGT 150
AGAGATGGAT ATGCGTGAGC TACTAAGCTT CTATGACTTT GACGGCGACA 200
40 AACTCCTGT CATCCGTGGT TCTGCTCTTG GTGCTCTCAA TGGTGAGCCT 250
AAGTGGGTAG AGAAGGTTAT GGAGCTCATG GAGGCTGTAG AACTTTGGAT 300
CCCACTACCT GAGCGCGACA TCGACAAGCC TTTCCCTAATG CCTGTAGAGG 350
ACGTATTCTC TATCACAGGT CGTGGTACTG TCGCTACTGG TCGTATCGAG 400
ACTGGTGTCTG TTAAGGTCAA CGATGAGGTT CAGATCATCG GTCTAGGTGC 450
45 TGAGGGTAAG AAGAGCGTCG TAACTGGCGT GGAAATGTTT CGCAAGATCC 500
TTGATGAGGG TGAAGCTGGT GATAACGTAG GTCTCCTACT CCGTGGTATC 550
GACAAGGACG AGATCAAGCG CGGTATGGTC CTAGCACACC CAGGTCAGGT 600
CAAGCCTCAC GATCACTTCA AGGCTGAGGT CTATATCCTG AAGAAGGAAG 650
AGGGTGGTCTG TCACACACCA TTCCACAACA AGTACCGTCC TCAGTTCTAC 700
50 ATCCGTACGC TAGACGTAAC GGGCGAGATC AACTCCCAG AGGGTGTAAG 750
GATGGTTATG CCTGGTGATA ACGTCACCAT CGATGTCAAG CTCATCTCTC 800
CAGTAGCTTG TAGCGTAGGT CTACGCTTCG C 831

```

55 2) INFORMATION FOR SEQ ID NO: 141

(i) SEQUENCE CHARACTERISTICS:

- 60 (A) LENGTH: 818 bases
 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*
(B) STRAIN: ATCC 33277

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141

CGGTGCTATA	ATCGTTGTAG	CAGCTACAGA	CGGTCCTATG	CCTCAGACTC	50
GCGAGCACAT	CCTTTTGGCT	CGCCAGGTAA	ACGTTCCTCG	TCTGGTTGTT	100
TTCATGAACA	AATGTGACAT	GGTAGACGAT	GAAGAGATGC	TCGAGCTTGT	150
TGAAATGGAC	ATGCGCGAAC	TCCTTTCTTT	CTACGATTTC	GATGGTGACA	200
ATACCCCTAT	CATCCGTGGT	TCTGCTCTGG	GCGCTTTGAA	TGGAGAGCCT	250
CAGTGGGAAG	ACAAGGTGAT	GGAGCTTATG	GAAGCTGTTG	ACAAC TGGGT	300
TCCCCTGCCT	GAGCGCGATA	TCGACAAACC	GTTCTTGATG	CCGGTTGAAG	350
ACGTGTTCTC	TATCACGGGT	CGTGGTACGG	TCGCTACAGG	ACGTATCGAA	400
ACCGGTATTG	TGAAGACCGG	TGACGAAGTT	CAAATCATCG	GCCTCGGTGC	450
AGAAGGAATG	AAGTCGGTTG	TTACGGGTGT	TGAAATGTTT	CGTAAGATTC	500
TTGACGAAGG	TCAGGCTGGT	GACAACGTTG	GTCTCCTCCT	GCGTGGTATC	550
GATAAGGATC	AGATCAAGCG	TGGTATGGTT	ATCTCTCACC	CGGGTAAGAT	600
TACTCCTCAC	AAGAGATTTA	AGGCCGAGGT	TTATATCTTG	AAGAAAGAAG	650
AAGGTGGTCG	CCACACTCCT	TTCCACAACA	AATATCGTCC	GCAGTTCTAC	700
ATCCGTACGC	TTGACGTGAC	CGGTGAAATC	ACTCTTCCCG	AAGGAACAGA	750
AATGGTTATG	CCCGGTGACA	ACGTAACGAT	CACTGTAGAA	CTCATCTACC	800
CGGTTGCATG	TAATGTAG				818

2) INFORMATION FOR SEQ ID NO: 142

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 830 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Pragia fontium*
(B) STRAIN: ATCC 49100

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142

CGGCGCTATT	CTGGTTGTTG	CTGCAACTGA	TGGTCCTATG	CCTCAAAC TC	50
GTGAGCACAT	CCTGTTAGGY	CGCCAGGTTG	GCGTACCATA	CATCATTGTG	100
TTCCTGAACA	AGTGTGACAT	GGTTGAYGAT	GAAGAGCTGT	TAGAACTGGT	150
TGAAATGGAA	GTTCTGTGAG	TTCTGTCTCA	GTACGATTTC	CCAGGTGATG	200
ATACTCCAGT	TGTTCTGGGT	TCTGCGCTGA	AAGCGTTRGA	AGGCGAAGCT	250
GAGTGGGAAG	CTAAAATCAT	TGAATTGGCT	GACTCCCTGG	AYAGCTACAT	300
TCCACAGCCA	GAGCGTGCAA	TTGATAAGCC	GTTCCCTGCTG	CCAATCGAAG	350
ACGTTTTCTC	AATCTCTGGC	CGTGGTACAG	TAGTAACCGG	TCGTGTAGAG	400
CGCGGTATCG	TTAAAGTTGG	TGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	450
TACTGTGAAA	ACAAC TTGTA	CTGGCGTTGA	AATGTTCCGT	AARTTACTGG	500
ATGAAGGCCG	TGCGGGTGAG	AACGTTGGTG	TTCTGCTGCG	TGGTACTAAG	550
CGTGATGAAA	TCGAACGTGG	TCAAGTATTA	GCAAAACCAG	GTTCAATCAA	600
CCCGCATACT	AACTTCGTAT	CAGAAGTTTA	TATCCTGAGC	AAAGATGAAG	650

GTGGTCGTCA	TACTCCATTC	TTCAAAGGCT	ACCGTCCACA	GTTYTACTTC	700
CGTACAACGT	ACGTGACCGG	TACCATCGAA	CTGCCAGAAG	GCGTAGAGAT	750
GGTAATGCCA	GGTGATAACA	TTCAGATGAC	TGTAAGTCTG	ATTGCCCCAA	800
TCGCGATGGA	CGAAGGTTTA	CGCTTCGCTA			830

5

2) INFORMATION FOR SEQ ID NO: 143

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 821 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

20 (A) ORGANISM: *Prevotella melaninogenica*
 (B) STRAIN: ATCC 25845

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143

25	TGGTGCTATC	TTGGTTGTAG	CTGCTACTGA	TGGTCCTATG	CCTCAGACTC	50
	GTGAGCACGT	ATTGCTCGCT	CGTCAGGTAA	ACGTACCTCG	CTTGGTTGTA	100
	TTCTTGAACA	AGTGTGATAT	GGTTGACGAT	GCTGAGATGC	TTGACCTCGT	150
	TGAGATGGAG	GTTTCGTGAGA	TCCTCGAGCA	GTACGGTTAT	GAGGAGGATA	200
	CTCCTATTAT	TCGTGGTTCT	GCACTCGGTG	CTTTGAACGG	TGTTGAGAAG	250
	TGGGTAGACT	CTGTAATGGA	GCTCATGGAT	ACTGTTGACA	CTTGGATTGA	300
30	AGAGCCAGAG	CGTGAGATTG	ACAAGCCATT	CTTGATGCCT	GTTGAGGACG	350
	TATTCTCTAT	CACAGGTCGT	GGTACTGTAG	CTACTGGTCG	TATCGAGACT	400
	GGTATCTGTA	AGGTAGGTGA	TGAGGTTTCA	TTGCTCGGTC	TCGGTGAGGA	450
	CAAGAAGTCT	GTTATCACTG	GTGTTGAGAT	GTTCCGTAAG	AACCTTCCAA	500
	CAGGTCAGGC	TGGTGACAAC	GTAGGTCTCC	TCCTTCGTGG	TATCGATAAG	550
35	GCTGAGGTTA	AGCGTGGTAT	GGTTGTTGTG	CACCCAGGTG	CTATTACTCC	600
	TCACGATCAC	TTCAAGGCAT	CTATCTATGT	ATTGAAGAAG	GAAGAGGGTG	650
	GTCGTCATAC	TCCATTCCGGT	AACAAGTATC	GTCCACAGTT	CTACCTCCGT	700
	ACAATGGACT	GTACAGGTGA	AATCCACCTC	CCAGAGGGCG	TTGAGATGGT	750
	TATGCCAGGT	GACAACGTAG	AGATTGAAGT	TGTATTGATC	TATAAGGTTG	800
40	CTTTGAACGA	GGGTCTTCGT	T			821

2) INFORMATION FOR SEQ ID NO: 144

45

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 827 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 50 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

55 (A) ORGANISM: *Prevotella oralis*
 (B) STRAIN: ATCC 33269

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144

60	TGGTGCTATT	CTTGTAGTAG	CTGCTACTGA	CGGTCCTATG	CCTCAAACCTC	50
----	------------	------------	------------	------------	-------------	----

	GTGAACACGT	GCTTCTTGCT	CGTCAGGTGA	ACGTACCTCG	TTTGGTCGTT	100
	TTCTTGAACA	AGTGCGATAT	GGTTGACGAT	GAAGAAATGC	TTGAGCTCGT	150
	AGAAATGGAG	CTTCATGAAC	TTCTCGAGCA	GTATGAATAT	GAGGAGGATA	200
	CTCCTATTGT	TCGTGGTTTCG	GCACCTGGCG	CTCTGAATGG	AGTAGAGAAG	250
5	TGGGTTGACA	GCGTGATGAA	GTTGATGGAT	ACCGTTGATG	AATGGATACA	300
	GGAACCACCG	CGTGATCTTG	ATAAGCCTTT	CTTGATGCCG	GTAGAGGATG	350
	TATTTTCTAT	TACTGGTCGT	GGAACGGTTG	TTACAGGCCG	TATTGAAACT	400
	GGTAAGGTTA	AGGTGGGCGA	TGAAGTTCAA	CTTCTTGGTC	TCGGTGAAGA	450
	TAAGAAGTCC	GTTGTGACAG	GCGTTGAGAT	GTTCCGTAAG	ATTCTTGACG	500
10	AAGGTGAAGC	TGGTGATAAT	GTAGGCTTGC	TGCTTCGTGG	TATCGATAAG	550
	ACGGAAGTAA	AGCGTGGTAT	GGTTGTCGTA	CATCCGGGGG	CTATTACTCC	600
	TCACGATCAT	TTCAAGGCTT	CAGTTTACGT	ATTGAAGAAA	GAAGAAGGCG	650
	GTCGCCATAC	TCCGTTTGGT	AMCAAGTATC	GTCCACAGTT	CTATCTTCGT	700
	ACCATGGACT	GTACTGGTGA	AATTACTCTT	CCGGAAGGAG	TTGAGATGGT	750
15	AATGCCGGGT	GATAACGTCG	AAATTGAAGT	TAAGTTGATC	TATCCGGTAG	800
	CTTTGAACGA	GGGACTTCGT	TTCGCTA			827

20 2) INFORMATION FOR SEQ ID NO: 145

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 833 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Propionibacterium acnes*
 (B) STRAIN: ATCC 6919

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145

35	CGGCGCCATC	CTCGTGGTTG	CTGCTACCGA	CGGCCCGATG	CCTCAGACTC	50
	GCGAGCACGT	TCTGCTCGCT	CGTCAGGTGG	GCGTGCCCGC	CATCGTCGTC	100
	GCCCTCAACA	AGTGCGACAT	GGTTGACGAT	GAGGAGCTCA	TTGAGCTCGT	150
	CGAGATGGAG	GTCCGCGAGC	TGCTGACCTC	GCAGGAGTTC	GACGGCGACA	200
40	ACTGCCCTGT	CGTTTCGCATC	TCCGCCTTCC	AGGCCCTCCA	GGGTGATGAG	250
	AAGTGGACCC	AGTCGATCCT	CGACCTCATG	GACGCCGTGG	ACGAGTACAT	300
	CCCGCAGCCT	GAGCGCGATC	TCGACAAGCC	CTTCCTTATG	CCGATCGAGG	350
	ACGTCTTCAC	CATCACCGGC	CGTGGCACCG	TTGTCACCGG	TCGTGTCGAG	400
	CGCGGCGTCG	TCAAGACTGG	CGAAGAGGTC	GAGATCGTCG	GTATCCACGA	450
45	GAAGACCCAG	AAGACCACCG	TTACCGGTGT	CGAGATGTTC	CGCAAGATCC	500
	TCGACGAGGG	CCGCGCTGGT	GAGAACGTCG	GCGTTCTGCT	CCGTGGCACC	550
	AAGAAGGAGG	ATGTCGTTTCG	CGGCATGGTC	CTCTCCAAGC	CTGGTTCCAC	600
	CACCCCCCAC	ACCGACTTCG	AGGGCCAGGT	CTACGTCCTC	AAGAAGGATG	650
	AGGGTGGCCG	CCACAAGCCG	TTCTTCTCCC	ACTACAGCCC	CCAGTTCTAC	700
50	TTCCGTACCA	CGGACGTGAC	TGGCACTGTT	GAGCTCCCCG	AGGGCACCGA	750
	GATGGTCATG	CCTGGCGACA	ACACCGACAT	GACTGTGCAC	CTGATTCAAC	800
	CGGTTGCCAT	GGAGGATCAG	CTCAAGTTCC	CTA		833

55

2) INFORMATION FOR SEQ ID NO: 146

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 745 bases
 60 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Proteus mirabilis*
(B) STRAIN: ATCC 35659

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146

	CACAAACTCG	TGAGCACATC	CTGTTAGGTC	GTCAGGTTGG	TGTTCTTAC	50
	ATCATCGTAT	TCCTGAACAA	ATGTGACATG	GATAGATGATG	AAGAGCTGTT	100
	AGAATTAGTT	GAAATGGAAG	TTCGTGAACT	TCTGTCTCAA	TACGATTTCC	150
15	CAGGTGATGA	CACTCCAGTA	ATCCGTGGTT	CAGCGCTGAA	AGCACTGGAA	200
	GGCGAAGCAG	AGTGGGAAGC	AAAAATTGTT	GAATTAGCAG	AAGCACTGGA	250
	TTCTTATATC	CCAGAGCCAG	AGCGTGCAAT	TGACAAACCA	TTCCTGTTAC	300
	CAATCGAAGA	TGTATTCTCA	ATCTCAGGCC	GTGGTACAGT	AGTTACTGGT	350
	CGTGTAGAGC	GTGGTATCAT	CAAAGTAGGT	GATGAAGTTG	AGATTGTTGG	400
20	TATCAAAGAA	ACCGCCAAAA	CAACTTGTAC	TGGCGTTGAA	ATGTTCCGTA	450
	AATTACTTGA	CGAAGGTCGT	GCAGGTGAGA	ACGTAGGTGT	TCTGCTGCGT	500
	GGTACAAAC	GTGAAGAAAT	CGAACGTGGA	CAAGTACTGG	CRAAACCAGG	550
	CTCAATCAAC	CCACACAACA	AATTTGAATC	AGAAGTTTAT	ATTCTGAGCA	600
	AAGATGAAGG	TGGTCGTCAC	ACTCCATTCT	TCAAAGGCTA	CCGTCCACAG	650
25	TTCTACTTCC	GTACAACTGA	CGTAACTGGT	ACTATCGAAT	TACCAGAAGG	700
	CGTAGAAATG	GTAATGCCAG	GCGACAACGT	GAACATGATC	GTTGA	745

30 2) INFORMATION FOR SEQ ID NO: 147

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 829 bases
(B) TYPE: Nucleic acid
35 (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Proteus penneri*
(B) STRAIN: ATCC 33519

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147

45	GGAGCTATCC	TGGTTGTTGC	TGCGACAGAT	GGCCCAATGC	CACAAACTCG	50
	TGAGCACATC	CTGTTAGGTC	GTCAGGTTGG	TGTTCTTAC	ATCATCGTAT	100
	TCCTGAACAA	ATGTGACATG	GATAGATGATG	AAGAGTTACT	GGAATTAGTM	150
	GAAATGGAAG	TTCGTGAACT	TCTGTCTCAG	TACGATTTCC	CAGGTGATGA	200
50	CACTCCAGTA	ATCCGTGGTT	CAGCGCTGAA	AGCACTGGAA	GGCGAAGCAG	250
	AGTGGGAAGC	AAAAATTGTT	GAATTAGCAG	AAGCACTGGA	TTCATACATC	300
	CCAGARCCAG	AGCGTGCAAT	TGACAAACCA	TTCCTGTTAC	CAATTGAAGA	350
	CGTATTCTCA	ATTTTCAGGCC	GTGGTACAGT	AGTAACAGGT	CGTGTGAGC	400
	GTGGCGTAAT	CAAAGTTGGT	GAAGAAGTTG	AAATCGTTGG	TATTAAACCA	450
55	ACAGCGAAAA	CAACTTGATC	TGGCGTTGAA	ATGTTCCGTA	AATTACTTGA	500
	CGAAGGTCGT	GCAGGTGAGA	ACGTAGGTGT	TCTTCTGCGT	GGTACTAAAC	550
	GTGAAGAAAT	CGAACGTGGA	CAAGTACTGG	CGAAACCAGG	TTCAATCAAC	600
	CCACACACTA	AATTTGAATC	AGAAGTTTAT	ATTCTGAGCA	AAGATGAAGG	650
	TGGTCGTCAT	ACTCCATTCT	TCAAAGGCTA	CCGTCCACAG	TTCTACTTCC	700
60	GTACAACTGA	CGTAACTGGT	ACTATCGAAT	TACCAGAAGG	CGTAGAAATG	750

GTAATGCCAG GTGACAACAT CAACATGATC GTTGAAGTGA TTCACCCAAT 800
CGCGATGGAC GACGGTTTAC GTTTCGCTA 829

5

2) INFORMATION FOR SEQ ID NO: 148

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 824 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Proteus vulgaris*
(B) STRAIN: ATCC 13315

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148

CGGAGCTATT CTGGTTGTTG CTGCGACTGA TGGCCCAATG CCACAAACTC 50
GTGAGCACAT CCTGTTAGGT CGCCAGGTTG GTGTACCTTA CATCATCGTA 100
TTCCTGAACA AATGTGACAT GGTTGATGAT GAAGAACTGC TGGAAATTAGT 150
25 AGAAATGGAA GTTCGTGAAC TTCTGTCTCA GTACGATTTC CCAGGTGATG 200
ACACTCCAGT AATCCGTGGT TCAGCGCTGA AAGCACTGGA AGGCGAAGCT 250
GAGTGGGAAG CAAAATTGT TGAATTAGCA GAAGCACTGG ATTCTTACAT 300
CCCAGAACCA GAGCGTGCAA TTGACAAACC ATTCCTGCTG CCTATCGAAG 350
ACGTATTCTC AATCTCTGGT CGTGGTACAG TAGTAACAGG CCGTGTTAGAG 400
30 CGTGGTGTGG TTAAAGTTGG TGAAGAAGTT GAGATTGTTG GTATTAAAGA 450
CACAGTTAAA ACAACTTGTA CTGGCGTTGA AATGTTCCGT AAATTACTTG 500
ACGAAGGTCG TGCAGGTGAG AACGTAGGTG TTCTTCTGCG TGGTACTAAA 550
CGTGAAGAAA TCGAACGTGG ACAAGTACTG GCTAAACCAG GTTCAATCAA 600
GCCACACACT AAATTCGAAT CAGAAGTTTA TATCCTGAGC AAAGATGAAG 650
35 GTGGTCGTCA CACTCCATTC TTCAAAGGTT ACCGTCCACA GTTCTACTTC 700
CGTACAACCTG ACGTAACTGG TACTATCGAA TTACCAGAAG GCGTAGAAAT 750
GGTAATGCCA GGTGACAACA TCAACATGAT CGTTGAAGT ATTACCCCTA 800
TCGCGTAGGA CGACGGTTTA CGTT 824

40

2) INFORMATION FOR SEQ ID NO: 149

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 745 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Providencia alcalifaciens*
(B) STRAIN: ATCC 9886

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149

60 CACAAACTCG TGAGCACATC CTGTTAGGTC GCCAAGTAGG TGTTCTTAC 50
ATCATCGTTT TCCTGAACAA ATGTGACATG GTAGACGACG AAGAACTGTT 100
AGAATTAGTT GAAATGGAAG TTCGTGAAC TCTGTCTCAG TACGATTTC 150


```

CAGGCGATGA CACTCCAGTT GTTCGCGGTT CAGCACTGAA AGCGCTGGAA 200
GGCAACCCAG AGTGGGAAGC AAAAATTGTT GAATTAGCAG GTTACCTGGA 250
TTCTTACATC CCAGAACCAG AGCGTGCAAT TGACAAGCCA TTCCTGCTGC 300
CAATCGAAGA CGTATTCTCA ATCTCTGGTC GTGGTACAGT AGTAACAGGC 350
5 CGTGTTGAGC GTGGTATCAT CAAAGTTGGT GAAGAAGTTG AAATCGTTGG 400
TATTCAAGCG ACTGCGAAAA CAACTGTGAC TGGCGTTGAA ATGTTCCGTA 450
AACTGCTGGA TGAAGGTCGT GCGGGTGAGA ACGTTGGTGT TCTGCTGCGT 500
GGTACTAAAC GTGAAGAAAT TCAACGTGGT CAAGTACTGG CTAAACCAGG 550
TTCAATCAAG CCACACACTC AATTCGAATC AGAAGTATAT ATTCTGAGCA 600
10 AAGATGAAGG TGGTCGTCAT ACTCCATTCT TCAAAGGCTA CCGTCCACAG 650
TTCTACTTCC GTACAACCTG CGTAACCGGT ACTATCGAAC TGCCAGAAGG 700
CGTAGAGATG GTAATGCCAG GCGACAACAT CAACATGATC GTGAC 745

```

15

2) INFORMATION FOR SEQ ID NO: 150

(i) SEQUENCE CHARACTERISTICS:

```

20 (A) LENGTH: 830 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

```

    (A) ORGANISM: Providencia rettgeri
    (B) STRAIN: ATCC 9250

```

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150

```

CGGTGCAATC CTGGTTGTTG CTGCGACTGA TGGCCCAATG CCACAAACTC 50
GTGAGCACAT CCTGTTAGGY CGCCAAGTAG GTGTWCCTTA CATCATCGTT 100
TTCCTGAACA AATGTGACAT GGTAGACGAC GAAGAACTGT TAGAATTAGT 150
35 TGAATGGAA GTTCGTGAAC TTCTGTCTCA ATACGATTTC CCAGGCGACG 200
ACACTCCAGT TGTCCGTGGT TCAGCTCTGA AAGCGCTGGA AGGCAACCCA 250
GAGTGGGAAG CGAAAATTGT TGAATTAGCA GGTCACCTGG ATTCTTACAT 300
CCCAGAACCA GAGCGTGCAA TTGACAAACC ATTCCTGCTG CCAATCGAAG 350
ACGTATTCTC AATCTCTGGT CGTGGTACAG TAGTAACAGG CCGTGTGAG 400
40 CGTGGTATCA TCAAAGTTGG TGAAGAAGTT GAAATCGTTG GTATCCAAGA 450
CACGGTTAAA ACAACTTGTA CTGGCGTTGA AATGTTCCGT AAAGTCTGG 500
ACGAAGGTCG TCGGGGTGAG AACGTTGGTG TTCTGCTGCG TGGTACTAAA 550
CGTGAAGAAA TTCAACGTGG TCAAGTACTG GCAAAACCAG GTTCAATCAA 600
GCCACACACT AAATTCGAAT CAGAAGTCTA TATTCTGAGC AAAGATGAAG 650
45 GTGGTCGTC CACTCCATTC TTCAAAGGTT ACCGTCCACA GTTCTACTTC 700
CGTACAACCTG ACGTAACAGG TACTATCGAA CTGCCAGAAG GCGTAGAGAT 750
GGTAATGCCA GGTGATAACA TCAACATGAT CGTTACCCTG ATCCACCCAA 800
TCGCGATGGA CGACGGTTTA CGTTTCGCAA 830

```

50

2) INFORMATION FOR SEQ ID NO: 151

(i) SEQUENCE CHARACTERISTICS:

```

55 (A) LENGTH: 826 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

60 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Providencia rustigianii*
 (B) STRAIN: ATCC 33673

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151

```

CGGTGCAATC CTGGTTGTTG CTGCGACTGA TGGCCCAATG CCACAAACTC      50
GTGAGCACAT CCTGTTAGGT CGCCAAGTAG GTGTTCTTA CATCATCGTT      100
10 TTCCTGAACA AATGTGACAT GGTGACGAC GAAGAACTGT TAGAATTAGT      150
TGAAATGGAA GTTCGTGAAC TTCTGTCTCA GTACGATTTC CCAGGCGACG      200
ACACTCCAGT TGTTTCGYGGT TCAGCACTGA AAGCGCTGGA AGGTATCCCT      250
GAGTGGGAAG CGAAAATTGT TGAATTAGCC GGTACCTGG ACAGCTACAT      300
CCCAGAACCA GAGCGCGCAA TTGACCGTCC ATTCCTGCTG CCAATCGAAG      350
15 ACGTATTCTC AATCTCTGGT CGTGGTACAG TAGTAACAGG SCGTGTTGAG      400
CGTGGTATCG TTAAAGTTGG TGAAGAAGTT GAAATCGTTG GTATCCAAGA      450
CACRGTAAAC ACAACTTGTA CTGGCGTTGA AATGTTCCGT AAAGTGCTTG      500
ACGAAGGTCG TGCTGGTGAG AACGTTGGTG TTTTACTGCG TGGTACTAAG      550
CGTGAAGAAA TTCAACGTGG TCAAGTACTG GCTAAACCAG GTTCAATCAA      600
20 GCCACACACT ACTTTTGAAT CAGAAGTTTA TATCTGAGC AAAGATGAAG      650
GTGGTCGTCA TACTCCATTC TTCAAAGGCT ACCGTCCACA GTTCTACTTC      700
CGTACAAC TGTAACCGG TACTATCGAA CTGCCAGAAG GCGTAGAGAT      750
GGTAATGCCA GCGGACAACA TCAACATGAT CGTGACACTG ATTCACCCAA      800
TCGCGATGGA TGATGGTTTA CGTTTC      826
25

```

2) INFORMATION FOR SEQ ID NO: 152

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 830 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Providencia stuartii*
 (B) STRAIN: ATCC 33672

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152

```

CGGTGCAATC CTAGTTGTTG CGGCAACAGA TGGCCCAATG CCACAAACTC      50
45 GTGAGCACAT CCTGTTAGGT CGTCAGGTTG GCGTTCCTTA CATCATCGTG      100
TTCCTGAACA AATGTGACAT GGTAGACGAC GAAGAGCTGC TGGAAGTGGT      150
TGAAATGGAA GTTCGTGAAC TTCTGTCTCA ATACGATTTC CCAGGTGATG      200
ACACTCCAGT TATCCGTGGT TCAGCGCTGA AAGCGTTGGA AGGCAACCCA      250
GAGTGGGAAG CGAAAATCGT TGAAGTAGCA GAAGCACTGG ACAGCTACAT      300
50 CCCAGAGCCA GAGCGTGCAA TTGACAAGCC ATTCCTGCTG CCAATCGAAG      350
ACGTATTCTC AATCTCAGGT CGTGGTACAG TAGTCACAGG CCGTGTGAG      400
CGTGGTATCA TCAAAGTTGG TGAAGAAGTT GAAATCGTAG GTATCAAAGA      450
GACTGCGAAA ACCACTTGTA CTGGCGTTGA AATGTTCCGT AAAGTGCTGG      500
ACGAAGGCCG TGCGGGTGAG AACGTAGGTG TTCTGCTGCG TGGTACTAAG      550
55 CGTGAAGAAA TCGAACGTGG TCAAGTTCTG GCGAAACCAG GTTCAATCAA      600
GCCACACACA ACTTTGCAAT CAGAAGTTTA TATCTGAGC AAAGATGAAG      650
GTGGTCGTCA CAGCCATTTC TTCAAAGGYT ACCGTCCACA GTTCTACTTC      700
CGTACAAC TGTAACCGG TACTATCGAA CTGCCAGAAG GCGTAGAGAT      750
GGTAATGCCA GCGGACAACG TGAACATGAA AGTAACTCTG ATTCACCCAA      800
60 TCGCGATGGA CGATGGTTTG CGTTTCGCAA      830

```

2) INFORMATION FOR SEQ ID NO: 153

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 827 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas aeruginosa*
 (B) STRAIN: ATCC 35554

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153

```

20 CCTGGTTTGC TCGGCTGCCG ACGGCCCAT GCCGCAGACC CGCGAGCACA      50
   TCCTGCTGTC CCGCCAGGTA GGCGTTCCCT ACATCGTCGT GTTCCTGAAC      100
   AAAGCCGACA TGGTCGACGA CGCCGAGCTG CTGGAAGTGG TCGAGATGGA      150
   AGTTCGCGAT CTGCTGAACA CCTACGACTT CCCGGGCGAC GACACTCCGA      200
   TCATCATCGG TTCCGCGCTG ATGGCGCTGG AAGGCAAGGA TGACAACGGC      250
25 ATCGGCGTAA GCGCCGTGCA GAAGCTGGTA GAGACCCTGG ACTCCTACAT      300
   TCCGGAGCCG GTTCGTGCCA TCGACCAGCC GTTCCTCATG CCGATCGAAG      350
   ACGTGTTCTC GATCTCCGGT CGCGGTACCG TGGTAACCGG TCGTGTAGAG      400
   CGCGGCATCA TCAAGGTCCA GGAAGAAGTG GAAATCGTCG GCATCAAGGC      450
   GACCACCAAG ACCACCTGCA CCGGCGTTGA AATGTTCCGC AAGCTGCTCG      500
30 ACGAAGGTCG TGCTGGTGAG AACGTTGGTA TCCTGCTGCG TGGCACC AAG      550
   CGTGAAGACG TAGAGCGTGG CCAGGTACTG GCCAAGCCGG GCACCATCAA      600
   GCCGCACACC AAGTTCGAGT GCGAAGTGTA CGTGCTGTCC AAGGAAGAAG      650
   GTGGTCGTCA CACCCCGTTC TTCAAGGGCT ACCGTCCGCA GTTCTACTTC      700
   CGTACCACKG ACGTGACCGG TAMCTGCGAG CTGCCGGAAG GCGTAGAGAT      750
35 GGTAATGCCG GGCGACAACA TCAAGATGGT TGTACCCTG ATCGCTCCGA      800
   TCGCCATGGA AGATGGCTGC GTTCGCGC                                827

```

2) INFORMATION FOR SEQ ID NO: 154

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 841 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas fluorescens*
 (B) STRAIN: ATCC 13525

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154

```

55 CGGCGCAATC CTGGTTTGCT CGGCCGCTGA TGGTCCGATG CCACAAACCC      50
   GTGAACACAT CCTGCTGTCC CGTCAGGTTG GCGTTCCGTA CATCGTGGTT      100
   TACCTGAACA AGGCTGACCT GGTAAGACGAC GCTGAGCTGC TGGAAGTGGT      150
   TGAGATGGAA GTGCGCGATC TGCTGAGCAC TTACGACTTC CCAGGCGACG      200
60 AACTCCGAT CATCATCGGT TCTGCTCGTA TGGCTCTGGA AGGCAAAGAC      250

```

```

GACAACGAAA TGGGCACCAC GTCCGTTCGT AAACTGGTTG AAACTCTGGA 300
CAGCTACATC CCAGATCCAG TTCGTGTTAT CGACAAGCCG TTCCTGATGC 350
CAATCGAAGA CGTGTTCTCG ATCTCCGGTG GCGGTACTGT TGTGACTGGT 400
CGTATCGAGC GCGGTATCGT TAAGGTTCAA GATCCACTGG AAATCGTTGG 450
5 TCTGCGTGAC ACTACCGTCA CCACCTGCAC CGGTGTTGAA ATGTTCCGTA 500
AGCTGCTCGA CGAAGGTCGT GCTGGCGAGA ACTGCGGCGT TCTGCTGCGT 550
GGTACCAAGC GTGACGACGT TGAGCGTGGC CAGGTTCTGG TTAAGCCAGG 600
TTCGGTTAAG CCGCACACCA AGTTCGAAGC TGAAGTCTAC GTACTGAGCA 650
AAGAAGAAGG CGGTCGTCAC ACTCCGTTCT TCAAAGGCTA CCGTCCACAG 700
10 TTCTACTTCC GTACTACTGA CGTGACTGGT AACTGCGAGC TGCCGGAAGG 750
CGTTGAAATG GTTATGCCAG GCGACAACAT CAAAATGGTT GTTACCCTGA 800
TCAAAACCAT CGCAATGGAA GACGGTCTGC GTTTCGCTAT T 841

```

15 2) INFORMATION FOR SEQ ID NO: 155

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 841 bases
 (B) TYPE: Nucleic acid
 20 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas stutzeri*
 (B) STRAIN: ATCC 17588

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155

```

30 CGGCGCGATC CTGGTCTGCT CGGCTGCTGA CGGCCCCATG CCGCAGACTC 50
GCGAGCACAT CCTGCTGTCC CGTCAGGTTG GTGTTCCGTA CATCGTCGTG 100
TTCCTGAACA AGGCCGACAT GGTTGATGAC GCCGAGCTGC TCGAGCTGGT 150
CGAGATGGAA GTTCGYGACC TGCTGTCGAC CTACGACTTC CCGGGTGAYG 200
35 ACACTCCGAT CATCATCGGC TCCGCGCTGA TGGCGCTGAA CGGCGAAGAC 250
GACAACGAGC TCGGCACCAC TGCGGTGAAG AAGCTGGTCG AGACCCTGGA 300
CAGCTACATT CCCGAGCCGG TTCGTGCCAT CGACAAGCCG TTCCTGATGC 350
CGATCGAAGA CGTGTTCTCG ATCTCCGGTC GCGGCACSGT GGTAACCGGT 400
CGCGTAGAGC GCGGCATCGT CAAGGTTGAG GAAGAGATCG AGATCGTCGG 450
40 TCTGCGTCCG ACCACCAAGA CTACCTGCAC CGGCGTTGAG ATGTTCCGCA 500
AGCTGCTCGA YGARGGTCGT GCTGGCGAGA ACTGCGGYGT GCTGCTGCGT 550
GGCACCAAGC GTGACGAAGT GGAGCGTGGT CAGGTTCTGG CCAAGCCGGG 600
CACCATCAAG CCGCACACCA AGTTCGAAGC CGAAGTGATG GTGCTGTCCA 650
AGGAAGAAGG TGGTCGTCAC ACCCCGTTCT TYAAGGGCTA CCGTCCKCAG 700
45 TTCTACTTCC GTACCACTGA YGTGACYGGW TCGTGCGARC TGCCGGAAGG 750
CGTCGAGATG GTAATGCCGG GCGACAACGT GAAGATGGTT GTCACCCTGA 800
TCAAGCCGAT CGCCATGGAA GACGGCCTGC GCTTCGCGAT T 841

```

50

2) INFORMATION FOR SEQ ID NO: 156

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 833 bases
 55 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Psychrobacter phenylpyruvicus*

(B) STRAIN: ATCC 23333

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156

GCTATTCTAG TAGTATCAGC AACTGACGGT CCAATGCCAC AAACACGTGA 50
 GCACATTCTA TTATCACGTC AGGTTGGTGT ACCATACATC ATCGTATTCA 100
 TGAACAAATG TGACATGGTA GATGACGAAG AGTTACTAGA GCTAGTAGAA 150
 10 ATGGAAGTGC GTGAATTACT TTCAGACTAC GACTTCCCAG GTGATGACAC 200
 TCCAATCATC AAAGGTTTCAG CTTTAGAAGC GTTAAATGGT AACGACGGTA 250
 AGTACGGTGA GCCAGCAGTT ATCGAACTAC TAAACACTCT AGACACTTAC 300
 ATTCCAGAGC CAGAGCGTGA CATCGATAAG CCATTCCCTAA TGCCAATCGA 350
 AGACGTATTC TCAATCTCAG GTCGTGGTAC AGTAGTAACA GGCCGTGTTG 400
 15 AATCTGGTAT CATCAAAGTT GGTGACGAAA TCGAAATCGT TGGTATCAAA 450
 GACACAGTTA AAACAACCTG TACTGGTATC GAGATGTTCC GTAAGTTACT 500
 AGACGAAGGT CGTGCTGGTG AGAACTGTGG TGTACTATTA CGTGGTACTA 550
 AGCGTGAAGA CGTACAACGT GGTCAAGTAC TTGCTAAGCC AGGTTCAATC 600
 ACTCCACACA CCAACTTCGA CGCAGAAGTA TACGTACTAT CAAAAGAAGA 650
 20 AGGTGGTCGT CACACTCCAT TCTTAAATGG TTACCGTCCA CAGTTCTACT 700
 TCCGTACTAC TGACGTAAAC GGTGCAATCA CGTTACAAGA AGGTACTGAA 750
 ATGGTAATGC CAGGCGATAA CGTTGAGATG AGCGTAGAGC TAATCCACCC 800
 AATCGCTAGG ACAAAGGTTT ACGTTTCGCA ATC 833

25

2) INFORMATION FOR SEQ ID NO: 157

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Rahnella aquatilis*

(B) STRAIN: ATCC 33071

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157

GGCGCTATCC TGGTTGTTGC TGCAACTGAC GGCCCTATGC CTCAGACTCG 50
 TGAGCACATC CTGCTGGGTC GCCAGGTGCG CGTTCCATAC ATGATCGTGT 100
 45 TCATGAACAA ATGCGACATG GTAGATGACG AAGAGCTGCT GGAAGTGGTA 150
 GAAATGGAAG TTCGCGAACT TCTGTCTGCT TACGAATTCC CAGGCGACGA 200
 CATCCCGGTC ATCAAAGGTT CAGCGCTGAA AGCACTGGAA GGCGATGCTA 250
 CTTGGGAAGC GAAAATCATC GAACTGGCAG AAGCACTGGA CAGCTACATT 300
 CCATTGCCAG AGCGTGCTAT CGATAAGCCA TTCCTGCTGC CAATCGAAGA 350
 50 CGTATTCTCC ATCTCCGGTC GTGGTACAGT GGTTACCGGT CGTGTAGAGC 400
 GCGGTATCGT TAAAGTGGGC GAAGAAGTTG AAATCGTCCG TATCAAGGAC 450
 ACTGTTAAGT CTACTTGTAC TGGCGTTGAA ATGTTCCGCA AACTGCTGGA 500
 CGAAGGCCGT GCGGGCGAGA ACGTGGGTGT TCTGCTGCGT GGTATCAAGC 550
 GTGAAGACAT CGAACGTGGT CAGGTTCTGG CTAAACCAGG TTCAATCAAA 600
 55 CCACACACCA AGTTTGATTG CGAAGTGTAC ATCCTGAGCA AAGATGAAGG 650
 TGGTCGTCAC ACTCCATTCT TCAAAGGCTA CCGTCCACAG TTCTACTTCC 700
 GTACAACTGA CGTGACCGGT ACTATCGAAC TGCCAGAAGG CGTTGAGATG 750
 GTTATGCCTG GTGACAACGT GAACATGGTT GTTACCCTGA TCCACCCAAT 800
 CGCGATGGAT GACGGTCTGC GTTTC 825

60

2) INFORMATION FOR SEQ ID NO: 158

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 830 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *arizonae*
 (B) STRAIN: ATCC 13314

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158

```

CGGCGCGATC CTGGTTGTTG CTGCGACTGA CGGCCCGATG CCGCAGACCC      50
20 GTGAGCACAT CCTGCTGGGC CGTCAGGTAG GCGTTCCGTA CATCATCGTG      100
TTCCTGAACA AATGCGACAT GGTTGATGAC GAAGAGCTGC TGGAAGTGGT      150
TGAAATGGAA GTTCGTGAAC TTCTGTCTCA GTACGACTTC CCGGGCGACG      200
ATACGCCGAT CGTTCGTGGT TCTGCTCTGA AAGCGCTGGA AGGCGACGCA      250
GAGTGGGAAG CGAAAATCAT CGAACTGGCT GGCTTCCTGG ACTCTTACAT      300
25 CCCGGAACCA GAGCGTGC GAAGCAAGCC GTTCCTGCTG CCGATCGAAG      350
ACGTATTCTC CATCTCCGGT CGTGGTACCG TTGTTACCGG TCGTGTAAGAA      400
CGCGGTATCA TCAAAGTGGG CGAAGAAGTT GAAATCGTTG GTATCAAAGA      450
GACTCAGAAG TCTACCTGTA CTGGCGTTGA AATGTTCCGC AAAGTGGTGG      500
ACGAAGGCCG TGCCGGTGAG AACGTAGGTG TTCTGCTGCG TGGTATCAAA      550
30 CGTGAAGAAA TCGAACGTGG TCAGGTACTG GCTAAGCCGG GCACCATCAA      600
GCCGCACACC AAGTTCGAAT CTGAAGTGTA CATCTGTGCC AAAGATGAAG      650
GCGGCCGTCA TACTCCGTTT TTCAAAGGCT ACCGTCCGCA GTTCTACTTC      700
CGTACTACTG ACGTGACTGG CACCATCGAA CTGCCGGAAG GCGTGGAGAT      750
GGTAATGCCG GGCGACAACA TCAAATGGT TGTACCCTG ATCCACCCGA      800
35 TCGCGATGGA CGACGGTCTG CGTTTCGCAA      830

```

2) INFORMATION FOR SEQ ID NO: 159

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 832 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
 serotype *Choleraesuis*
 (B) STRAIN: ATCC 7001

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159

```

CGGCGCGATC CTGGTTGTTG CTGCGACTGA CGGYCCGATG CCGCAGACCC      50
GTGAGCACAT CCTGCTGGGT CGTCAGGTAG GCGTTCCGTA CATCATCGTG      100
TTCCTGAACA AATGCGACAT GGTTGATGAC GAAGAGCTGC TGGAAGTGGT      150
TGAAATGGAA GTTCGTGAAC TTCTGTCTCA GTACGACTTC CCGGGCGACG      200
60 ACACGCCGAT CGTTCGTGGT TCTGCTCTGA AAGCGCTGGA AGGTGACGCA      250

```

```

GAGTGGGAAG CGAAAATCAT CGAACTGGCT GGCTTCCTGG ATTCTTACAT 300
TCCGGAACCA GAGCGTGCGA TTGACAAGCC GTTCCTGCTG CCGATCGAAG 350
ACGTATTCTC CATCTCCGGT CGTGGTACCG TTGTTACCGG TCGTG TAGAG 400
CGCGGTATCA TCAAAGTGGG YGAAGAAGTT GAAATCGTTG GTATCAAAGA 450
5 GACTCAGAAG TCTACCTGTA CTGGCGTTGA AATGTTCCGC AAAGTGTGG 500
ACGAAGGCCG TGCCGGTGAG AACGTAGGTG TTCTGCTGCG TGGTATCAAA 550
CGTGAAGAAA TCGAACGTGG TCAGGTACTG GCTAAGCCGG GCACCATCAA 600
GCCGCACACC AAGTTCGAAT CTGAAGTGTA CATTCGTGTC AAAGATGAAG 650
GCGGCCGTCA TACTCCGTTT TTCAAAGGCT ACCGTCCGCA GTTCTACTTC 700
10 CGTACTACTG ACGTGACTGG CACCATCGAA CTGCCGGAAG GCGTAGAGAT 750
GGTAATGCCG GCGGACAACA TCAAATGGT TGTACCCTG ATCCACCCGA 800
TCGCAATGGA CGACGGTCTG CGTTTCGCAA TC 832

```

15

2) INFORMATION FOR SEQ ID NO: 160

(i) SEQUENCE CHARACTERISTICS:

```

20 (A) LENGTH: 807 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

```

(A) ORGANISM: Salmonella choleraesuis subsp. diarizonae
(B) STRAIN: ATCC 43973

```

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160

```

CCTGGTTGTT GCTGCGACTG ACGGCCCCGAT GCCGCAGACC CGTGAGCACA 50
TCCTGCTGGG TCGTCAGGTA GCGGTTCCGT ACATTATCGT GTTCCTGAAC 100
AAATGCCACA TGGTTGATGA CGAAGAGCTG CTGGAAGTGG TAGAAATGGA 150
35 AGTTCGTGAA CTTCTGTCTC AGTACGACTT CCCGGGCGAC GACACGCCAA 200
TCGTTTCGTGG TTCTGCTCTG AAAGCGCTGG AAGGCGACGC AGAGTGGGAA 250
GCGAAAATCA TCGAACTGGC TGGCTTCCTG GATTCTTACA TCCCGGAACC 300
AGAGCGTGCG ATTGACAAGC CGTTCCCTGCT GCCGATCGAA GACGTATTCT 350
CCATCTCCGG TCGTGGTACC GTTGTTACCG GTCGTGTAGA GCGCGGTATC 400
40 ATCAAAGTGG GCGAAGAAGT TGAAATCGTT GGTATCAAAG AGACTCAGAA 450
GTCTACCTGT ACTGGCGTTG AAATGTTCCG CAARCTGCTG GACGAAGGCC 500
GTGCWGGTGA GAACGTAGGT GTTCTGCTGC GTGGTATCAA ACGTGAAGAA 550
ATCGAACGTG GTCAGGTACT GGCTAAGCCG GGCACCATCA AGCCGCACAC 600
CAAGTTCGAA TCTGAAGTGT ATATTCTGTC CAAAGATGAA GCGGCCGTC 650
45 AACTCCGTT CTTCAAAGGC TACCGTCCGC AGTCTACTT CCGTACCACT 700
GACGTGACTG GCACCATCGA ACTGCCGGAA GCGGTGGAGA TGGTAATGCC 750
GGGCGACAAC ATCAAATGG TTGTTACCCT GATCCACCCG ATCGCGATGG 800
ACGACGG 807

```

50

2) INFORMATION FOR SEQ ID NO: 161

(i) SEQUENCE CHARACTERISTICS:

```

55 (A) LENGTH: 832 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

60 (ii) MOLECULE TYPE: Genomic DNA

300

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
serotype Heidelberg
(B) STRAIN: ATCC 8326

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161

```

10  CGGCGCGATC CTGGTTGTTG CTGCGACTGA CGGCCCGATG CCGCAGACCC      50
    GTGAGCACAT CCTGCTGGGT CGTCAGGTAG GCGTTCCGTA CATCATCGTG      100
    TTCCTGAACA AATGCGACAT GGTTGATGAC GAAGAGCTGC TGGAAGTGGT      150
    TGAAATGGAA GTTCGTGAAC TTCTGTCTCA GTACGACTTC CCGGGCGACG      200
    AACTCCGAT  CGTTCGTGGT TCTGCTCTGA AAGCGCTGGA AGGCGACGCA      250
    GAGTGGGAAG CGAAAATCAT CGAACTGGCT GGCTTCCTGG ATTCTTACAT      300
15  CCCGGAACCA GAGCGTGC GA GAGCGTGC GA GTTCCTGCTG CCGATCGAAG      350
    ACGTATTCTC CATCTCCGGT CGTGGTACCG TTGTTACCGG TCGTGTAGAA      400
    CGCGGTATCA TCAAAGTGGG CGAAGAAGTT GAAATCGTTG GTATCAAAGA      450
    GACTCAGAAG TCTACCTGTA CTGGCGTTGA AATGTTCCGC AAAGTGTGCTGG      500
    ACGAAGGCCG TGCCGGTGAG AACGTAGGTG TTCTGCTGCG TGGTATCAAA      550
20  CGTGAAGAAA TCGAACGTGG TCAGGTACTG GCTAAGCCGG GCACCATCAA      600
    GCCGCACACC AAGTTCGAAT CTGAAGTGTA CATTCGTGTC AAAGATGAAG      650
    GCGGCCGTCA YACTCCGTTT TTCAAAGGCT ACCGTCCGCA GTTCTACTTC      700
    CGTACTACTG ACGTGACTGG CACCATCGAA TTGCCGGAAG GCGTAGAGAT      750
    GGTAATGCCG GCGACAACA TCAAATGGT TGTACCCTG ATCCACCCGA      800
25  TCGCGATGGA CGACGGTCTG CGTTTCGCAA TC                      832

```

2) INFORMATION FOR SEQ ID NO: 162

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 807 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Salmonella choleraesuis* subsp. *houtenae*
(B) STRAIN: ATCC 43974

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162

```

45  CCTGGTTGTT GCTGCGACTG ACGGCCCGAT GCCGCAGACC CGTGAGCACA      50
    TCCTGCTGGG TCGTCAGGTA GGCGTTCCGT ACATCATCGT GTTCCTGAAC      100
    AAATGCGACA TGGTTGATGA CGAAGAGCTG CTGGAAGTGG TAGAAATGGA      150
    AGTTCGTGAA CTTCTGTCTC AGTACGATTT CCCGGGCGAC GACACGCCGA      200
    TCGTGCGTGG TTCTGCTCTG AAAGCGCTGG AAGGCGACGC AGAATGGGAA      250
50  GCGAAAATCA TCGAACTGGC TGGCTACCTG GATTCTTACA TCCCGGAACC      300
    AGAGCTGCGC ATTGACAAAC CGTTCCTGCT GCCGATCGAA GACGTATTCT      350
    CTATCTCCGG TCGTGGTACC GTTGTTACCG GTCGTGTAGA GCGCGGTATC      400
    ATCAAAGTGG GCGAAGAAGT TGAAATCGTT GGTATCAAAG AGACTCAGAA      450
    GTCGACCTGT ACTGGCGTTG AAATGTTCCG CAAACTGCTG GACGAAGGCC      500
55  GTGCTGCGCA GAACGTAGGT GTTCTGCTGC GTGGTATCAA ACGTGAAGAA      550
    ATCGAACGTG GTCAGGTACT GGCTAAGCCG GGCACCATCA AGCCGCACAC      600
    CAAGTTCGAA TCTGAAGTGT ACATTCTGTC CAAAGATGAA GCGCGCCGTC      650
    ATACTCCGTT CTTCAAAGGC TACCTCCGC AATTCTACTT CCGTACGACT      700
    GACGTGACTG GCACCATCGA ACTGCCGGAA GCGGTGGAGA TGGTAATGCC      750
60  GGGCGACAAC ATCAAATGG TTGTTACCCT GATCCACCCG ATCGCGATGG      800

```


ACGACGG

807

5 2) INFORMATION FOR SEQ ID NO: 163

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 827 bases
 (B) TYPE: Nucleic acid
 10 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *indica*
 (B) STRAIN: ATCC 43976

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163

20 CGCGATCCTG GTTGTGCTG CGACTGACGG CCCGATGCCC CAGACCCGTG 50
 AGCACATCCT GCTGGGTCGT CAGGTAGGCG TTCCGTACAT CATCGTGTTT 100
 CTGAACAAAT GCGACATGGT TGATGACGAA GAGCTGCTGG AACTGGTTGA 150
 AATGGAAGTT CGTGAAC TTCGCTCAGTA CGACTTCCCG GGTGACGACA 200
 25 CGCCGATCGT GCGTGGTTCT GCTCTGAAAG CGCTGGAAGG CGACGCAGAG 250
 TGGGAAGCGA AAATCATCGA ACTGGCTGGC TTCCTGGATT CTTACATTCC 300
 GGAACCAGAG CGTGCGATTG ACAAGCCGTT CCTGCTGCCG ATCGAAGACG 350
 TATTCTCCAT CTCCGGTCGT GGTACYGTTG TTACCGGTCG TGTAGAGCGC 400
 GGTATCATCA AAGTGGGCGA AGAAGTTGAA ATCGTTGGTA TCAAAGAGAC 450
 30 TCAGAACTCT ACCTGTACTG GCGTTGAAAT GTTCCGCAA CTGCTGGACG 500
 AAGGCCGTGC CGGTGAGAAC GTAGGTGTTT TGCTGCGTGG TATCAAACGT 550
 GAAGAAATCG AACGTGGTCA GGTACTGGCT AAGCCGGGCA CCATCAAGCC 600
 GCACACCAAG TTCGAATCTG AAGTGTACAT TCTGTCCAAA GATGAAGGCG 650
 CCCGTCATAC TCGTTCTTTC AAAGGCTACC GTCCGCAGTT CTAATTCCGT 700
 35 ACTACTGACG TGACTGGCAC CATCGAACTG CCGGAAGGCG TAGAGATGGT 750
 AATGCCGGGC GACAACATCA AAATGGTTGT TACCCTGATC CATCCGATCG 800
 CRATGGACGA CGGTCTGCGT TTCGCAA 827

40 2) INFORMATION FOR SEQ ID NO: 164

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 807 bases
 45 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *salamae*
 (B) STRAIN: ATCC 43972

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164

CCTGGTTGTT GCTGCGACTG ACGGCCCCGAT GCCGCAGACC CGTGAGCACA 50
 TCCTGCTGGG TCGTCAGGTA GGCGTTCGTT ACATCATCGT GTTCCTGAAC 100
 AAATGCGACA TGGTTGATGA CGAAGAGCTG CTGGAAGTGG TAGAAATGGA 150
 60 AGTTCGTGAA CTTCTGTCTC AGTACGACTT CCCGGGCGAC GACACGCCGA 200

	TCGTGCGTGG	TTCCGCTCTG	AAAGCGCTGG	AAGGCGAMGC	TGAGTGGGAA	250
	GMGAAAATCA	TCGAACTGGC	TGGCTWCCTG	GATTCTTACA	TTCCGGAACC	300
	AGAGCGTGCG	ATTGACAAGC	CGTTCCTGCT	GCCGATCGAA	GACGTATTCT	350
	CCATCTCCGG	TCGTGGTACC	GTTGTTACCG	GTCGTGTAGA	GCGCGGTATC	400
5	ATCAAAGTGG	GCGAAGAAGT	TGAAATCGTT	GGTATCAAAG	AGACTCAGAA	450
	GTCTACCTGT	ACTGGCGTTG	AAATGTTCCG	CAAAC TGCTG	GACGAAGGCC	500
	GTGCCGGTGA	GAACGTAGGT	GTTCTGCTGC	GTGGTATCAA	ACGTGAAGAA	550
	ATCGAACGTG	GTCAGGTACT	GGCTAAGCCG	GGCACCATCA	AGCCGCACAC	600
	CAAGTTCGAA	TCTGAAGTGT	ACATTCTGTC	CAAAGATGAA	GGCGGCCGTC	650
10	ATACTCCGTT	CTTCAAAGGC	TACCGTCCGC	AGTTCTACTT	CCGTACCACT	700
	GACGTGACTG	GCACCATCGA	ACTGCCGGAA	GGCGTGAGAA	TGGTAATGCC	750
	GGGCGACAAC	ATCAAAATGG	TTGTTACCCT	GATCCACCCG	ATCGCGATGG	800
	ACGACGG					807

15

2) INFORMATION FOR SEQ ID NO: 165

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 832 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
serotype Typhi

(B) STRAIN: ATCC 10749

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165

	CGGCGCGATC	CTGGTTGTTG	CTGCGACTGA	CGGCCCGATG	CCGCAGACCC	50
35	GTGAGCACAT	CCTGCTGGGT	CGTCAGGTAG	GCGTTCCGTA	CATCATCGTG	100
	TTCTTGAACA	AATGCGACAT	GGTTGATGAC	GAAGAGCTGC	TGGAAGTGGT	150
	TGAAATGGAA	GTTCGTGAAC	TTCTGTCTCA	GTACGACTTC	CCGGGCGACG	200
	ACACGCCGAT	CGTTCGTGGT	TCTGCTCTGA	AAGCGCTGGA	AGGCGACGCA	250
	GAGTGGGAAG	CGAAAATCAT	CGAACTGGCT	GGCTTCCTGG	ATTCTTACAT	300
40	CCCGGAACCA	GAGCGTGCGA	TTGACAAGCC	GTTCTGCTG	CCGATCGAAG	350
	ACGTATTCTC	CATCTCCGGT	CGTGGTACCG	TTGTTACCGG	TCGTGTAGAA	400
	CGCGGTATCA	TCAAAGTGGG	CGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	450
	GACTCAGAAG	TCTACCTGTA	CTGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
	ACGAAGGCCG	TGCNNGTGAG	AACGTAGGTG	TTCTGCTGCG	TGGTATCAAA	550
45	CGTGAAGAAA	TCGAACGTGG	TCAGGTACTG	GCTAAGCCGG	GCACCATCAA	600
	GCCGCACACY	AAGTTCGAAT	CTGAAGTGTA	CATTCTGTCC	AAAGATGAAG	650
	GCGGCCGTCA	TACTCCGTTT	TTCAAAGGCT	ACCGTCCGCA	GTTCTACTTC	700
	CGTACTACTG	ACGTGACTGG	CACCATCGAA	CTGCCGGAAG	GCGTAGAGAT	750
	GGTAATGCCG	GGCGACAACA	TCAAAATGGT	TGTTACCCTG	ATCCACCCGA	800
50	TCGCAATGGA	CGACGGTCTG	CGTTTCGCAA	TC		832

2) INFORMATION FOR SEQ ID NO: 166

55

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 817 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Serratia fonticola*
(B) STRAIN: DSM 4576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166

10	CGGCGCTATC	CTGGTTGTAG	CTGCGACTGA	CGGCCCTATG	CCTCAGACTC	50
	GTGAGCACAT	CCTGCTGGGT	CGTCAGGTTG	GCGTTCCTTA	CATCATCGTA	100
	TTCATGAACA	AATGCGACAT	GGTTGATGAT	GAAGAGCTGC	TGGAAGTGGT	150
	AGAAATGGAA	GTTTCGTGAAC	TTCTGTCTGC	TTATGACTTC	CCTGGTGATG	200
	ACCTGCCGGT	TGTTTCGTGGT	TCAGCGCTGA	AAGCACTGGA	AGGCGAAGCT	250
15	GAGTGGGAAG	CTAAAATCAT	CGAGCTGGCC	GGTCACCTGG	ATTCCCTACAT	300
	CCCAGAACCA	GAGCGTGCTA	TCGATCAGCC	GTTCCCTGCTG	CCAATCGAAG	350
	ACGTATTCTC	CATCTCCGGT	CGTGGTACCG	TAGTTACCGG	TCGTGTTGAG	400
	CGCGGTATCG	TTAAAGTTGG	CGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	450
	CACCGTTAAG	TCTACCTGTA	CTGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
20	ACGAAGGCCG	TGCTGGTGAG	AACGTTGGTG	TTCTGCTGCG	TGGTATCAAG	550
	CGTGAAGACA	TCGAACGTGG	TCAGGTACTG	GCTAAACCAG	GTTCCATCAA	600
	GCCGCACACT	CAGTTCGATT	CAGAAGTGTA	TATCCTGAGC	AAAGAAGAAG	650
	GTGGTCGTCA	TACTCCATTC	TTCAAAGGCT	ACCGTCCACA	GTTCTACTTC	700
	CGTACAACCTG	ACGTGACCGG	TACCATCGAA	CTGCCAGAAG	GCGTAGAGAT	750
25	GGTAATGCCA	GGCGATAACG	TGAACATGGT	TGTTACCCTG	ATCCACCCAA	800
	TCGCTATGGA	CCAAGGC				817

30 2) INFORMATION FOR SEQ ID NO: 167

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 787 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Serratia liquefaciens*
(B) STRAIN: ATCC 27592

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167

45	GCTGCGACTG	ACGGCCCAAT	GCCTCAGACC	CGTGAGCACA	TCCTGCTGGG	50
	TCGTACAGGT	GGCGTTCCTT	TCATCATCGT	ATTCATGAAC	AAATGCGACA	100
	TGGTTGATGA	TGAAGAGCTG	CTGGAAGTGG	TAGAAATGGA	AGTTCGTGAA	150
	CTTCTGTCTG	CTTACGACTT	CCCTGGTGAT	GACCTGCCGG	TTGTTCGTGG	200
50	TTCAGCGCTG	AAAGCACTGG	AAGGCGAAGC	TGAGTGGGAA	GCTAAAATCA	250
	TCGAGCTGGC	CGGTTACCTG	GATTCCTTACA	TCCCAGAACC	AGAGCGTGCT	300
	ATCGACAAGC	CGTTCCTGCT	GCCAATCGAA	GACGTCTTCT	CCATCTCCGG	350
	TCGTGGTACC	GTGTTACC	GTCGTGTTGA	GCGCGGTATC	GTTAAAGTTG	400
	GCGAAGAAGT	TGAAATCGTT	GGTATCAAAG	ACACCGTTAA	GTCTACCTGT	450
55	ACTGGCGTTG	AAATGTTCCG	CAAACCTGCTG	GACGAAGGCC	GTGCTGGTGA	500
	GAACGTTGGT	GTTCTGCTGC	GTGGTATCAA	GCGTGAAGAC	ATCGAACGTG	550
	GTCAGGTACT	GGCTAAACCA	GGTTCATCA	AGCCACACAC	CAAGTTCGAC	600
	TCAGAAGTGT	ACATCCTGAG	CAAAGAAGAA	GGTGGTCGTC	ATACTCCATT	650
	CTTCAAAGGC	TACCGTCCAC	AGTTCTACTT	CCGTACAAC	GACGTGACCG	700
60	GTACCATCGA	ACTGCCAGAA	GGCGTTGAA	TGGTAATGCC	AGGTGACAAC	750

GTGAACATGG TTGTTACCCT GATCCACCCA ATCGCGA

787

5 2) INFORMATION FOR SEQ ID NO: 168

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 745 bases
 (B) TYPE: Nucleic acid
 10 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Serratia marcescens*
 (B) STRAIN: ATCC 13880

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168

20 GCCTCAGACT CGTGAGCACA TCCTGCTGGG TCGTCAGGTT GGCGTTCCTT 50
 TCATCATCGT ATTCATGAAC AAATGCGACA TGTTTGATGA TGAAGAGCTG 100
 YTGGAACTGG TAGAAATGGA AGTTCGCGAA CTGCTGTCCG CTTACGACTT 150
 CCCTGGCGAC GACCTGCCGG TAATCCGCGG TTCCGCGCTG AAAGCGCTGG 200
 25 AAGGCGAAGC TGAGTGGGAA GCGAAAATCA TCGAACTGGC CGAAGCCCTG 250
 GACAGCTACA TCCCAGAGCC AGAGCGTGCT ATCGACAAGC CGTTCCTGCT 300
 GCCAATCGAA GACGTATTCT CCATCTCCGG TCGTGGTACC GTTGTTACCG 350
 GTCGTGTTGA GCGCGGCATC ATCAAAGTTG GCGAAGAAGT TGAAATCGTT 400
 GGTATCAAAG ACACCGTTAA GTCTACCTGT ACTGGCGTTG AAATGTTCCG 450
 30 CAAACTGCTG GACGAAGGCC GTGCTGGTGA GAACGTAGGT GTTCTGCTGC 500
 GTGGTATCAA ACGTGAAGAA ATCGAACGTG GTCAGGTACT GGCTAAGCCA 550
 GGCTCCATCA AGCCGCACAC CCAGTTCGAA TCTGAAGTGT ACATCCTGAG 600
 CAAAGATGAA GGTGGTCTGC ACACKCCATT CTTCAAAGGC TACCGTCCAC 650
 AGTTCTACTT CCGTACCACT GACGTGACCG GTACCATCGA ACTGCCAGAA 700
 35 GGCGTAGAGA TGGTAATGCC AGGCGACAAC GTGAACATGG TTGTA 745

2) INFORMATION FOR SEQ ID NO: 169

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 45 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Serratia odorifera*
 50 (B) STRAIN: ATCC 33077

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169

55 GGCGCAATCC TGGTTGTTGC TGCAGCTGAC GGCCCTATGC CTCAGACCCG 50
 TGAGCACATC CTGCTGGGTC GCCAGGTTGG CGTTCCTTTC ATCATCGTGT 100
 TCATGAACAA ATGTGACATG GTTGATGACG AAGAGCTGCT GGAAGTGGTA 150
 GAAATGGAAG TTCGCGAGCT GCTGTCTGCT TACGATTTCC CTGGCGACGA 200
 CCTGCCAGTA ATCCGCGGTT CTGCGCTGAA AGCGCTGGAA GGCGAAGCAG 250
 60 AGTGGGAAGC TAAGATTGTA GAACTGGCTG AAGCGCTGGA TTCTTACATC 300

	CCAGAACCAG	AGCGTGCTAT	CGACAAGCCG	TTCCTGCTGC	CAATCGAAGA	350
	CGTATTCTCC	ATCTCCGGTC	GTGGTACCGT	TGTTACCGGT	CGTGTTGAGC	400
	GCGGTATCAT	CAAAGTTGGC	GAAGAAGTTG	AAATCGTTGG	TATCAAAGAC	450
	ACCGTTAAGT	CTACCTGTAC	CGGTGTAGAA	ATGTTCCGCA	AACTGCTGGA	500
5	CGAAGGCCGT	GCTGGTGAGA	ACGTTGGTGT	TCTGCTGCGT	GGTATCAAGC	550
	GTGAAGACAT	CGAACGTGGT	CAGGTTCTGG	CTAAACCAGG	TTCTATCAAG	600
	CCGCACACCA	AATTCGACTC	AGAAGTGTAC	ATCCTGAGCA	AAGAAGAAGG	650
	TGGTCGTCAC	ACGCCATTCT	TCAAAGGCTA	CCGTCCACAG	TTCTACTTCC	700
	GTACTACTGA	CGTGACCGGT	ACCATCGAAC	TGCCAGAAGG	CGTAGAGATG	750
10	GTAATGCCAG	GCGATAACGT	GAACATGGTT	GTTACCCTGA	TTCACCCAAT	800
	CGCAATGGAC	GACGGTCTGC	GTTTCGCAA			829

15 2) INFORMATION FOR SEQ ID NO: 170

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 830 bases
	(B)	TYPE: Nucleic acid
20	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

	(A)	ORGANISM: <i>Serratia plymuthica</i>
	(B)	STRAIN: DSM 4540

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170

30	CGGCGCAATC	CTGGTTGTTG	CTGCGACTGA	CGGCCCAATG	CCTCAGACCC	50
	GTGAGCACAT	CCTGCTGGGT	CGTCAGGTTG	GCGTTCCTTT	CATCATCGTA	100
	TTCATGAACA	AATGCGACAT	GGTTGATGAT	GAAGAGCTGC	TGGAAGTGGT	150
	AGAAATGGAA	GTTTCGTGAAC	TTCTGTCTGC	TTACGACTTC	CCTGGTGATG	200
35	ACCTGCCGGT	TGTTCCGTGGT	TCAGCGCTGA	AAGCACTGGA	AGGCGAACCA	250
	GAGTGGGAAG	CTAAAATCAT	CGAGCTGGCT	GGTTTCCTGG	ATTCTTACAT	300
	CCCAGAACCA	GAGCGTGCTA	TCGACAAGCC	GTTCCCTGCTG	CCAATCGAAG	350
	ACGTATTCTC	CATCTCCGGT	CGTGGTACCG	TTGTTACCGG	TCGTGTTGAG	400
	CGCGGTATCG	TTAAAGTTGG	CGAAGAAGTT	GAAATCGTGG	GTATCAAAGA	450
40	CACCGTTAAG	TCTACCTGTA	CCGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
	ACGAAGGCCG	TGCTGGTGAG	AACGTGGGTG	TTCTGCTGCG	TGGTATCAAG	550
	CGCGAAGATA	TCGAACGTGG	TCAGGTCCTG	GCTAAACCAG	GTTCAATCAA	600
	GCCACACACC	AAGTTTGACT	CAGAAGTGTA	CATCCTGAGC	AAAGAAGAAG	650
	GTGGTCGTCA	TACTCCATTC	TTCAAAGGCT	ACCGTCCACA	GTTCTACTTC	700
45	CGTACAACCTG	ACGTGACCGG	TACCATCGAA	CTGCCAGAAG	GCGTAGAGAT	750
	GGTAATGCCA	GGTGACAACG	TGAACATGGT	TGTAACCTTG	ATCCACCCAA	800
	TCGCGATGGA	CGACGGCCTG	CGTTTCGCAA			830

50

2) INFORMATION FOR SEQ ID NO: 171

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 829 bases
55	(B)	TYPE: Nucleic acid
	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Serratia rubidaea*
 (B) STRAIN: ATCC 27593

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171

	GGCGCAATCC	TGGTAGTAGC	AGCGACTGAC	GGCCCAATGC	CTCAGACCCG	50
	TGAGCACATC	CTGCTGGGCC	GCCAGGTAGG	CGTACCTTAC	ATCATCGTAT	100
	TCATGAACAA	ATGCGACATG	GATAGTGATG	AAGAGCTGCT	GGAAGCTGGTA	150
10	GAGATGGAAG	TTCGCGAACT	GCTGTCTGCT	TACGACTTCC	CAGGCGACGA	200
	CCTGCCGGTA	ATCCGTGGTT	CCGCGCTGAA	AGCGCTGGAA	GGCGAAGCCG	250
	AGTGGGAAGC	GAAAATCGTT	GAGCTGGCAG	AAGCGCTGGA	CAGCTACATC	300
	CCAGAGCCAG	AGCGTGCTGT	AGACAAGCCG	TTCCTGCTGC	CAATCGAAGA	350
	CGTATTCTCC	ATCTCCGGTC	GTGGTACCGT	TGTTACCGGT	CGTGTAGAGC	400
15	GCGGTATCAT	CAAAGTTGGT	GAAGAAGTAG	AAATCGTAGG	TATCAAAGAC	450
	ACCGTTAAGT	CTACCTGTAC	TGGCGTAGAA	ATGTTCCGCA	AACTGCTGGA	500
	CGAAGGCCGT	GCTGGTGAGA	ACGTAGGTGT	TCTGCTGCGT	GGTATCAAGC	550
	GTGAAGAAAT	CGAACGTGGT	CAGGTACTGG	CGAAGCCAGG	TTCAATCAAG	600
	CCGCACACCC	AGTTCGAATC	TGAAGTGATC	ATTCTGTCCA	AAGACGAAGG	650
20	CGGCCGTCAT	ACTCCGTTCT	TCAAAGGCTA	CCGTCCACAG	TTCTACTTCC	700
	GTACAACCTGA	CGTGACCGGT	ACCATCGAAC	TGCCAGAAGG	CGTAGAGATG	750
	GTAATGCCAG	GCGACAACGT	GAACATGAAA	GTTACTCTGA	TTCACCCAAT	800
	CGCAATGGAC	GACGGTCTGC	GTTTCGCAA			829

25

2) INFORMATION FOR SEQ ID NO: 172

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 826 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Shigella boydii*
 (B) STRAIN: ATCC 9207

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172

	CGGCGCGATC	YTGGTAGTTG	CTGCGACTGA	CGGCCCGATG	CCGCAGACTC	50
	GTGAGCACAT	CCTGCTGGGT	CGTCAGGTAG	GCGTTCCGTA	CATCATCGTG	100
45	TTCCTGAACA	AATGCGACAT	GGTTGATGAC	GAAGAGCTGC	TGGAAGTGGT	150
	TGAAATGGAA	GTTTCGTGAAC	TTCTGTCTCA	GTACGACTTC	CCGGGCGACG	200
	AACTCCGAT	CGTTCGTGGT	TCTGCTCTGA	AAGCGCTGGA	AGGCGACGCA	250
	GAGTGGGAAG	CGAAAATCCT	GGAAGTGGCT	GGCTTCCTGG	ATTCTTACAT	300
	TCCGGAACCA	GAGCGTGCGA	TTGACAAGCC	GTTCTGCTG	CCGATCGAAG	350
50	ACGTATTCTC	CATCTCCGGT	CGTGGTACCG	TTGTTACCGG	TCGTGTAGAA	400
	CGCGGTATCA	TCAAAGTTGG	TGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	450
	GACTCAGAAG	TCTACCTGTA	CTGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
	ACGAAGGCCG	TGCTGGTGAG	AACGTAGGTG	TTCTGCTGCG	TGGTATCAAA	550
	CGTGAAGAAA	TCGAACGTGG	TCAGGTACTG	GCTAAGCCGG	GCACCATCAA	600
55	GCCGCACACC	AAGTTCGAAT	CTGAAGTGTA	CATTCTGTCC	AAAGATGAAG	650
	GCGGCCGTCA	TACTCCGTTT	TTCAAAGGCT	ACCGTCCGCA	GTTCTACTTC	700
	CGTACTACTG	ACGTGACTGG	TACCATCGAA	CTGCCGGAAG	GCGTAGAGAT	750
	GGTAATGCCG	GGCGACAACA	TCAAAGTGGT	TGTTACCCTG	ATCCACCCGA	800
60	TCGCGATGGA	CGACGGTCTG	CGTTTC			826

2) INFORMATION FOR SEQ ID NO: 173

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 818 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Shigella dysenteriae*
 (B) STRAIN: ATCC 11835

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173

20	TGGTAGTTGC	TGCGACTGAC	GGCCCGATGC	CGCAGACTCG	TGAGCACATC	50
	CTGCTGGGTC	GTCAGGTAGG	CGTTCCGTAC	ATCATCGTGT	TCCTGAACAA	100
	ATGCGACATG	GTTGATGACG	AAGAGCTGCT	GGAAGCTGGT	GAAATGGAAG	150
	TTCGTGAAC	TCTGTCTCAG	TACGACTTCC	CGGGCGACGA	CACTCCGATC	200
	GTTTCGTGGT	CTGCTCTGAA	AGCGCTGGAA	GGCGACGCAG	AGTGGGAAGC	250
	GAAAATCCTG	GAAGTGGCTG	GCTTCCTGGA	TTCYTAYATT	CCGGAACCCAG	300
25	AGCGTGCGAT	TGACAAGCCG	TTCTTGCTGC	CGATCGAAGA	CGTATTCTCC	350
	ATCTCCGGTC	GTGGTACCGT	TGTTACCGGT	CGTGTAGAAC	GCGGTATCAT	400
	CAAAGTTGGT	GAAGAAGTTG	AAATCGTTGG	TATCAAAGAG	ACYCAGAAGT	450
	CTACCTGTAC	TGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	CGAAGGCCGT	500
	GCTGGTGAGA	ACGTAGGTGT	TCTGCTGCGT	GGTATCAAAC	GTGAAGAAAT	550
30	CGAACGTGGT	CAGGTACTGG	CGAAGCCRG	CACCATCAAG	CCGCACACCA	600
	AGTTCGAATC	TGAAGTGATC	ATTCTGTCCA	AAGATGAAGG	CGGCCGTCAT	650
	ACTCCGTTCT	TCAAAGGCTA	CCGTCCGCAG	TTCTACTTCC	GTACTACTGA	700
	CGTGACTGGT	ACCATCGAAT	TGCCGGAAGG	CGTAGAGATG	GTAATGCCGG	750
	GCGACAACAT	CAAAATGGTT	GTTACCCTGA	TCCACCCGAT	CGCGATGGAC	800
35	GACGGTCTGC	GTTTCGCA				818

2) INFORMATION FOR SEQ ID NO: 174

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 806 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Shigella flexneri*
 (B) STRAIN: ATCC 12022

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174

55	CCTGGTAGTT	GCTGCGACTG	ACGGCCCGAT	GCCGCAGACT	CGTGAGCACA	50
	TCCTGCTGGG	TCGTCAGGTA	GGCGTTCCGT	ACATCATCGT	GTTCTTGAAC	100
	AAATGCGACA	TGGTTGATGA	CGAAGAGCTG	CTGGAACTGG	TTGAAATGGA	150
	AGTTCGTGAA	CTTCTGTCTC	AGTACGACTT	CCCGGGCGAC	GACACTCCGA	200
	TCGTTCGTGG	TTCTGCTCTG	AAAGCGCTGG	AAGGCGACGC	AGAGTGGGAA	250
60	GCGAAAATCC	TGGAAGTGGC	TGGCTTCCTG	GATTCTTACA	TTCCGGAACC	300

```

AGAGCGTGCG ATTGACAAGC CGTTCCTGCT GCCGATCGAA GACGTATTCT 350
CCATCTCCGG TCGTGGTACC GTTGTTACCG GTCGTGTAGA ACGCGGTATC 400
ATCAAAGTTG GTGAAGAAGT TGAAATCGTT GGTATCAAAG AGACTCAGAA 450
GTCTACCTGT ACTGGCGTTG AAATGTTCCG CAAACTGCTG GACGAAGGCC 500
5 GTGCTGGTGA GAACGTAGGT GTTCTGCTGC GTGGTATCAA ACGTGAAGAA 550
ATCGAACGTG GTCAGGTACT GGCTAAGCCG GGCACCATCA AGCCGCACAC 600
CAAGTTCGAA TCTGAAGTGT ACATTCTGTC CAAAGATGAA GGCGGMCCTC 650
ATACTCCGTT CTTCAAAGGC TACCGTCCGC AGTTCTACTT CCGTACTACT 700
GACGTGACTG GTACCATCGA ACTGCCGGAA GGCGTAGAGA TGGTAATGCC 750
10 GGGCGACAAC ATCAAATGG TTGTTACCCT GATCCACCCG ATCGCGATGG 800
ACGACG 806

```

15 2) INFORMATION FOR SEQ ID NO: 175

(i) SEQUENCE CHARACTERISTICS:

```

(A) LENGTH: 832 bases
(B) TYPE: Nucleic acid
20 (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

```

(A) ORGANISM: Shigella sonnei
(B) STRAIN: ATCC 29930

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175

```

30 CGGCGCGATC CTGGTAGTTG CTGCGACTGA CGGCCCGATG CCGCAGACTC 50
GTGAGCACAT CCTGCTGGGT CGTCAGGTAG GCGTTCCGTA CATCATCGTG 100
TTCCTGAACA AATGCGACAT GGTTGATGAC GAAGAGCTGC TGGAAGTGGT 150
TGAAATGGAA GTTCGTGAAC TTCTGTCTCA GTACGACTTC CCGGGCGACG 200
35 ACACTCCGAT CGTTCGTGGT TCTGCTCTGA AAGCGCTGGA AGGCGACGCA 250
GAGTGGGAAG CGAAAATCCT GGAAGTGGCT GGCTTCCTGG ATTCTTACAT 300
TCCGGAACCA GAGCGTGCGA TTGACAAGCC GTTCTGCTG CCGATCGAAG 350
ACGTATTCTC CATCTCCGGT CGTGGTACCG TTGTTACCGG TCGTGTAGAA 400
CGCGGTATCA TCAAAGTTGG TGAAGAAGTT GAAATCGTTG GTATCAAAGA 450
40 GACTCAGAAG TCTACCTGTA CTGGCGTTGA AATGTTCCGC AAAGTGGTGG 500
ACGAAGGCCG TGCTGGTGAG AACGTAGGTG TTCTGCTGCG TGGTATCAAA 550
CGTGAAGAAA TCGAACGTGG TCAGGTACTG GCTAAGCCGG GCACCATCAA 600
GCCGCACACC AAGTTCGAAT CTGAAGTGTA CATTCTGTCC AAAGATGAAG 650
GCGGYCGTCA TACTCCGTTT TTCAAAGGCT ACCGTCCGCA GTTCTACTTC 700
45 CGTACTACTG ACGTGACTGG TACCATCGAA CTGCCGGAAG GCGTAGAGAT 750
GGTAATGCCG GGCACACAAC TCAAATGGT TGTTACCCTG ATCCACCCGA 800
TCGCGATGGA CGACGGTCTG CGTTTCGCAA TC 832

```

50

2) INFORMATION FOR SEQ ID NO: 176

(i) SEQUENCE CHARACTERISTICS:

```

(A) LENGTH: 716 bases
55 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
 (B) STRAIN: ATCC 13301

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 176

```

TCTGCTGCTG ACGGTCCAAT GCCACAAACT CGTGAACACA TTCTTTTATC      50
ACGTAACGTT GGTGTACCAG CATTAGTAGT ATTCTTAAAC AAAGTTGACA      100
TGGTTGACGA TGAAGAATTA TTAGAATTAG TAGAAATGGA AGTTCGTGAC      150
10 TTATTAAGCG AATATGACTT CCCAGGTGAC GATGTACCTG TAATCGCTGG      200
TTCAGCATTA AAAGCTTTAG AAGGCGATGC TCAATACGAA GAAAAAATCT      250
TAGAATTAAT GGAAGCTGTA GATACTTACA TTCCAACCTCC AGAACGTGAT      300
TCTGACAAAC CATTATGATG GCCAGTTGAG GACGTATTCT CAATCACTGG      350
TCTGTTGTTG GTTGCTACAG GCCGTGTTGA ACGTGGTCAA ATCAAAGTTG      400
15 GTGAAGAAGT TGAAATCATC GGTTTACATG ACACATCTAA AACAACTGTT      450
ACAGGTGTTG AAATGTTCCG TAAATTATTA GACTACGCTG AAGCTGGTGA      500
CAACATTGGT GCATTATTAC GTGGTGTGTC TCGTGAAGAC GTACAACGTG      550
GTCAAGTATT AGCTGCTCCT GGTTC AATTA CACCACATAC TGAATTCAA      600
GCAGAAGTAT ACGTATTATC AAAAGACGAA GGTGGACGTC AACTCCATT      650
20 CTTCTCAAAC TATCGTCCAC AATTCTATTT CCGTACTACT GACGTAAC TG      700
GTGTTGTTCA CTTACC                                     716

```

25 2) INFORMATION FOR SEQ ID NO: 177

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 719 bases
 (B) TYPE: Nucleic acid
 30 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
 (B) STRAIN: ATCC 29247

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177

```

40 TTCTTTTATC ACGTAACGTT GGTGTACCAG CATTAGTAGT ATTCTTAAAC      50
AAAGTTGACA TGGTTGACGA TGAAGAATTA TTAGAATTAG TAGAAATGGA      100
AGTTCGTGAC TTATTAAGCG AATATGACTT CCCAGGTGAC GATGTACCTG      150
TAATCGCTGG TTCAGCATTA AAAGCTTTAG AAGGCGATGC TCAATACGAA      200
45 GAAAAAATCT TAGAATTAAT GGAAGCTGTA GATACTTACA TTCCAACCTCC      250
AGAACGTGAT TCTGACAAAC CATTATGATG GCCAGTTGAG GACGTATTCT      300
CAATCACTGG TCGTGGTACT GTTGCTACAG GCCGTGTTGA ACGTGGTCAA      350
ATCAAAGTTG GTGAAGAAGT TGAAATCATC GGTTTACATG ACACATCTAA      400
AACAACGTGT ACAGGTGTTG AAATGTTCCG TAAATTATTA GACTACGCTG      450
50 AAGCTGGTGA CAACATTGGT GCATTATTAC GTGGTGTGTC TCGTGAAGAC      500
GTACAACGTG GTCAAGTATT AGCTGCTCCT GGTTC AATTA CACCACATAC      550
TGAATTCAA GCAGAAGTAT ACGTATTATC AAAAGACGAA GGTGGACGTC      600
ACACTCCATT CTTCTCAAAC TATCGTCCAC AATTCTATTT CCGTACTACT      650
GACGTAAC TG      700
55 TGGTGATAAC GTTGAAATG                                     719

```

2) INFORMATION FOR SEQ ID NO: 178

60

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 625 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
 (B) STRAIN: ATCC 33591

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 178

```

15 GTGAACACAT TCTTTTATCA CGTAACGTTG GTGTACCAGC ATTAGTAGTA      50
   TTCTTAAACA AAGTTGACAT GGTTGACGAT GAAGAATTAT TAGAATTAGT      100
   AGAAATGGAA GTTCGTGACT TATTAAGCGA ATATGACTTC CCAGGTGACG      150
   ATGTACCTGT AATCGCTGGT TCAGCATTA AAGCTTTAGA AGGCGATGCT      200
   CAATACGAAG AAAAAATCTT AGAATTAATG GAAGCTGTAG ATACTTACAT      250
20 TCCAACGCCA GAACGTGATT CTGACAAACC ATTCATGATG CCAGTTGAGG      300
   ACGTATTCTC AATCACTGGT CGTGGTACTG TTGCTACAGG CCGTGTTGAA      350
   CGTGGTCAAA TCAAAGTTGG TGAAGAAGTT GAAATCATCG GTTTACATGA      400
   CACATCTAAA ACAACTGTTA CAGGTGTTGA AATGTTCCGT AAATTATTAG      450
   ACTACGCTGA AGCTGGTGAC AACATTGGTG CATTATTACG TGGTGTTGCT      500
25 CGTGAAGACG TACAACGTGG TCAAGTATTA GCTGCTCCTG GTTCAATTAC      550
   ACCACATACT GAATTCAAAG CAGAAGTATA CGTATTATCA AAAGACGAAG      600
   GTGGACGTCA CACTCCATTC TTCTC                                     625

```

2-) INFORMATION FOR SEQ ID NO: 179

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 704 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
 (B) STRAIN: ATCC 43300

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179

```

GTTGGTGTAC CAGCATTAGT AGTATTCTTA AACAAAGTTG ACATGGTTGA      50
CGATGAAGAA TTATTAGAAT TAGTAGAAAT GGAAGTTCGT GACTTATTAA      100
GCGAATATGA CTTCCCAGGT GACGATGTAC CTGTAATCGC TGGTTCAGCA      150
50 TTAAAAGCTT TAGAAGGCGA TGCTCAATAC GAAGAAAAAA TCTTAGAATT      200
   AATGGAAGCT GTAGATACTT ACATTCCAAC TCCAGAACGT GATTCTGACA      250
   AACCATTCAAT GATGCCAGTT GAGGACGTAT TCTCAATCAC TGGTCGTGGT      300
   ACTGTTGCTA CAGGCCGTGT TGAACGTGGT CAAATCAAAG TTGGTGAAGA      350
   AGTTGAAATC ATCGGTTTAC ATGACACATC TAAAACAAC TTTACAGGTG      400
55 TTGAAATGTT CCGTAAATTA TTAGACTACG CTGAAGCTGG TGACAACATT      450
   GGTGCATTAT TACGTGGTGT TGCTCGTGAA GACGTACAAC GTGGTCAAGT      500
   ATTAGCTGCT CCTGGTTCAA TTACACCACA TACTGAATTC AAAGCAGAAG      550
   TATACGTATT ATCAAAGAC GAAGGTGGAC GTCACACTCC ATTCTTCTCA      600
   AACTATCGTC CACAATTCTA TTTCCGTACT ACCTGACGTAA CTGGTGTGTG      650
60 TCACTTACCA GAAGGTACTG AAATGGTAAT GCCTGGTGAT AACGTTGAAA      700

```

TGAC

704

5 2) INFORMATION FOR SEQ ID NO: 180

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 730 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus* subsp. *aureus*
 (B) STRAIN: ATCC 6538

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 180

20 GTGAACACAT TCTTTTATCA CGTAACGTTG GTGTACCAGC ATTAGTAGTA 50
 TTCTTAAACA AAGTTGACAT GGTGACGAT GAAGAATTAT TAGAATTAGT 100
 AGAAATGGAA GTTCGTGACT TATTAAGCGA ATATGACTTC CCAGGTGACG 150
 ATGTACCTGT AATCGCTGGT TCAGCATTA AAGCTTTAGA AGGCGATGCT 200
 25 CAATACGAAG AAAAAATCTT AGAATTAATG GAAGCTGTAG ATAATTACAT 250
 TCCAACCTCA GAACGTGATT CTGACAAACC ATTTCATGAT CCAGTTGAGG 300
 ACGTATTCTC AATCACTGGT CGTGGTACTG TTGCTACAGG CCGTGTGAA 350
 CGTGGTCAAA TCAAAGTTGG TGAAGAAGTT GAAATCATCG GTTTACATGA 400
 CACATCTAAA ACAACTGTTA CAGGTGTTGA AATGTTCCGT AAATTATTAG 450
 30 ACTACGCTGA AGCTGGTGAC AACATTGGTG CATTATTACG TGGTGTGCT 500
 CGTGAAGACG TACAACGTGG TCAAGTATTA GCTGCTCCTG GTTCAATTAC 550
 ACCACATACT GAATTCAAAG CAGAAGTATA CGTATTATCA AAAGACGAAG 600
 GTGGACGTCA CACTCCATTC TTCTCAAAC ATCGTCCACA ATTCTATTTC 650
 CGTACTACTG ACGTAACTGG TGTGTTTCAC TTACCAGAAG GTACTGAAAT 700
 35 GGTAATGCCT GGTGATAACG TTGAAATGAC 730

2) INFORMATION FOR SEQ ID NO: 181

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 834 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 45 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 50 (A) ORGANISM: *Staphylococcus auricularis*
 (B) STRAIN: ATCC 33753

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181

55 CGGTGCGATC TTAGTTGTAT CTGCAGCTGA TGGTCCAATG CCACAAACTC 50
 GTGAACACAT CTTATTATCA CGTAACGTTG GTGTACCAGC ATTAGTTGTA 100
 TTCTTAAACA AAGTTGACCA AGTTGACGAC GAAGAATTAT TAGAATTAGT 150
 AGAAATGGAA GTTCGTGACT TATTAAGCGA ATACGACTAC CCAGGTGACG 200
 ATGTACCTGT AATCTCTGGT TCTGCGTTGA AAGCATTAGA AGGCGACAAA 250
 60 GAATACGAAC AAAAAATCTT AGACTTAATG CAACAAGTTG ACGATTACAT 300

```

TCCAACCTCCA GAACGTGACT CTGATAAACC ATTCATGATG CCAGTTGAAG      350
ACGTATTCTC  AATCACTGGT CGTGGTACTG TTGCAACAGG CCGTGTTGAA      400
CGTGGTCAAA  TCAAAGTCGG  TGAAGAAGTT GAAATCATCG GTATGAAAGA      450
CGGTTACAAA  AAAACAACAG  TTACTGGTGT AGAAATGTTT CGTAAATTAT      500
5  TAGACTACGC TGAAGCTGGT GACAACATCG GTGCTTTATT ACGTGGTATT      550
TCACGTGAAG  AAGTACAACG  TGGTCAAGTT TTAGCTGCTC CTGGTTCAAT      600
TACACCACAC  ACTAAATTCA  CTGCAGAAGT TTACGTATTA TCTAAAGATG      650
AAGGTGGACG  TCACACTCCA  TTCTTCTCTA ACTACCGTCC ACAATTCTAT      700
TTCCGTACTA  CTGACGTAAC  AGGTGTTGTT ACTTTACCAG AAGGTACAGA      750
10 AATGGTAATG  CCTGGCGATA  ACGTTAAAT  GGAAGTTGAA TTAATTTCTC      800
CAATCGCTAT  CGAAGACGGT  ACTCGTTTCT CAAT      834

```

15 2) INFORMATION FOR SEQ ID NO: 182

(i) SEQUENCE CHARACTERISTICS:

```

20 (A) LENGTH: 835 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

```

    (A) ORGANISM: Staphylococcus capitis subsp. capitis
    (B) STRAIN: ATCC 27840

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182

```

30 CGGCGGTATC TTAGTÀGTAT CTGCTGCTGA CGGTCCAATG CCACAAACTC      50
   GTGAACACAT CTTATTATCA CGTAACGTTG GTGTACCAGC ATTAGTTGTA      100
   TTCTTAAACA AAGTTGACAT GGTAGACGAC GAAGAATTAT TAGAATTAGT      150
   TGAAATGGAA GTTCGTGACT TATTAAGCGA ATATGACTTC CCAGGTGATG      200
35 ATGTACCTGT AATCGCTGGT TCAGCATTAA AAGCTTTAGA AGGCGATGCT      250
   CAATACGAAG AAAAAATCTT AGAATTAATG CAAGCAGTTG ATGATTACAT      300
   TCCAACCTCCA GAACGTGATT CTGACAAACC ATTCATGATG CCAGTTGAGG      350
   ACGTATTCTC AATCACTGGT CGTGGTACTG TTGCTACAGG CCGTGTTGAA      400
   CGTGGTCAAA TCAAAGTTGG TGAAGAAGTT GAAATCATCG GTATCCACGA      450
40 AACTTCTAAA ACAACTGTTA CTGGTGTAGA AATGTTCCGT AAATTATTAG      500
   ACTACGCTGA AGCTGGTGAC AACATCGGTG CTTTATTACG TGGTGTGCT      550
   CGTGAAGACG TACAACGTGG TCAAGTATTA GCTGCTCCTG GTTCAATCAC      600
   ACCACACACT AAATTCAAAG CGGAAGTTTA CGTTTTATCT AAAGACGAAG      650
   GTGGACGTCA CACTCCATTC TTCAGTAACT ACCGCCCACA ATTCTATTTC      700
45 CGTACTACTG ACGTAACTGG TGTGTTAAC TTACCAGAAG GTACTGAAAT      750
   GGTATGCCT  GGCGACAACG TTGAAATGAC AGTTGAATTA ATCGCTCCTA      800
   TCGCTATTGA AGACGGTACT CGTTTCTCAA TCGGA      835

```

50

2) INFORMATION FOR SEQ ID NO: 183

(i) SEQUENCE CHARACTERISTICS:

```

55 (A) LENGTH: 804 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Macrococcus caseolyticus*
 (B) STRAIN: ATCC 13548

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183

```

GTATCTTAGT AGTATCTGCT GCTGACGGTC CAATGCCACA AACTCGTGAA      50
CACATCCTTT TATCACGTAA CGTTGGTGTA CCAGCATTAG TAGTATTCTT      100
GAACAAAGTT GACATGGTTG ACGATGAAGA ATTATTAGAA TTAGTTGAAA      150
10 TGGAAGTTCG TGACTTATTA TCTGAATATG ACTTCCCTGG TGACGATGTA      200
CCTGTAATCG CTGGATCTGC TTTAAAAGCA TTAGAAGGCG TTGAAGAATA      250
CGAAGACAAA ATCATGGAAT TAATGGACGC AGTTGATGAG TACATCCCAA      300
CTCCAGAACG TGATTCTGAC AAACCATTC A TGATGCCAGT TGAGGACGTA      350
TTCTCAATCA CTGGTCGTGG TACAGTTGCA ACTGGACGTG TTGAGCGTGG      400
15 ACAAGTTAAA GTTGGTGAAG AAGTTGAAAT CATTGGTTTA ACTGAAGAAC      450
CAGCAAAAAC TACAGTTACA GGTGTAGAAA TGTTCCGTAA ATTATTAGAT      500
TACGCTGAAG CTGGAGATAA CATCGGTGCT TTATTACGTG GTGTTTCTCG      550
TGAAGACGTA CAACGTGGAC AAGTATTAGC TAAACCAGGT TCAATTACTC      600
CACATACTAA ATTCAAAGCT GAAGTTTACG TATTATCTAA AGAAGAAGGT      650
20 GGACGTCATA CTCCATTCTT CACTAACTAC CGCCCTCAGT TCTACTTCCG      700
TACAAC TGAC GTAAGTGGTG TAGTTAACTT ACCAGAAGGT ACTGAAATGG      750
TAATGCCTGG AGATAACATC GAAATGAACG TTGAATTAAT TTCTCCAATC      800
GCGA                                                                804

```

25

2) INFORMATION FOR SEQ ID NO: 184

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 832 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus cohnii*
 (B) STRAIN: DSM 20260

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 184

```

CGGAGCTATC TTAGTAGTAT CTGCTGCTGA TGGCCCAATG CCACAAACTC      50
GTGAACATAT CCTTTTATCA CGTAACGTTG GTGTTCCAGC ATTAGTTGTA      100
45 TTCTTAAACA AAGTTGACAT GGTGACGAT GAAGAATTAT TAGAATTAGT      150
AGAAATGGAA GTTCGTGACT TATTAAGCGA ATATGACTTC CCAGGTGACG      200
ATGTACCTGT AATCTCTGGT TCAGCATTA AAGCTCTTGA AGGCGACGCT      250
GACTATGAGC AAAAAATCTT AGACTTAATG CAAGCTGTTG ATGACTTCAT      300
TCCAACACCA GAACGTGATT CTGACAAACC ATTCATGATG CCAGTTGAGG      350
50 ACGTATTCTC AATCACTGGT CGTGGTACTG TTGCTACAGG GCGTGTGAA      400
CGTGGTCAAA TCAAAGTCGG TGAAGAAGTT GAAATCATCG GTATGCAAGA      450
AGATTCAAGC AAAACAAC TG TACTGGTGT AGAAATGTTC CGTAAATTAT      500
TAGACTACGC TGAAGCTGGT GACAACATTG GTGCGTTATT ACGTGGTGT      550
GCACGTGAAG ACATCCAACG TGGTCAAGTT TTAGCTGCTC CTGGTTCAAT      600
55 TACACCACAC ACAAAC TTTA AAGCGGAAGT TTACGTTTTA TCAAAGATG      650
AAGGTGGCCG TCATACGCCA TTCTTCAGTA ACTATCGCCC ACAATTCTAT      700
TTCCGTACTA CTGACGTAAC AGGTGTTGTT ACTTTACCAG AAGGTACTGA      750
AATGGTTATG CCTGGCGACA ACGTAGAAAT GGAAGTTGAA CTAATTTCTC      800
CAATCGCTAT CGAAGACGGT ACACGTTTCT CT                                                                832

```

60

2) INFORMATION FOR SEQ ID NO: 185

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 699 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus epidermidis*
 (B) STRAIN: CSG 269

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 185

20	ATCTGCTGCT	GACGGTCCAA	TGCCACAAAC	TCGTGAACAC	ATCTTATTAT	50
	CACGTAACGT	TGGTGTACCA	GCATTAGTTG	TATTCTTAAA	CAAAGTTGAC	100
	ATGGTAGACG	ACGAAGAATT	ATTAGAATTA	GTTGAAATGG	AAGTTCGTGA	150
	CTTATTAAGC	GAATATGACT	TCCCAGGTGA	CGATGTACCT	GTAATCGCTG	200
	GTTCTGCATT	AAAAGCATT	GAAGGCGATG	CTGAATACGA	ACAAAAAATC	250
25	TTAGACTTAA	TGCAAGCAGT	TGATGATTAC	ATTCCAATC	CAGAACGTGA	300
	TTCTGACAAA	CCATTCATGA	TGCCAGTTGA	GGACGTATTC	TCAATCACTG	350
	GTCGTGGTAC	TGTTGCTACA	GGCCGTGTTG	AACGTGGTCA	AATCAAAGTT	400
	GGTGAAGAAG	TTGAAATCAT	CGGTATGCAC	GAAACTTCTA	AAACAACTGT	450
	TACTGGTGTA	GAAATGTTCC	GTAAATTATT	AGACTACGCT	GAAGCTGGTG	500
30	ACAACATCGG	TGCTTTATTA	CGTGGTGTTG	CACGTGAAGA	CGTACAACGT	550
	GGTCAAGTAT	TAGCTGCTCC	TGGTTCTATT	ACACCACACA	CAAAATTCAA	600
	AGCTGAAGTA	TACGTATTAT	CTAAAGATGA	AGGTGGACGT	CACACTCCAT	650
	TCTTCACTAA	CTATCGCCCA	CAATTCTATT	TCCGTACTAC	TGACGTAAC	699

2) INFORMATION FOR SEQ ID NO: 186

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus haemolyticus*
 (B) STRAIN: ATCC 29970

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 186

	CGGCGGTATC	TTAGTAGTAT	CTGCTGCTGA	CGGTCCAATG	CCACAAACTC	50
	GTGAACACAT	TCTTTTATCA	CGTAACGTTG	GTGTACCAGC	ATTAGTAGTA	100
55	TTCTTAAATA	AAGTTGACAT	GGTTGACGAT	GAAGAATTAT	TAGAATTAGT	150
	TGAAATGGAA	GTACGTGACT	TATTATCTGA	ATACGACTTC	CCAGGTGACG	200
	ATGTACCTGT	AATCGCTGGT	TCAGCATTA	AAGCTTTAGA	AGGCGATGCT	250
	CAATACGAAG	AAAAAATCTT	AGAATTAATG	CAAGCAGTTG	ATGACTACAT	300
	TCCAACCTCA	GAACGTGATT	CTGACAAACC	ATTCATGATG	CCAGTTGAGG	350
60	ACGTATTCTC	AATCACTGGT	CGTGGTACTG	TTGCTACAGG	CCGTGTTGAA	400

10
 5
 CGTGGGCAAA TCAAAGTTGG TGAAGAAGTT GAAATCATTG GTATCCATGA 450
 CACTTCTAAA ACAACTGTTA CTGGTGTAGA AATGTTCCGT AAATTATTAG 500
 ACTACGCTGA AGCTGGTGAC AACATCGGTG CATTATTACG TGGTGTGCT 550
 CGTGAAGACG TACAACGTGG TCAAGTATTA GCTGCTCCAG GTTCAATCAC 600
 ACCTCACACA AAATTTAAAG CAGACGTATA CGTTTTATCT AAAGACGAAG 650
 GTGGACGTCA CACTCCATTC TTCACAAACT ATCGTCCACA ATTCTATTTC 700
 CGTACTACTG ACGTAACTGG TGTGTTAAC TTACCAGAAG GTACTGAAAT 750
 GGTATGCCT GCGGACAACG TTGAAATGAC AGTAGAATTA ATCGCTCCTA 800
 TCGCGATTGA AGACGGTACT CGTTTCTCA 829

2) INFORMATION FOR SEQ ID NO: 187

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 705 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 20 (ii) MOLECULE TYPE: Genomic DNA
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Staphylococcus warneri*
 25 (B) STRAIN: CSG 123

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 187

30 CACAACTCG TGAACACATT CTTTTATCAC GTAACGTTGG TGTACCAGCT 50
 TTAGTTGTAT TCTTAAACAA AGTTGATATG GTAGACGACG AAGAATTATT 100
 AGAATTAGTA GAAATGGAAG TTCGTGACTT ATTATCTGAA TATGACTTCC 150
 CAGGTGACGA CGTACCTGTA ATCGCTGGTT CAGCATTAAG AGCTTTAGAA 200
 GCGGACGAAA AATACGAAGA AAAAATCTTA GAATTAATGC AAGCAGTTGA 250
 TGACTACATT CCAACTCCAG AACGTGATTC TGACAAACCA TTCATGATGC 300
 35 CAGTTGAGGA CGTATTCTCA ATCACTGGTC GTGGTACTGT TGCTACAGGC 350
 CGTGTTGAAC GTGGTCAAAT CAAAGTTGGT GAAGAAGTTG AAATCATCGG 400
 TTTACATGAC ACTTCTAAAA CAACTGTTAC TGGTGTAGAA ATGTTCCGTA 450
 AGTTATTAGA CTACGCTGAA GCTGGTGACA ACATCGGTGC TTTATTACGT 500
 GGTGTTGCTC GTGAAGACGT ACAACGTGGT CAAGTATTAG CTGCTCCTGG 550
 40 TTCAATTACA CCACATACAA AATTCAAAGC GGAAGTTTAC GTTTTATCTA 600
 AAGACGAAGG TGGACGTCAC ACTCCATTCT TCAGTAACTA CCGCCACAA 650
 TTCTATTTCC GTACTACTGA CGTAACTGGC GTTGTTCAAT TACCAGAAGG 700
 TACTG 705

45

2) INFORMATION FOR SEQ ID NO: 188

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 678 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 55 (ii) MOLECULE TYPE: Genomic DNA
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Staphylococcus haemolyticus*
 60 (B) STRAIN: CSG 23

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 188

```

5   TTTTATCACG TAACGTTGGT GTACCAGCAT TAGTAGTATT CTTAAACAAA    50
   GTTGACATGG TTGACGATGA AGAATTATTA GAATTAGTTG AAATGGAAGT    100
   ACGTGACTTA TTATCTGAAT ACGACTTCCC AGGTGACGAC GTACCTGTAA    150
   TCGCTGGTTC AGCTTTAAAA GCTTTAGAAG GCGATGCTCA ATACGAAGAA    200
   AAAATCTTAG AATTAATGCA AGCAGTTGAT GATTACATTC CAACTCCAGA    250
   ACGTGACTCT GATAAACCAT TCATGATGCC AGTTGAGGAC GTATTCTCAA    300
   TCACTGGTCTG TGGTACTGTT GCTACAGGTC GTGTTGAACG TGGTCAAATC    350
10  AAAGTTGGTG AAGAAGTTGA AATTATTGGT ATCAAAGAAA CTTCTAAAAC    400
   AACTGTTACT GGTGTAGAAA TGTTCCGTAA ATTATTAGAC TACGCTGAAG    450
   CTGGTGACAA CATCGGTGCT TTATTACGTG GTGTTGCTCG TGAAGATGTA    500
   CAACGTGGTC AAGTATTAGC TGCTCCAGGT TCAATTACAC CTCACACAAA    550
   ATTCAAAGCA GACGTATACG TTTTATCAAA AGATGAAGGT GGACGTCATA    600
15  CTCCATTCTT CACTAACTAT CGTCCACAAT TCTATTTCCG TACTACTGAC    650
   GTAACGGTG  TTGTTAACTT ACCAGAAG                                678

```

20 2) INFORMATION FOR SEQ ID NO: 189

(i) SEQUENCE CHARACTERISTICS:

```

25  (A) LENGTH: 668 bases
   (B) TYPE: Nucleic acid
   (C) STRANDEDNESS: Double
   (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

```

   (A) ORGANISM: Staphylococcus haemolyticus
   (B) STRAIN: CSG 33

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189

```

35  ACCAGCATTG TAGTATTCTT TAAATAAAGT TGACATGGTT GACGATGAAG    50
   AATTATTAGA ATTAGTTGAA ATGGAAGTAC GTGACTTATT ATCTGAATAC    100
   GACTTCCCAG GTGACGATGT ACCTGTAATC GCTGGTTCAG CATTAAAAGC    150
   TTTAGAAGGC GATGCTCAAT ACGAAGAAAA AATCTTAGAA TTAATGCAAG    200
40  CAGTTGATGA CTACATTCCA ACTCCAGAAC GTGATTCTGA CAAACCATTC    250
   ATGATGCCAG TTGAGGACGT ATTCTCAATC ACTGGTCGTG GTACTGTTGC    300
   TACAGGCCGT GTTGAACGTG GTCAAATCAA AGTTGGTGAA GAAGTTGAAA    350
   TCATTGGTAT CCATGACACT TCTAAAACAA CTGTTACTGG TGTAGAAATG    400
   TTCCGTAAAT TATTAGACTA CGCTGAAGCT GGTGACAACA TCGGTGCATT    450
45  ATTACGTGGT GTTGCTCGTG AAGACGTACA ACGTGGTCAA GTATTAGCTG    500
   CTCCAGGTTC AATCACACCT CACACAAAAT TTAAAGCAGA CGTATACGTT    550
   TTATCTAAAG ACGAAGGTGG ACGTCACACT CCATTCTTCA CAAACTATCG    600
   TCCACAATTC TATTTCCGTA CTACTGACGT AACTGGTGTT GTTAACTTAC    650
50  CAGAAGGTAC TGAAATGG                                668

```

2) INFORMATION FOR SEQ ID NO: 190

(i) SEQUENCE CHARACTERISTICS:

```

55  (A) LENGTH: 593 bases
   (B) TYPE: Nucleic acid
   (C) STRANDEDNESS: Double
60  (D) TOPOLOGY: Linear

```


(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus haemolyticus*
 (B) STRAIN: CSG 8

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 190

	AAAGTTGACA	TGGTTGACGA	TGAAGAATTA	TTAGAATTAG	TTGAAATGGA	50
10	AGTACGTGAC	TTATTATCTG	AATACGACTT	CCCAGGTGAC	GATGTACCTG	100
	TAATCGCTGG	TTCAGCATT	AAAGCTTTAG	AAGGCGATGC	TCAATACGAA	150
	GAAAAAATCT	TAGAATTAAT	GCAAGCAGTT	GATGATTACA	TTCCAACCTCC	200
	AGAACGTGAT	TCTGACAAAC	CATTTCATGAT	GCCAGTTGAG	GACGTATTCT	250
	CAATCACTGG	TCGTGGTACT	GTTGCTACAG	GCCGTGTTGA	ACGTGGTCAA	300
15	ATCAAAGTTG	GTGAAGAAGT	TGAAATCATT	GGTATCCATG	ACACTTCTAA	350
	AACAACGTGT	ACTGGTGTAG	AAATGTTCCG	TAAATTATTA	GACTACGCTG	400
	AAGCTGGTGA	CAACATTGGT	GCATTATTAC	GTGGTGTTCG	TCGTGAAGAC	450
	GTACAACGTG	GTCAAGTATT	AGCTGCTCCA	GGTTCATCA	CACCTCACAC	500
	AAAATTTAAA	GCAGACGTAT	ACGTTTTATC	TAAAGACGAA	GGTGGACGTC	550
20	ACACTCCATT	CTTCACAAAC	TATCGTCCAC	AATTCTATTT	CCG	593

2) INFORMATION FOR SEQ ID NO: 191

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus hominis* subsp. *hominis*
 (B) STRAIN: ATCC 27844

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 191

40	CGGCGCTATC	TTAGTAGTAT	CTGCTGCTGA	TGGTCCAATG	CCACAACTC	50
	GTGAACACAT	TCTTTTATCA	CGTAACGTTG	GTGTACCAGC	ATTAGTAGTA	100
	TTCTTAAACA	AAGTTGACAT	GGTTGACGAT	GAAGAATTAT	TAGAATTAGT	150
	TGAAATGGAA	GTACGTGACT	TATTATCTGA	ATACGACTTC	CCAGGTGACG	200
	ACGTACCTGT	AATCGCTGGT	TCAGCTTTAA	AAGCTTTAGA	AGGCGATGCT	250
45	CAATACGAAG	AAAAAATCTT	AGAATTAATG	CAAGCAGTTG	ATGATTATAT	300
	TCCAACCTCCA	GAACGTGACT	CTGATAAACC	ATTCATGATG	CCAGTTGAGG	350
	ACGTATTCTC	AATCACTGGT	CGTGGTACTG	TTGCTACAGG	CCGTGTTGAA	400
	CGTGGTCAAA	TCAAAGTTGG	TGAAGAAGTT	GAAATTATTG	GTATCAAAGA	450
	AACTTCTAAA	ACAACGTGTA	CTGGTGTAGA	AATGTTCCGT	AAATTATTAG	500
50	ACTACGCTGA	AGCTGGTGAC	AACATCGGTG	C'TTTATTACG	TGGTGTTCCT	550
	CGTGAAGATG	TACAACGTGG	TCAAGTATTA	GCTGCTCCAG	GTTCAATTAC	600
	ACCTCACACA	AAATTCAAAG	CAGACGTATA	CGTTTTATCA	AAAGATGAAG	650
	GTGGACGTCA	TACTCCATTG	TTCTCTAACT	ATCGTCCACA	ATTCTATTTT	700
	CGTACTACTG	ACGTAACCTG	TGTTGTTAAC	TTACCAGAAG	GTACTGAAAT	750
55	GGTAATGCCT	GGTGACAACG	TTGAAATGAC	AGTAGAATTA	ATCGCTCCTA	800
	TCGCGATTGA	AGACGGTACT	CGTTTCTC			828

60 2) INFORMATION FOR SEQ ID NO: 192

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 620 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus warneri*
 (B) STRAIN: ATCC 35982

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 192

15	ATGGTCCAAT	GCCACAAACT	CGTGAACACA	TTCTTTTATC	ACGTAACGTT	50
	GGTGTACCAG	CTTTAGTTGT	ATTCTTAAAC	AAAGTTGATA	TGGTAGACGA	100
	CGAAGAATTA	TTAGAATTAG	TAGAAATGGA	AGTTCGTGAC	TTATTATCTG	150
	AATATGACTT	CCCAGGTGAC	GACGTACCTG	TAATCGCTGG	TTCAGCATTA	200
20	AAAGCTTTAG	AAGGCGACGA	AAAATACGAA	GAAAAAATCT	TAGAATTAAT	250
	GCAAGCAGTT	GATGACTACA	TTCCAACCTCC	AGAACGTGAT	TCTGACAAAC	300
	CATTCATGAT	GCCAGTTGAG	GACGTATTCT	CAATCACTGG	TCGTGGTACT	350
	GTTGCTACAG	GCCGTGTTGA	ACGTGGTCAA	ATCAAAGTTG	GTGAAGAAGT	400
	TGAAATCATC	GGTTTACATG	ACACTTCTAA	AACAACTGTT	ACTGGTGTAG	450
25	AAATGTTCCG	TAAAGTTATTA	GACTACGCTG	AAGCTGGTGA	CAACATCGGT	500
	GCTTTATTAC	GTGGTGTTGC	TCGTGAAGAC	GTACAACGTG	GTCAAGTATT	550
	AGCTGCTCCT	GGTTCAATTA	CACCACATAC	AAAATTCAAA	GCGGAAGTTT	600
	ACGTTTTATC	TAAAGACGAA				620

2) INFORMATION FOR SEQ ID NO: 193

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 692 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus hominis*
 (B) STRAIN: CSG 170

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193

	CCAGCATTAG	TAGTATTCTT	AAACAAAGTT	GACATGGTTG	ACGATGAAGA	50
	ATTATTAGAA	TTAGTTGAAA	TGGAAGTACG	TGACTTATTA	TCTGAATACG	100
50	ACTTCCCAGG	TGACGACGTA	CCTGTAATCG	CTGGTTCAGC	TTTAAAAGCT	150
	TTAGAAGGCG	ATGCTCAATA	CGAAGAAAAA	ATCTTAGAAT	TAATGCAAGC	200
	AGTTGATGAT	TATATTCCAA	CTCCAGAACG	TGACTCTGAT	AAACCATTCA	250
	TGATGCCAGT	TGAGGACGTA	TTCTCAATCA	CTGGTCGTGG	TACTGTTGCT	300
	ACAGGCCCGTG	TTGAACGTGG	TCAAATCAAA	GTTGGTGAAG	AAGTTGAAAT	350
55	TATTGGTATC	AAAGAAACTT	CTAAAACAAC	TGTTACTGGT	GTAGAAATGT	400
	TCCGTAAATT	ATTAGACTAC	GCTGAAGCTG	GTGACAACAT	CGGTGCTTTA	450
	TTACGTGGTG	TTGCTCGTGA	AGATGTACAA	CGTGGTCAAG	TATTAGCTGC	500
	TCCAGGTTCA	ATTACACCTC	ACACAAAATT	CAAAGCAGAC	GTATACGTTT	550
	TATCAAAGA	TGAAGGTGGA	CGTCATACTC	CATTCTTCTC	TAACATCGT	600
60	CCACAATTCT	ATTTCCGTAC	TACTGACGTA	ACTGGTGTTG	TTAACTTACC	650

AGAAGGTACT GAAATGGTAA TGCCTGGTGA CAACGTTGAA AT

692

5 2) INFORMATION FOR SEQ ID NO: 194

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 684 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus hominis*
 (B) STRAIN: CSG 36

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 194

20 CATTCTTTTA TCACGTAACG TTGGTGTACC AGCATTAGTA GTATTCTTAA 50
 ACAAAGTTGA CATGGTTGAC GATGAAGAAT TATTAGAATT AGTTGAAATG 100
 GAAGTACGTG ACTTATTATC TGAATACGAC TTCCCAGGTG ACGACGTACC 150
 TGTAATCGCT GGTTTCAGCTT TAAAAGCTTT AGAAGGCGAT GCTCAATACG 200
 25 AAGAAAAAAT CTTAGAATTA ATGCAAGCAG TTGATGATTA TATTCCAAC T 250
 CCAGAACGTG ACTCTGATAA ACCATTTCATG ATGCCAGTTG AGGACGTATT 300
 CTCAATCACT GGTCTGGTGA CTGTTGCTAC AGGCCGTGTT GAACGTGGTC 350
 AAATCAAAGT TGGTGAAGAA GTTGAAATTA TTGGTATCAA AGAAACTTCT 400
 AAAACAAC TG TACTGGTGT AGAAATGTTT CGTAAATTAT TAGACTACGC 450
 30 TGAAGCTGGT GACAACATCG GTGCTTTATT ACGTGGTGTT GCTCGTGAAG 500
 ATGTACAACG TGGTCAAGTA TTAGCTGCTC CAGGTTCAAT TACACCTCAC 550
 ACAAATTC AAGCAGACGT ATACGTTTTA TCAAAAGATG AAGGTGGACG 600
 TCATACTCCA TTCTTCTCTA ACTATCGTCC ACAATTCTAT TTCCGTACTA 650
 CTGACGTAAC TGGTGTGTTT AACTTACCAG AAGG 684

2) INFORMATION FOR SEQ ID NO: 195

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 685 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus hominis*
 (B) STRAIN: CSG 6

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195

55 ACCAGCATTA GTAGTATTCT TAAACAAAGT TGACATGGTT GACGATGAAG 50
 AATTATTAGA ATTAGTTGAA ATGGAAGTAC GTGACTTATT ATCTGAATAC 100
 GACTTCCCAG GTGACGACGT ACCTGTAATC GCTGGTTCAG CTTTAAAAGC 150
 TTTAGAAGGC GATGCTCAAT ACGAAGAAAA AATCTTAGAA TTAATGCAAG 200
 CAGTTGATGA TTACATTCCA ACTCCAGAAC GTGACTCTGA TAAACCATTC 250
 ATGATGCCAG TTGAGGACGT ATTCTCAATC ACTGGTCGTG GTACTGTTGC 300
 60 TACAGGCCGT GTTGAACGTG GTCAAATCAA AGTTGGTGAA GAAGTTGAAA 350

TTATTGGTAT CAAAGAACT TCTAAAACAA CTGTTACTGG TGTAGAAATG 400
 TTCCGTAAAT TATTAGACTA CGCTGAAGCT GGTGACAACA TCGGTGCTTT 450
 ATTACGTGGT GTTGCTCGTG AAGATGTACA ACGTGGTCAA GTATTAGCTG 500
 CTCCAGGTTC AATTACACCT CACACAAAAT TCAAAGCAGA CGTATACGTT 550
 5 TTATCAAAAG ATGAAGGTGG ACGTCATACT CCATTCTTCA CTAACATCG 600
 TCCACAATTC TATTTCCGTA CTACTGACGT AACTGGTGTG GTTAACCTAC 650
 CAGAAGGTAC TGAAATGGTA ATGCCTGGCG ACAAC 685

10

2) INFORMATION FOR SEQ ID NO: 196

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 611 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus hominis*
 (B) STRAIN: CSG 62

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 196

GACTTATTAT CTGAATACGA CTTCCCAGGT GACGACGTAC CTGTAATCGC 50
 TGGTTCAGCT TTAAAAGCTT TAGAAGGCGA TGCTCAATAC GAAGAAAAAA 100
 TCTTAGAATT AATGCAAGCA GTTGATGATT ACATTCCAAC TCCAGAACGT 150
 30 GACTCTGATA AACCATTTCAT GATGCCAGTT GAGGACGTAT TCTCAATCAC 200
 TGGTCGTGGT ACTGTTGCTA CAGGCCGTGT TGAACGTGGT CAAATCAAAG 250
 TTGGTGAAGA AGTTGAAATT ATTGGTATCA AAGATACTTC TAAAACAACT 300
 GTTACTGGTG TAGAAATGTT CCGTAAATTA TTAGACTACG CTGAAGCTGG 350
 TGACAACATC GGTGCTTTAT TACGTGGTGT TGCTCGTGAA GATGTACAAC 400
 35 GTGGTCAAGT ATTAGCTGCT CCAGGTTCAA TCACACCTCA CACAAAATTC 450
 AAAGCAGACG TATATGTTTT ATCAAAAGAT GAAGGTGGAC GTCATACTCC 500
 ATTCTTCACT AACTATCGTC CACAATTCTA TTTCCGTACT ACTGACGTAA 550
 CTGGTGTTGT TAACCTACCA GAAGGTACTG AAATGGTAAT GCCTGGCGAC 600
 AACGTTGAAA T 611
 40

2) INFORMATION FOR SEQ ID NO: 197

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 828 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

55 (A) ORGANISM: *Staphylococcus lugdunensis*
 (B) STRAIN: ATCC 43809

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197

CGGCGGTATC TTAGTAGTTT CTGCTGCAGA TGGTCCAATG CCACAAACTC 50
 60 GTGAACACAT TCTTTTATCA CGTAACGTTG GTGTGCCAGC ATTAGTAGTA 100

```

TTCTTAAACA AAGTTGACAT GGTGACGAT GAAGAATTAT TAGAATTAGT 150
AGAAATGGAA GTTCGTGATT TATTAAGTGA ATATGACTTC CCAGGTGACG 200
ATGTGCCTGT AATCGCTGGT TCAGCATTAA AAGCTTTAGA AGGCGACGAA 250
AAATACGAAG CTAAATCTT AGAATTAATG GATGCAGTTG ATAAGTACAT 300
5 TCCAACCTCA GAACGTGACT CTGACAAACC ATTCATGATG CCAGTTGAGG 350
ACGTATTCTC AATCACTGGT CGTGGTACTG TTGCTACAGG CCGTGTTGAA 400
CGTGGTCAAA TCAAAGTCGG TGAAGAAGTT GAAATTATTG GTATCCACGA 450
TACTACTAAA ACAACTGTGA CTGGTGTAGA AATGTTCCGT AAATTATTAG 500
ACTACGCTGA AGCTGGTGAC AACATCGGTG CGTTATTACG TGGTGTTGCT 550
10 CGTGAAGATG TACAACGTGG ACAAGTATTA GCTGCTCCAG GTTCAATTAC 600
ACCTCACACT AAATTTAAAG CTGACGTATA TGTTTTATCT AAAGATGAAG 650
GTGGACGTCA TACACCATTG TTCTCAAAC ACCGCCACA ATTCTATTTT 700
CGTACTACAG ACGTAACTGG TGTTGTTAAC TTACCAGAAG GTACAGAAAT 750
GGTTATGCCT GCGGACAACG TTGAAATGAC AGTTGAATTA ATCGCTCCAA 800
15 TCGCTATCGA AGACGGAAC CGTTTCTC 828

```

2) INFORMATION FOR SEQ ID NO: 198

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 690 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus saprophyticus*
 (B) STRAIN: ATCC 35552

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 198

```

35 AGTAGTATCT GCTGCTGATG GCCCAATGCC ACAAACTCGT GAACACATTC 50
TTTTATCACG TAACGTTGGT GTTCCAGCAT TAGTTGTATT CTTAAACAAA 100
GTTGACATGG TTGACGATGA AGAATTATTA GAATTAGTAG AAATGGAAGT 150
TCGTGACTTA TTAAGCGAAT ATGACTTCCC AGGTGACGAT GTACCTGTAA 200
TCTCTGGTTC TGCATTAAAA GCTTTAGAAG GCGACGCTGA CTATGAGCAA 250
40 AAAATCTTAG ACTTAATGCA AGCTGTTGAT GACTTCATTC CAACACCAGA 300
ACGTGATTCT GACAAACCAT TCATGATGCC AGTTGAGGAC GTATTCTCAA 350
TCACTGGTTCG TGGTACTGTT GCTACAGGCC GTGTTGAACG TGGTCAAATC 400
AAAGTCGGTG AAGAAATCGA AATCATCGGT ATGCAAGAAG AATCAAGCAA 450
AACAACTGTT ACTGGTGTAG AAATGTTCCG TAAATTATTA GACTACGCTG 500
45 AAGCTGGTGA CAACATTGGT GCATTATTAC GTGGTGTTTC ACGTGATGAC 550
GTACAACGTG GTCAAGTTTT AGCTGCTCCT GGTACTATTA CACCACATAC 600
AAAATTCAAA GCGGATGTTT ACGTTTTATC TAAAGATGAA GGTGGTCGTC 650
ATACACCATT CTTCACTAAC TACCGCCAC AATTCTATTT 690

```

2) INFORMATION FOR SEQ ID NO: 199

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 723 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus saprophyticus*
 (B) STRAIN: CSG 83

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199

GCATTAGTTG TATTCTTAAA CAAAGTTGAC ATGGTTGACG ATGAAGAATT 50
 ATTAGAATTA GTAGAAATGG AAGTTCGTGA TTTATTAAGC GAATATGACT 100
 10 TCCCAGGTGA CGATGTACCT GTAATCTCTG GTTCTGCATT AAAAGCTTTA 150
 GAAGGCGACG CTGACTATGA GCAAAAAATC TTAGACTTAA TGCAAGCTGT 200
 TGATGACTTC ATTCCAACAC CAGAACGTGA TTCTGACAAA CCATTTCATGA 250
 TGCCAGTTGA GGACGTATTC TCAATCACTG GTCGTGGTAC TGTTGCTACA 300
 GGCCGTGTTG AACGTGGTCA AATCAAAGTC GGTGAAGAAA TCGAAATCAT 350
 15 CGGTATGCAA GAAGAATCAA GCAAAACAAC TGTTACTGGT GTAGAAATGT 400
 TCCGTAAATT ATTAGACTAC GCTGAAGCTG GTGACAACAT TGGTGCATTA 450
 TTACGTGGTG TTTACACGTG TGACGTACAA CGTGGTCAAG TTTTAGCTGC 500
 TCCTGGTACT ATTACACCAC ATACAAAATT CAAAGCGGAT GTTTACGTTT 550
 TATCTAAAGA TGAAGGTGGT CGTCATACAC CATTCCTTAC TAACTACCGC 600
 20 CCACAATTCT ATTTCCGTAC TACTGACGTA ACTGGTGTG TTAACCTACC 650
 AGAAGGTACT GAAATGGTTA TGCCTGGCGA TAACGTTGAA ATGGATGTTG 700
 AATTAATTTT TCCAATCGCT ATT 723

25

2) INFORMATION FOR SEQ ID NO: 200

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 697 bases
 30 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus saprophyticus*
 (B) STRAIN: CSsa 18

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 200

CGTTGGTGTG CCAGCATTAG TTGTATTCTT AAACAAAGTT GACATGGTTG 50
 ACGATGAAGA ATTATTAGAA TTAGTAGAAA TGGAAGTTCG TGAATTATTA 100
 AGCGAATATG ACTTCCCAGG TGACGATGTA CCTGTAATCT CTGGTTCTGC 150
 45 ATTAAAAGCT TTAGAAGGCG ACGCTGACTA TGAGCAAAAA ATCTTAGACT 200
 TAATGCAAGC TGTTGATGAC TTCATTCCAA CACCAGAACG TGATTCTGAC 250
 AAACCATTCA TGATGCCAGT TGAGGACGTA TTCTCAATCA CTGGTCGTGG 300
 TACTGTTGCT ACAGGCCGTG TTGAACGTGG TCAAATCAAA GTCGGTGAAG 350
 AAATCGAAAT CATCGGTATG CAAGAAGAAT CAAGCAAAAC AACTGTTACT 400
 50 GGTGTAGAAA TGTTCCGTAA ATTATTAGAC TACGCTGAAG CTGGTGACAA 450
 CATTGGTGCA TTATTACGTG GTGTTTCACG TGATGACGTA CAACGTGGTC 500
 AAGTTTTAGC TGCTCCTGGT ACTATTACAC CACATACAAA ATTCAAAGCG 550
 GATGTTTACG TTTTATCTAA AGATGAAGGT GGTGTCGATA CACCATTCTT 600
 CACTAACTAC CGCCACAAT TCTATTTCCG TACTACTGAC GTAACCTGGT 650
 55 TTGTTAACCT ACCAGAAGGT ACTGAAATGG TTATGCCTGG CGATAAC 697

60

2) INFORMATION FOR SEQ ID NO: 201

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus sciuri* subsp. *sciuri*
 (B) STRAIN: ATCC 29060

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201

```

15  CGGCGGTATC TTAGTAGTAT CTGCTGCTGA CGGTCCAATG CCTCAAACCTC      50
    GTGAGCACAT TCTTTTATCA CGTAACGTAG GTGTTCCCTGC ATTAGTAGTA      100
    TTCTTAAACA AAGTTGACAT GGTTGACGAT GAAGAATTAT TAGAATTAGT      150
    TGAATGGGAA GTTCGTGACT TATTATCTGA ATATGACTTC CCAGGCGACG      200
    ACGTTCCTGT AATTGCTGGT TCAGCATTA AAGCATTAGA AGGCGACGAA      250
20  GCTTACGAAG ACAAAATCAT GGAATTAATG GATGCTGTTG ATACATTCAT      300
    CCCAACTCCA GAACGTGACT CTGACAAACC ATTCATGATG CCAGTTGAGG      350
    ACGTATTCTC AATCACTGGT CGTGGTACTG TTGCTACAGG CCGTGTGTA      400
    CGTGGTCAAA TCACTGTTGG TGAAGAAGTT GAAATCATCG GTTTAACTGA      450
    AGAATCTTCT AAAACAACCTG TAACTGGTGT TGAAATGTTC CGTAAATTAT      500
25  TAGACTTCGC TGAAGCTGGA GATAACATCG GTGCATTATT ACGTGGTGTT      550
    GCTCGTGAAG ACGTTAACC GGTCAAGTA TTAGCTAAAC CAGGTTCAAT      600
    CACACCTCAC ACTAAATTCA AAGCTGAAGT TTATGTATTA TCTAAAGACG      650
    AAGGTGGACG TCATACTCCA TTCTTCACAA ACTACCGCCC ACAATTCTAT      700
    TTCCGTAATA CTGACGTAAC TGGTGTAGTT AACTTACCAG AAGGTACTGA      750
30  AATGGTTATG CCTGGCGACA ACGTTGAAAT GGACGTTGAA TTAATTTTAC      800
    CAATEGETAT TGAAGACGGT ATCGTTTCTC AATCA                      835
  
```

35 2) INFORMATION FOR SEQ ID NO: 202

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus warneri*
 (B) STRAIN: ATCC 27836

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 202

```

50  CGGCGGTATC TTAGTTGTAT CTGCAGCTGA TGGTCCAATG CCACAAACTC      50
    GTGAACACAT TCTTTTATCA CGTAACGTTG GTGTACCAGC TTAGTTGTA      100
    TTCTTAAACA AAGTTGATAT GGTAGACGAC GAAGAATTAT TAGAATTAGT      150
    AGAAATGGAA GTTCGTGACT TATTATCTGA ATATGACTTC CCAGGTGACG      200
55  ACGTACCTGT AATCGCTGGT TCAGCATTA AAGCTTTAGA AGGCGACGAA      250
    AAATACGAAG AAAAATCTT AGAATTAATG CAAGCAGTTG ATGACTACAT      300
    TCCAACCTCA GAACGTGATT CTGACAAACC ATTCATGATG CCAGTTGAGG      350
    ACGTATTCTC AATCACTGGT CGTGGTACTG TTGCTACAGG CCGTGTGTA      400
    CGTGGTCAAA TCAAAGTTGG TGAAGAAGTT GAAATCATCG GTTTACATGA      450
60  CACTTCTAAA ACAACTGTTA CTGGTGTAAG AATGTTCCGT AAGTTATTAG      500
  
```

ACTACGCTGA AGCTGGTGAC AACATCGGTG CTTTATTACG TGGTGTGCT 550
 CGTGAAGACG TACAACGTGG TCAAGTATTA GCTGCTCCTG GTTCAATTAC 600
 ACCACATACA AAATTCAAAG CGGAAGTTTA CGTTTTATCT AAAGACGAAG 650
 GTGGACGTCA CACTCCATTC TTCAGTAACT ACCGCCCACA ATTCTATTTC 700
 5 CGTACTACTG ACGTAACTGG CGTTGTTCAA TTACCAGAAG GTACTGAAAT 750
 GGTATATGCCT GGTGATAACG TTGAAATGAC AGTAGAATTA ATCGCTCCTA 800
 TCGCGATTGA AGACGGTACT CGTTTCTCAA C 831

10

2) INFORMATION FOR SEQ ID NO: 203

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus warneri*
 (B) STRAIN: CSG 50

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203

CGGCGGTATC TTAGTTGTAT CTGCAGCTGA TGGTCCAATG CCACAACTC 50
 GTGAACACAT TCTTTTATCA CGTAACGTTG GTGTACCAGC TTTAGTTGTA 100
 TTCTTAAACA AAGTTGATAT GGTAGACGAC GAAGAATTAT TAGAATTAGT 150
 30 AGAAATGGAA GTTCGTGACT TATTATCTGA ATATGACTTC CCAGGTGACG 200
 ACGTACCTGT AATCGCTGGT TCAGCATTA AAGCTTTAGA AGGCGACGAA 250
 AAATACGAAG AAAAAATCTT AGAATTAATG CAAGCAGTTG ATGACTACAT 300
 TCCAACCTCA GAACGTGATT CTGACAAACC ATTCATGATG CCAGTTGAGG 350
 ACGTATTCTC AATCACTGGT CGTGGTACTG TTGCTACAGG CCGTGTTGAA 400
 35 CGTGGTCAAA TCAAAGTTGG TGAAGAAGTT GAAATCATCG GTTTACATGA 450
 CACTTCTAAA ACAACTGTTA CTGGTGTAGA AATGTTCCGT AAGTTATTAG 500
 ACTACGCTGA AGCTGGTGAC AACATCGGTG CTTTATTACG TGGTGTGCT 550
 CGTGAAGACG TACAACGTGG TCAAGTATTA GCTGCTCCTG GTTCAATTAC 600
 ACCACATACA AAATTCAAAG CGGAAGTTTA CGTTTTATCT AAAGACGAAG 650
 40 GTGGACGTCA CACTCCATTC TTCAGTAACT ACCGCCCACA ATTCTATTTC 700
 CGTACTACTG ACGTAACTGG CGTTGTTCAA TTACCAGAAG GTACTGAAAT 750
 GGTATATGCCT GGTGATAACG TTGAAATGAC AGTAGAATTA ATCGCTCCTA 800
 TCGCGATTGA AGACGGTACT CGTTTCTCA 829

45

2) INFORMATION FOR SEQ ID NO: 204

(i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 839 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bifidobacterium longum*
 (B) STRAIN: ATCC 15707

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 204

```

5  TGGCGCTATC CTCGTTGTGG CCGCCACCGA CGGCCCGATG GCCCAGACTC 50
   GCGAGCACGT GCTGCTCGCC CGTCAGGTTG GCGTTCCGAA GATCCTCGTC 100
   GCCCTGAACA AGTGCGACAT GGTCGACGAT GAAGAGCTCA TCGAGCTCGT 150
   CGAAGAAGAG GTCCGCGACC TCCTCGACGA GAACGGCTTC GACCGTGA CT 200
   GCCCGGTCAT CCACACCTCC GCTTACGGTG CTCTGCACGA CGACGCTCCG 250
   GACCACGAGA AGTGGGTCCA GTCCGTTAAG GACCTCATGG ACGCTGTCTG 300
   CGACTACATC CCGACCCCGG TTCACGACCT GGACAAGCCG TTCCTGATGC 350
10  CGATCGAGGA CGTCTTCACC ATCTCCGGCC GTGGTACCGT TGTACCCGGT 400
   CGTGTGCGAG GTGGCCAGCT GGCCGTCAAC ACCCCGGTCG AGATCGTTGG 450
   TATCCGTCCG ACCCAGCAGA CCACCGTCAC CTCCATCGAG ACCTTCCACA 500
   AGACCATGGA CGCCTGCGAG GCTGGCGACA ACACCGGTCT GCTTCTGCGT 550
   GGTCTCGGCC GTGACGATGT CGAGCGTGCG CAGGTTGTGG CCAAGCCGGG 600
15  CTCCGTCACC CCGCACACCA AGTTCGAGGG CGAAGTCTAC GTGCTGACCA 650
   AGGACGAAGG CGGCCGTCAC TCGCCGTTCT TCTCCAACTA CCGTCCGCAG 700
   TTCTACTTCC GCACCACCGA CGTCACCGGC GTCATCGAGC TGCCGGAAGG 750
   CGTCGAGATG GTTCAGCCGG GCGACCACGC TACCTTCACC GTTGAGCTGA 800
   TTCAGCCCAT CGCTATGGAG GAAGGCCTGA CCTTCGCTG 839
20

```

2) INFORMATION FOR SEQ ID NO: 205

```

25  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 754 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear

```

```

30  (ii) MOLECULE-TYPE: Genomic DNA

```

```

      (vi) ORIGINAL SOURCE:

```

```

35  (A) ORGANISM: Stenotrophomonas maltophilia
      (B) STRAIN: CDC F3338

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205

```

40  CGGCGCGATC CTGGTGTGCT CGGCCGCTGA CGGCCCGATG CCGCAGACCC 50
   GTGAGCACAT CCTGCTGTCG CGCCAGGTCG GCGTGCCGTA CATCGTCGTG 100
   TTCCTGAACA AGGCCGACAT GGTCGACGAC GCCGAGCTGC TCGAGCTGGT 150
   CGAGATGGAA GTGCGCGAAC TGCTGAGCAA GTACGAGTTC CCGGGCGACG 200
   ACACCCCGAT CATCGCCGGT TCGGCCCGCC TGGCGCTGGA AGGCGACCAG 250
   AGCGACATCG GCGTGCCGGC CATCCTGAAG CTGGTCGACG CGCTGGACAG 300
45  CTGGATTCCG GAGCCGGAGC GTGCGATCGA CAAGCCGTTT CTGATGCCCG 350
   TGGAAGACGT GTTCTCGATC TCGGGCCGCG GCACCGTGGT GACCGGTCGT 400
   ATCGAGCGCG GCGTGATCAA GGTTGGCGAC GAAATCGAAA TCGTCGGCAT 450
   CCGTCCGGTG CAGAAGACCA CCGTGACCGG CGTTGAAATG TTCCGCAAGC 500
   TGCTGGACCA GGGTCAGGCA GGCGACAACG CTGGCCTGCT GCTGCGCGGC 550
50  ACCAAGCGTG ATGACGTCGA GCGTGCCAG GTGCTGGCCA AGCCGGGCAC 600
   GATCAAGCCG CACACCAAGT TCGAAGGCGA AGTGACGTC CTGTCGAAGG 650
   ACGAGGGCGG CCGCCACACC CCGTTCCTCA ACGGCTACCG TCCGCAGTTC 700
   TACTTCGCA CCACCGACAT CACCGGCGCC GCTGCACTGC CGGAAGGCGT 750
   CGAA
55

```

2) INFORMATION FOR SEQ ID NO: 206

```

60  (i) SEQUENCE CHARACTERISTICS:

```

(A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus acidominimus*
 (B) STRAIN: ATCC 51726

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 206

	TGGTGCTATC	CTTG TAGTAG	CTTCAACTGA	CGGACCAATG	CCACAAACTC	50
15	GTGAGCACAT	CCTTCTTTCA	CGTCAAGTTG	GTGTTAAAAA	CCTTATCGTT	100
	TTCATGAACA	AAGTTGACCT	TGTTGATGAT	GAAGAATTGC	TTGAATTGGT	150
	TGAAATGGAA	ATCCGTGACC	TTCTTTCAGA	ATACGATTTC	CCAGGTGATG	200
	ATCTTCCAGT	TGTTCAAGGT	TCAGCTCTTA	AAGCGCTTGA	AGGTGATTCA	250
	GCACAAGAAG	ATGTTATCAT	GGAATTGATG	TCAATCGTTG	ACACATACAT	300
20	TCCAGAACCA	GAACGTGATA	CTGACAAACC	ATTGCTTCTT	CCAGTCGAGG	350
	ATGTATTCTC	AATCACTGGA	CGTGGTACTG	TTGCTTCAGG	ACGTATCGAC	400
	CGTGGTACTG	TTAAAGTTAA	TGACGAAGTT	GAAATCGTTG	GTATCAAAGA	450
	CGAAATCTCT	AAAGCAGTTG	TTACTGGTGT	TGAAATGTTT	CGTAAACAAC	500
	TTGACGAAGG	TCTTGCTGGA	GATAACGTTG	GTGTTCTTCT	TCGTGGTGTA	550
25	CAACGTGATG	AAATCGAACG	TGGTCAAGTT	CTTGCTAAAC	CAGGTTCAAT	600
	CAACCCACAC	ACTAAATTCA	AAGGTGAAGT	TTACGTTCTT	TCTAAAGAAG	650
	AAGGTGGACG	TCACACTCCA	TTCTTCGATA	ACTACCGTCC	TCAGTTCTAC	700
	TTCCGTACAA	CTGACGTAAC	TGGTTCAATC	AAATTGCCAG	AAGGTACTGA	750
	AATGGTAATG	CCTGGTGATA	ACGTAACAT	CGAAGTTGAG	TTGATCCACC	800
30	CAATCGCCGT	TGAACAAGGT	ACTACTTTCT	CTATC		835

2) INFORMATION FOR SEQ ID NO: 207

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 819 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus agalactiae*
 (B) STRAIN: ATCC 12403

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207

50	CTATCCTTGT	AGTTGCTTCA	ACTGATGGAC	CAATGCCACA	AACTCGTGAG	50
	CACATCCTTC	TTTCACGTCA	AGTTGGTGTT	AAACACCTTA	TCGTATTCAT	100
	GAACAAAGTT	GACCTTGTTG	ATGATGAAGA	ATTGCTTGAA	TTGGTTGAAA	150
	TGGAAATTCTG	TGACCTTCTT	TCAGAATACG	ACTTCCCAGG	TGATGACCTT	200
	CCAGTTATCC	AAGGTTTCAGC	TCTTAAAGCA	CTTGAAGGCG	ACGAAAAATA	250
55	CGAAGACATC	ATCATGGAAT	TGATGAGCAC	TGTTGATGAG	TACATTCCAG	300
	AACCAGAACG	TGATACTGAC	AAACCTTTAC	TTCTTCCAGT	TGAAGATGTA	350
	TTCTCAATCA	CTGGACGTGG	TACAGTTGCT	TCAGGACGTA	TCGACCGTGG	400
	TACTGTTCGT	GTCAACGACG	AAGTTGAAAT	CGTTGGTATT	AAAGAAGATA	450
	TCCAAAAAGC	AGTTGTTACT	GGTGTGAAA	TGTTCCGTAA	ACAACCTGAC	500
60	GAAGGTCTTG	CAGGGGACAA	CGTTGGTGTT	CTTCTTCGTG	GTGTTCAACG	550

	TGATGAAATC	GAACGTGGTC	AAGTTCTTGC	TAAACCAGGT	TCAATCAACC	600
	CACACACTAA	ATTTAAAGGT	GAAGTTTACA	TCCTTTCTAA	AGAAGAAGGT	650
	GGACGTCATA	CTCCATTCTT	CAACAACACTAC	CGTCCACAAT	TCTACTTCCG	700
	TACAACAGGAC	GTAACAGGTT	CAATCGAACT	TCCAGCAGGA	ACAGAAATGG	750
5	TTATGCCTGG	TGATAACGTT	ACTATCGAAG	TTGAATTGAT	TCACCCAATC	800
	GCCGTAGAAC	AAGGTACTA				819

10 2) INFORMATION FOR SEQ ID NO: 208

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 819 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus agalactiae*
 (B) STRAIN: ATCC 12973

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 208

25	CTATCCTTGT	AGTTGCTTCA	ACTGATGGAC	CAATGCCACA	AACTCGTGAG	50
	CACATCCTTC	TTTCACGTCA	AGTTGGTGTT	AAACACCTTA	TCGTATTTCAT	100
	GAACAAAGTT	GACCTTGTTG	ATGATGAAGA	ATTGCTTGAA	TTGGTTGAAA	150
	TGGAAATTCTG	TGACCTTCTT	TCAGAATACG	ACTTCCCAGG	TGATGACCTT	200
30	CCAGTTATCC	AAGGTTTCAGC	TCTTAAAGCA	CTTGAAGGCG	ATGAAAAATA	250
	CGAAGACATC	ATCATGGAAT	TGATGAGCAC	TGTTGATGAG	TACATTCCAG	300
	AACCAGAACG	TGATACTGAC	AAACCTTTAC	TTCTTCCAGT	CGAAGATGTA	350
	TTCTCAATCA	CTGGACGTGG	TACAGTTGCT	TCAGGACGTA	TCGACCGTGG	400
	TACTGTTCGT	GTCAACGACG	AAGTTGAAAT	CGTTGGTATT	AAAGAAGATA	450
35	TCCAAAAAGC	AGTTGTTACT	GGTGTTGAAA	TGTTCCGTAA	ACAACCTTGAC	500
	GAAGGTCTTG	CAGGGGACAA	CGTTGGTGTT	CTTCTTCGTG	GTGTTCAACG	550
	TGATGAAATC	GAACGTGGTC	AAGTTCTTGC	TAAACCAGGT	TCAATCAACC	600
	CACACACTAA	ATTTAAAGGT	GAAGTTTACA	TCCTTTCTAA	AGAAGAAGGT	650
	GGACGTCATA	CTCCATTCTT	CAACAACACTAC	CGTCCACAAT	TCTACTTCCG	700
40	TACAACAGGAC	GTAACAGGTT	CAATCGAACT	TCCAGCAGGA	ACAGAAATGG	750
	TTATGCCTGG	TGATAACGTT	ACTATCGAAG	TTGAATTGAT	TCACCCAATC	800
	GCCGTAGAAC	AAGGTACTA				819

45 2) INFORMATION FOR SEQ ID NO: 209

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 bases
 50 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus agalactiae*
 (B) STRAIN: ATCC 13813

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 209

```

AGCTATCCTT GTAGTTGCTT CAACTGATGG ACCAATGCCA CAAACTCGTG      50
AGCACATCCT TCTTTCACGT CAAGTTGGTG TTAAACACCT TATCGTATTC      100
ATGAACAAAG TTGACCTTGT TGATGATGAA GAATTGCTTG AATTGGTTGA      150
5  AATGGAAATT CGTGACCTTC TTTCAGAATA CGACTTCCCA GGTGATGACC      200
TTCCAGTTAT CCAAGGTTCA GCTCTTAAAG CACTTGAAGG CGATGAAAAA      250
TACGAAGACA TCATCATGGA ATTGATGAGC ACTGTTGATG AGTACATTCC      300
AGAACCAGAA CGTGATACTG ACAAACCTTT ACTTCTTCCA GTCGAAGATG      350
TATTCTCAAT CACTGGACGT GGTACAGTTG CTTCAGGACG TATCGACCGT      400
10 GGTACTGTTC GTGTCAACGA CGAAGTTGAA ATCGTTGGTA TTAAAGAAGA      450
TATCCAAAAA GCAGTTGTTA CTGGTGTTGA AATGTTCCGT AAACAACCTG      500
ACGAAGGTCT TGCAGGGGAC AACGTTGGTG TTCTTCTTCG TGGTGTTCAA      550
CGTGATGAAA TCGAACGTGG TCAAGTTCTT GCTAAACCAG GTTCAATCAA      600
CCCACACACT AAATTTAAAG GTGAAGTTTA CATCCTTTCT AAAGAAGAAG      650
15 GTGGACGTCA TACTCCATTC TTCAACAAC ACTCGTCCACA ATTCTACTTC      700
CGTACAAC TGACGTAACAGG TTCAATCGAA CTTCCAGCAG GAACAGAAAT      750
GGTTATGCCT GGTGATAACG TTAATATCGA AGTTGAATTG ATTCACCCAA      800
TCGCCGTAGA ACAAGGTACT AC                                     822

```

20

2) INFORMATION FOR SEQ ID NO: 210

```

25 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 825 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

```

30 (ii) MOLECULE TYPE: Genomic DNA

```

(vi) ORIGINAL SOURCE:

```

    (A) ORGANISM: Streptococcus agalactiae
    (B) STRAIN: CDCss-1073

```

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 210

```

CGGAGCTATC CTTGTAGTTG CTTCAACTGA TGGACCAATG CCACAAACTC      50
GTGAGCACAT CCTTCTTTCA CGTCAAGTTG GTGTTAAACA CCTTATCGTA      100
40 TTCATGAACA AAGTTGACCT TGTTGATGAT GAAGAATTGC TTGAATTGGT      150
TGAAATGGAA ATTCGTGACC TTCTTTCAGA ATACGACTTC CCAGGTGATG      200
ACCTTCCAGT TATCCAAGGT TCAGCTCTTA AAGCACTTGA AGGCGACGAA      250
AAATACGAAG ACATCATCAT GGAATTGATG AGCACTGTTG ATGAGTACAT      300
TCCAGAACCA GAACGTGATA CTGACAAACC TTTACTTCTT CCAGTTGAAG      350
45 ATGTATTCTC AATCACTGGA CGTGGTACAG TTGCTTCAGG ACGTATCGAC      400
CGTGGTACTG TTCGTGTCAA CGACGAAGTT GAAATCGTTG GTATTAAAGA      450
AGATATCCAA AAAGCAGTTG TTAAGTGGTG TGAAATGTTT CGTAAACAAC      500
TTGACGAAGG TCTTGCAGGG GACAACGTTG GTGTTCTTCT TCGTGGTGTT      550
CAACGTGATG AAATCGAACG TGGTCAAGTT CTTGCTAAAC CAGGTTCAAT      600
50 CAACCCACAC ACTAAATTTA AAGGTGAAGT TTACATCCTT TCTAAAGAAG      650
AAGGTGGACG TCATACTCCA TTCTTCAACA ACTACCGTCC ACAATTCTAC      700
TTCCGTACAA CTGACGTAAC AGGTTCATC GAACTTCCAG CAGGAACAGA      750
AATGGTTATG CCTGGTGATA ACGTTACTAT CGAAGTTGAA TTGATTACAC      800
CAATCGCCGT AGAACAAGGT ACTAC                                     825
55

```

2) INFORMATION FOR SEQ ID NO: 211

```

60 (i) SEQUENCE CHARACTERISTICS:

```

(A) LENGTH: 826 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus anginosus*
 (B) STRAIN: ATCC 33397

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 211

15	GGAGCTATCC	TTGTAGTAGC	TTCAACTGAC	GGACCAATGC	CTCAAACCTCG	50
	TGAACACATC	CTTCTTTTCAC	GCCAAGTAGG	TGTTAAATAC	CTTATCGTCT	100
	TCATGAATAA	AGTTGACTTG	GTTGACGATG	AAGAATTGCT	TGAATTGGTT	150
	GAAATGGAAA	TCCGTGACCT	TCTTTCAGAA	TACGATTTCC	CAGGTGATGA	200
	AATCCCAGTT	ATCCAAGGTT	CAGCTCTTAA	AGCTCTTGAA	GGTGATGAAA	250
	AATATGAAGA	CATCATCATG	GAATTGATGG	ATACTGTTGA	TGAATACATT	300
20	CCAGAACCAG	AACGTGACAC	TGACAAACCA	TTGCTTCTTC	CAGTTGAAGA	350
	TGTATTCTCA	ATTACTGGAC	GTGGTACTGT	TGCTTCAGGA	CGTATCGACC	400
	GTGGTACTGT	TAAAGTCAAC	GACGAAGTTG	AAATCGTTGG	TATCCGTGAT	450
	GAAATCCAAA	AAGCAGTTGT	TACTGGTGTT	GAAATGTTCC	GTAAACAATT	500
	GGACGAAGGT	CTTGCTGGAG	ATAACGTAGG	GGTTCCTTCT	CGTGGTATCC	550
25	AACGTGACGA	AATCGAACGT	GGACAAGTTC	TTGCTAAACC	AGGTTCAATT	600
	CATCCACACA	CTAAATTCAA	AGGTGAAGTT	TACATCCTTA	CTAAAGAAGA	650
	AGGTGGACGT	CATACTCCAT	TCTTCAACAA	CTACCGTCCT	CAATTCTACT	700
	TCCGTACTAC	AGACGTTACA	GGTTCATCG	AACTTCCTGC	AGGTACTGAA	750
	ATGGTAATGC	CTGGTGATAA	CGTAACAATC	GACGTTGAAT	TGATCCACCC	800
30	AATTGCCGTA	GAACAAGGAA	CTACAT			826

2) INFORMATION FOR SEQ ID NO: 212

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 827 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus bovis*
 (B) STRAIN: ATCC 33317

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 212

50	TGGTGCTATC	CTTG TAGTAG	CTTCTACAGA	TGGTCCAATG	CCACAAACAC	50
	GTGAACACAT	CCTTCTTTCA	CGTCAAGTTG	GTGTTAAACA	CCTTATCGTC	100
	TTCATGAACA	AAGTTGACCT	TGTTGATGAC	GAAGAATTGC	TTGAATTGGT	150
	TGAAATGGAA	ATCCGTGACC	TTCTTTTCAGA	ATATGATTTT	CCAGGTGATG	200
	AAATCCCTGT	AATCCAAGGT	TCAGCTCTTA	AAGCCCTTGA	AGGTGACACT	250
55	CACTACGAAG	ACATCATCAT	GGAATTGATG	AACACTGTAG	ATGAATACAT	300
	TCCAGAACCA	AAACGTGATA	CTGACAAACC	ATTGCTTCTT	CCAGTCGAAG	350
	ACGTATTCTC	AATCACTGGT	CGTGGTACTG	TAGCATCAGG	ACGTATCGAC	400
	CGTGGTACTG	TTAAAGTCAA	CGACGAAGTT	GAAATCGTTG	GTATCCGTGA	450
	CGACATCCAA	AAAGCTGTTG	TTACTGGTGT	TGAAATGTTT	CGTAAACAAC	500
60	TTGATGAAGG	TATCGCAGGG	GATAACGTTG	GTGTTCTTCT	TCGTGGTATC	550

CAACGTGATG AAATCGAACG TGGTCAAGTT CTTGCTAAAC CAGGTTCAAT 600
 CCACCCACAC ACTAAATTCA AAGGTGAAGT TTACATCCTT ACTAAAGAAG 650
 AAGGTGGACG TCACACTCCA TTCTTCAACA ACTACCGTCC TCAATTCTAC 700
 TTCCGTACAA CTGACGTTAC AGGTTCAATC GAACTTCCAG CAGGTACTGA 750
 5 AATGGTAATG CCTGGTGATA ACGTTACTAT CGACGTTGAA TTGATTCACC 800
 CAATCGCCGT TGAACAAGGT ACTACAT 827

10 2) INFORMATION FOR SEQ ID NO: 213

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 821 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus anginosus* (deposited as
Streptococcus constellatus)
 (B) STRAIN: ATCC 27823

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 213

GCTATCCTCG TAGTAGCTTC AACTGATGGA CCAATGCCTC AAACTCGTGA 50
 ACATATCCTT CTTTCACGTC AAGTAGGTGT TAAATACCTT ATCGTCTTCA 100
 TGAACAAAGT TGACTTGGTT GACGATGAAG AATTGCTTGA ATTGGTTGAA 150
 30 ATGGAAATCC GTGACCTTCT TTCAGAATAC GATTTCCTCAG GTGATGAAAT 200
 CCCAGTTATC CAAGGTTTCAG CTCTTAAAGC TCTTGAAGGT GATGAAAAAT 250
 ATGAAGACAT CATCATGGAA TTGATGGATA CTGTTGATGA ATACATTCCA 300
 GAACCAGAAC GTGACACTGA CAAACCACTT CTTCTTCCAG TCGAAGATGT 350
 ATTCTCAATC ACTGGACGTG GTACTGTTGC TTCAGGACGT ATCGACCGTG 400
 35 GTACTGTTAA AGTCAATGAT GAAGTTGAAA TTGTTGGTAT TCGTGACGAA 450
 ATCCAAAAAG CAGTTGTTAC TGGTGTTGAA ATGTTCCGTA AACAAATTGGA 500
 CGAAGGTCTT GCTGGAGATA ACGTAGGGGT TCTTCTTCGT GGTATCCAAC 550
 GTGACGAAAT CGAACGTGGA CAAGTTCTTG CTAAACCAGG TTCAATTTCAT 600
 CCACACACTA AATTCAAAGG TGAAGTTTAC ATCCTTACTA AAGAAGAAGG 650
 40 TGGACGTCAT ACTCCATTCT TCAACAATA CCGTCCTCAA TTCTACTTCC 700
 GTACTACAGA CGTTACAGGT TCAATCGAAC TTCCTGCAGG TACTGAAATG 750
 GTAATGCCTG GTGATAACGT AACAAATTGAT GTTGAGTTGA TCCACCCAAT 800
 TGCCGTAGAA CAAGGAACTA C 821

45

2) INFORMATION FOR SEQ ID NO: 214

(i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 821 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus cricetus*
 60 (B) STRAIN: ATCC 19642

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 214

```

5  GCTATCCTTG TAGTAGCTTC TACAGACGGA CCAATGCCAC AAACCTCGTGA 50
   ACACATCTTG CTTTCACGCC AAGTTGGTGT TAAGAGCCTT ATCGTCTTCA 100
   TGAACAAGGT TGACTTGGTT GACGATGAAG AATTGCTTGA ATTGGTTGAA 150
   ATGGAAATCC GTGATCTTCT TTCAGAATAC GATTTCCTCAG GTGATGATAT 200
   CCTGTGTGTT CAAGGTTTCAG CTCTTAAAGC CCTTGAAGGT GATACAGCTG 250
   CCGAAGACAA GATCATGGAA TTGATGGACA TCGTTGATGA CTACATTCCA 300
   GAACCAAAAC GTGATACTGA TAAGCCATTG CTTCTTCCAG TCGAAGACGT 350
10 ATTCTCAATC ACTGGACGTG GTACTGTTGC TTCAGGACGT ATCGACCGTG 400
   GTACTGTTAA GGTCAATGAC GAAGTTGAAA TCGTTGGTAT CAAGGACGAA 450
   ATCCAAAAAG CGGTTGTTAC CGGAGTTGAA ATGTTCCGTA AACAATTGGA 500
   TGAAGGTCTT GCAGGGGATA ACGTTGGTGT GCTTCTTCGT GGTATCCAAC 550
   GTGATGAAAT CGAACGTGGT CAAGTATTGG CTGCACCTGG TTCAATCCAT 600
15 CCACACACTA AATTCAAGGG TGAAGTTTAC ATCCTTTCTA AAGATGAAGG 650
   TGGACGTCAC ACTCCATTCT TCAACAACCTA CCGTCCACAG TTCTACTTCC 700
   GTACAACCTGA CGTAACTGGT TCAATCGAAT TGCCAGCAGG TACTGAAATG 750
   GTTATGCCTG GTGATAACGT TACTATCGAC GTTGAATTGA TCCACCCAAT 800
   CGCTGTTGAA AAAGGTACTA C 821
20

```

2) INFORMATION FOR SEQ ID NO: 215

```

25 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 821 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear
30

```

```

---(ii) MOLECULE TYPE: Genomic DNA

```

(vi) ORIGINAL SOURCE:

```

35 (A) ORGANISM: Streptococcus cristatus
    (B) STRAIN: ATCC 51100

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 215

```

40 TATCCTTGTA GTAGCTTCAA CTGACGGACC AATGCCACAA ACTCGTGAGC 50
   ACATCCTTCT TTCACGTCAG GTTGGTGTTA AACACCTTAT CGTCTTCATG 100
   AACAAGATCG ACTTGGTTGA TGACGAAGAA TTGCTTGAAT TGGTTGAAAT 150
   GGAAATCCGT GACCTCTTGT CAGAATACGA CTTCCCAGGT GACGATCTTC 200
   CAGTTATCCA AGGTTTCAGCT CTTAAAGCTC TTGAAGGTGA TACTAAGTAC 250
   GAAGACATCA TCATGGAATT GATGAACACT GTTGATGAGT ACATCCCAGA 300
45 ACCAGAACGT GATACTGACA AACCTCTTCT TCTTCCAGTC GAAGACGTAT 350
   TCTCAATCAC TGGTCGTGGT ACAGTTGCTT CAGGACGTAT CGACCGTGGT 400
   ACTGTTTCGTG TCAACGATGA AATCGAAATC GTTGGTATCA AAGAAGAAAT 450
   CCAAAAAGCA GTTGTTACTG GTGTTGAAAT GTTCCGTAAA CAGCTTGACG 500
   AAGGTCTTGC AGGGGACAAC GTAGGTGTAC TTCTTCGTGG TATCCAACGT 550
50 GATGAAATCG AACGTGGTCA AGTTATCGCT AAACCAGGTT CAATCAACCC 600
   ACACACTAAA TTCAAGGGTG AAGTTTACAT CCTTACTAAA GAAGAAGGTG 650
   GACGTCACAC TCCATTCTTC AACAACTACC GTCCACAGTT CTACTTCCGT 700
   ACAACTGACG TTACAGGTTT AATCGAACTT CCAGCAGGTA CTGAAATGGT 750
   AATGCCTGGT GATAACGTAA CTATCGACGT TGAGTTGATC CACCCAATCG 800
55 CCGTTGAACA AGGTACTCCT T 821

```

2) INFORMATION FOR SEQ ID NO: 216

60

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 792 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus downei*
 (B) STRAIN: ATCC 33748

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 216

```

15  AGTAGCTTCT ACTGATGGAC CAATGCCACA AACTCGTGAA CACATCTTGC      50
    TTTCACGTCA GGTGTTGGTGT AAGAACCTTA TCGTCTTCAT GAACAAGGTT      100
    GACTTGGTTG ACGATGAAGA ATTGCTTGAA TTGGTTGAAA TGGAAATCCG      150
    TGACCTGCTT TCAGAATACG ATTTCCCAGG TGATGATATC CCTGTTGTTC      200
    AAGGTTTCAGC TCTTAAGGCT CTTGAAGGTG ATACAGCTGC CGAAGACAAG      250
20  ATCATTGAAT TGATGGACAT CGTTGATGAC TACATTCCAG AACCAAAACG      300
    TGATACTGAT AAGCCTTTGC TTCTTCCAGT CGAAGATGTA TTCTCAATCA      350
    CTGGACGTGG TACTGTAGCT TCAGGACGTA TCGACCGTGG TACTGTTAAG      400
    GTCAACGACG AAGTTGAAAT CGTTGGTATC AAGGACGAAA TCCAAAAAGC      450
    AGTTGTTACC GGAGTTGAAA TGTTCCGTAA ACAATTGGAC GAAGGTCTTG      500
25  CAGGGGATAA CGTTGGTGTG CTTCTTCGTG GTATCCAACG TGATGAAATC      550
    GAACGTGGTC AAGTGTTGGC TGC GCCTGGT TCGATTACC CACACACTAA      600
    GTTTAAAGGT GAAGTTTACA TCCTTTCTAA AGAAGAAGGT GGACGTCATA      650
    CTCCATTCTT TAACAACACT CGTCCACAGT TCTACTTCCG TACAACGAC      700
    GTAACGTTT CAATCGAATT GCCAGCGGGT ACTGAAATGG TTATGCCTGG      750
30  TGATAACGTT ACTATCGACG TTGAATTGAT CCACCCAATT GC              792
  
```

2) INFORMATION FOR SEQ ID NO: 217

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 795 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus dysgalactiae*
 (B) STRAIN: ATCC 43078

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 217

```

50  GTAGTTGCTT CAACAGACGG ACCAATGCCA CAAACTCGTG AGCACATCCT      50
    CCTTTCACGT CAGGTTGGTG TTAAACACCT TATCGTGTTT ATGAACAAAA      100
    TTGACCTTGT TGACGATGAA GAATTGCTTG AATTGGTTGA AATGGAAATC      150
    CGTGACCTTC TTTCAGAAATA CGATTCCCA GGTGATGACC TTCCAGTTAT      200
    CCAAGGTTCA GCTCTTAAAG CTCTTGAAGG CGACACTAAA TTTGAAGACA      250
55  TCATCATGGA ATTGATGGAT ACTGTTGATT CATAATTCC AGAACCAGAA      300
    CGTGACACTG ACAAACCAT TCTTCTTCCA GTCGAAGACG TATTCTCAAT      350
    CACAGGTCGT GTTACAGTTG CTTGAGGACG TATCGACCGT GGTACTGTTC      400
    GTGTCAACGA CGAAATCGAA ATCGTTGGTA TCAAAGAAGA AACTAAAAAA      450
    GCTGTTGTGA CTGGTGTGTA AATGTTCCGT AAACAACCTG ACGAAGGTCT      500
60  TGCAGGAGAC AACGTAGGTA TCCTTCTTCG TGGTGTTCAG CGTGACGAAA      550
  
```


	TCGAACGTGG	TCAAGTTATT	GCTAAACCAG	GTTCAATCAA	CCCACACACT	600
	AAATTCAAAG	GTGAAGTATA	TATCCTTTCT	AAAGACGAAG	GTGGACGTCA	650
	CACTCCATTC	TTCAACAAC	ATCGTCCACA	ATTCTACTTC	CGTACAAC	700
	ACGTAACAGG	TTCAATCGAA	CTTCCAGCTG	GTACAGAAAT	GGTTATGCCT	750
5	GGTGATAACG	TGACAATCAA	CGTTGAGTTG	ATCCACCCAA	TCGCC	795

2) INFORMATION FOR SEQ ID NO: 218

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus equi* subsp. *equi*
- (B) STRAIN: ATCC 9528

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 218

25	CGGAGCTATC	CTTGTAGTTG	CTTCAACTGA	CGGACCAATG	CCACAAACTC	50
	GTGAGCACAT	CCTTCTTTCA	CGTCAGGTTG	GTGTTAAGCA	CCTTATCGTG	100
	TTCATGAACA	AGGTTGACCT	TGTTGACGAT	GAAGAATTGC	TTGAGCTTGT	150
	TGAAATGGAA	ATTCGTGACC	TTCTTTCAGA	ATATGATTTC	CCAGGTGATG	200
	ACCTTCCAGT	TATCCAAGGT	TCAGCGCTTA	AGGCTCTTGA	AGGCGACAGC	250
30	AAATACGAAG	ATATCATCAT	GGAATTGATG	GATACTGTTG	ATTCATACAT	300
	TCCAGAACCA	GAACGTGACA	CAGACAAGCC	ATTGCTTCTT	CCAGTCGAGG	350
	ACGTATTCTC	AATCACTGGA	CGTGGTACTG	TTGCTTCAGG	ACGTATCGAC	400
	CGCGGTACTG	TTTCGTGTTAA	CGACGAAATC	GAAATCGTTG	GTATCAGAGA	450
	CGAGATCAAA	AAAGCAGTTG	TTACTGGTGT	CGAAATGTTT	CGTAAACAGC	500
35	TTGACGAAGG	TCTTGCAGGG	GACAACGTTG	GTGTTCTTCT	TCGTGGTGTA	550
	CAACGTGATG	AAATCGAACG	TGGTCAAGTT	ATTGCTAAGC	CAGGTTCTAT	600
	CAACCCACAC	ACTAAATTTA	AAGGTGAAGT	ATATATCCTT	ACTAAAGAAG	650
	AAGGTGGACG	TCACACACCA	TTCTTCAACA	ACTATCGTCC	ACAATTCTAC	700
	TTCCGTACTA	CTGACGTAAC	AGGTTCAATC	GAGCTTCCAG	CAGGTACAGA	750
40	AATGGTTATG	CCTGGTGATA	ACGTGACTAT	TGACGTTGAG	TTGATCCACC	800
	CAATCGCCGT	AGAACAAGGT	ACTACATT			828

45 2) INFORMATION FOR SEQ ID NO: 219

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus ferus*
- (B) STRAIN: ATCC 33477

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 219

5 CGGTGCAATC CTTGTAGTAG CTTCTACAGA TGGACCAATG CCACAAACTC 50
 GTGAGCACAT CCTTCTTTCA CGTCAGGTAG GTGTAAACA CCTTATCGTC 100
 TTCATGAACA AAGTTGACTT GGTGACGAT GAAGAATTGC TTGAATTGGT 150
 TGAAATGGAA ATCCGTGACC TGCTTTCAGA ATATGATTTC CCAGGTGATG 200
 ACCTTCCAGT TATCCAAGGT TCAGCTCTTA AAGCGCTTGA AGGTGATACT 250
 GCTCAAGAAG ATGTTATCAT GGAATTGATG AAAACCGTTG ATGAGTACAT 300
 CCCAGAACCA GAACGTGATA CTGACAAACC ATTGCTTCTT CCAGTCGAAG 350
 ATGTATTCTC AATCACAGGT CGTGGTACTG TAGCTTCAGG ACGTATCGAT 400
 CGTGGTACTG TAAGAGTCAA CGATGAAGTT GAAATCGTTG GTATCAAAGA 450
 10 CGAAATCACT AAAGCAGTTG TTACCGGTGT TGAAATGTTT CGTAAACAAT 500
 TGGACGAAGG TCTTGCTGGT GATAACGTTG GTGTGCTTCT CCGTGGTGTT 550
 CAACGTGATG AAATCGAACG TGGTCAAGTA TTGGCTAAAC CAGGTTCAAT 600
 CAACCCACAC ACTAAATTTA AAGGTGAAGT TTACATCCTT ACTAAGAAG 650
 AAGGTGGACG TCATACACCA TTCTTCAACA ACTACCGTCC ACAGTTCTAC 700
 15 TTCCGTACAA CTGACGTAAC TGGTTCAATC GAATTGCCAG CAGGTACTGA 750
 AATGGTTATG CCTGGTGATA ACGTGACTAT CGACGTTGAA TTGATCCACC 800
 CAATCGCCGT TGAACAAGGT ACTAC 825

20

2) INFORMATION FOR SEQ ID NO: 220

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 826 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus gordonii*
 (B) STRAIN: ATCC 10558

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 220

40 CGGAGCTATC CTTGTAGTAG CTTCAACTGA TGGTCCTATG CCACAAACTC 50
 GTGAGCACAT CCTTCTCTCA CGCCAAGTTG GTGTTAAACA CTTGATCGTG 100
 TTCATGAACA AAGTTGACTT GGTGACGAT GAAGAATTGC TTGAGTTGGT 150
 TGAAATGGAA ATCCGTGACC TCTTGTCAGA ATACGACTTC CCAGGTGACG 200
 ATCTTCCAGT TATCCAAGGT TCAGCTCTTA AAGCTCTTGA AGGTGACTCT 250
 AAATATGAAG ATATCATCAT GGAATTGATG AACACTGTTG ATGAGTACAT 300
 CCCAGAACCA GAACGCGACA CTGACAAACC ATTGCTTCTT CCAGTCGAAG 350
 ACGTATTCTC AATCACTGGA CGTGGTACAG TTGCTTCAGG ACGTATCGAC 400
 45 CGTGGTATCG TTAAAGTCAA TGACGAAATC GAAATCGTTG GTATCAAAGA 450
 AGAAATCCAA AAAGCAGTTG TTAGTGGTGT TGAAATGTTT CGTAAACAGC 500
 TTGACGAAGG TCTTGCAGGG GACAACGTTG GTGTGCTTCT TCGTGGTATC 550
 CAACGTGATG AAATCGAACG TGGACAAGTT ATTGCTAAAC CAGGTTCAAT 600
 CAACCCACAC ACTAAATTTA AAGGTGAAGT TTATATCCTT ACTAAGAAG 650
 50 AAGGTGGACG TCACACTCCA TTCTTCAACA ACTACCGTCC ACAGTTCTAC 700
 TTCCGTACAA CTGACGTTAC AGGTTCAATC GAACTTCCAG CAGGTACTGA 750
 AATGGTAATG CCTGGTGATA ACGTAACTAT CGACGTTGAG TTGATCCACC 800
 CAATCGCCGT TGAACAAGGT ACTACT 826

55

2) INFORMATION FOR SEQ ID NO: 221

(i) SEQUENCE CHARACTERISTICS:

60 (A) LENGTH: 799 bases

(B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus anginosus*
 (B) STRAIN: ATCC 27335

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 221

	TG	TA	GT	AG	TA	GC	T	T	C	A	A	T	G	C	C		50
	TT	CT	TT	C	A	G	T	A	G	T	A	G	G	T			100
15	GT	T	G	A	C	T	T	G	G								150
	CC	GT	G	A	T	C	T	T									200
	T	C	C	A	A	G	G	T	T	C							250
	A	T	C	A	T	C	A	T	G	G	A						300
	A	C	G	T	G	A	T	A	C	T							350
20	T	C	A	C	T	G	G	A	C	G							400
	A	A	A	G	T	C	A	A	C	G	A	T	T	C	G		450
	A	G	C	A	G	T	T	G	T								500
	T	T	G	C	T	G	G	A	G	A							550
	A	T	T	G	A	A	C	G	T	G							600
25	T	A	A	A	T	T	C	A	A								650
	A	T	A	C	T	C	A	T									700
	G	A	C	G	T	T	A	C	A	G							750
	T	G	G	T	G	A	T	A	C								799

30

2) INFORMATION FOR SEQ ID NO: 222

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus macacae*
 (B) STRAIN: ATCC 35911

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 222

	TG	GT	G	C	T	A	T										50
	GT	G	A	A	C	A	T	A	T								100
50	TT	C	A	T	G	A	A	T	A								150
	T	G	A	A	T	G	G	A									200
	A	A	C	T	T	C	A	G	T								250
	A	A	G	T	A	C	G	A	A	G							300
	C	C	C	A	G	A	A	C	C	A							350
55	A	T	G	T	T	T	C	T	C								400
	C	G	T	G	G	T	A	C	T	T							450
	C	G	A	T	A	T	C	A									500
	T	T	G	A	C	G	A	A	G								550
	C	A	A	C	G	T	G	A	T								600
60	T	C	A	T	C	C	A	C	A	T							650

AAGGTGGACG	TCATACTCCA	TTCTTTAACA	ACTACCGTCC	ACAGTTCTAC	700
TTCCGTACAA	CTGATGTAAC	TGGTTCAATT	GATTTGCCAG	CAGGTACTGA	750
AATGGTTATG	CCTGGTGATA	ATGTTACGAT	TGATGTTGAA	CTGATCCACC	800
CAATCGCTGT	TGAACAAGGT	ACAAC			825

5

2) INFORMATION FOR SEQ ID NO: 223

10 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 822 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus gordonii* (deposited as

20 *Streptococcus mitis*)

(B) STRAIN: ATCC 33399

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 223

25	CTATCCTTGT	AGTAGCTTCA	ACTGACGGAC	CAATGCCACA	AATCGTGAG	50
	CACATCCTTC	TTTCACGTCA	GGTTGGTGTT	AAACACCTTA	TCGTCTTCAT	100
	GAACAAAGTT	GACTTGGTTG	ACGACGAAGA	ATTGCTTGAA	TTGGTTGAAA	150
	TGGAAATCCG	TGACCTATTG	TCAGAATACG	ACTTCCCAGG	TGACGATCTT	200
	CCAGTTATCC	AAGGTTTCAGC	TCTTAAAGCC	CTTGAAGGTG	ACACTAAATA	250
30	CGAAGACATC	GTTATGGAAT	TGATGAACAC	AGTTGATGAG	TACATCCCAG	300
	AACCAGAACG	TGACACTGAC	AAACCATTGC	TTCTTCCAGT	CGAAGACGTA	350
	TTCTCAATCA	CTGGTCGTGG	TACAGTTGCT	TCAGGACGTA	TCGACCGTGG	400
	TATCGTTAAA	GTCAACGACG	AAATCGAAAT	CGTTGGTATC	AAAGAAGAAA	450
	CTCAAAAAGC	AGTTGTTACT	GGTGTGAAA	TGTTCCGTAA	ACAACCTGAC	500
35	GAAGGTCTTG	CCGAGATAA	TGTAGGTGTC	CTTCTTCGTG	GTGTTCAACG	550
	TGATGAAATC	GAACGTGGAC	AAGTTATTGC	TAAACCAGGT	TCAATCAACC	600
	CACACACTAA	ATTCAAAGGT	GAAGTTTACA	TCCTTACTAA	AGAAGAAGGT	650
	GGACGTCACA	CTCCATTCTT	CAACAACACT	CGTCCACAAT	TCTACTTCCG	700
	TACTACTGAC	GTTACAGGTT	CAATCGAACT	TCCAGCAGGT	ACTGAAATGG	750
40	TAATGCCTGG	TGATAACGTG	ACAATCGACG	TTGAGTTGAT	CCACCCAATC	800
	GCCGTAGAAC	AAGGTACTAC	AT			822

45 2) INFORMATION FOR SEQ ID NO: 224

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 827 bases

(B) TYPE: Nucleic acid

50 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus mutans*

(B) STRAIN: ATCC 25175

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 224

60

CCCTGGTGCT ATCCTTGTAG TAGCTTCAAC TGATGGACCA ATGCCACAAA 50
 CTCGTGAACA CATTCTTCTT TCACGTCAAG TTGGTGTTAA ATACCTCATT 100
 GTCTTCATGA ATAAAGTTGA TTTGGTTGAC GATGAAGAAT TGCTTGAATT 150
 GGTGAAATG GAAATCCGTG ATCTTCTTTC AGAATATGAT TTCCCAGGTG 200
 5 ATGATATTCC AGTTATTCAA GGTTTCAGCTC TTAAAGCTCT TGAAGGCGAT 250
 ACTGCTCAAG AAGATATCAT CATGGAATTA ATGCATACTG TTGATGACTA 300
 CATTCCAGAT CCAGAACGTG ATACTGACAA GCCGCTCCTT CTTCCAGTCG 350
 AAGATGTTTT CTCAATCACT GGTCGTGGTA CTGTTGCTTC AGGACGTATT 400
 GATCGTGGTA CTGTTAAAGT TAACGATGAA GTTGAAATCG TTGGTATCCG 450
 10 TGATGACATT CAAAAAGCTG TTGTTACTGG TGTTGAAATG TTCCGTAAAC 500
 AATTGGATGA AGGTATTGCA GGGGATAATG TTGGTGTTCT CCTTCGTGGT 550
 ATCCAACGTG ATGAAATCGA ACGTGGTCAA GTTCTTGCTA AACCAGGTTC 600
 AATTCACCCA CATACTAAAT TCAAAGGTGA AGTTTATATC CTTACTAAAG 650
 AGGAAGGTGG ACGTCATACA CCATTCTTCA ATAACATCG TCCACAATTC 700
 15 TACTTCCGTG CAACTGACGT AACTGGTTCA ATTGAGTTGC CAGCAGGTAC 750
 TGAAATGGTT ATGCCTGGTG ATAACGTTAC TATTGACGTT GAATTGATCC 800
 ATCCAATCGC TGTTGAACAA GGTACTA 827

20

2) INFORMATION FOR SEQ ID NO: 225

(i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 824 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus parasanguinis*
 (B) STRAIN: ATCC 15912

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 225

AGCTATCCTT GTAGTAGCTT CAACTGACGG ACCAATGCCA CAAACACGTG 50
 AACACATCCT TCTTTCACGT CAGGTTGGTG TTAAACACTT GATCGTCTTC 100
 ATGAACAAAG TTGACTTGGT TGATGATGAA GAATTGCTTG AATTGGTTGA 150
 40 AATGGAAATC CGTGACCTTC TTTCAGAATA CGATTTCCCA GGTGATGACC 200
 TTCCAGTTAT CCAAGGTTCA GCTCTTAAAG CTCTTGAAGG TGA CTCTAAA 250
 TATGAAGATA TCATCATGGA ATTGATGGAT ACTGTTGATG AGTACATCCC 300
 AGAACCAGAA CGCGATACTG ACAAACCATT GCTTCTTCCA GTCGAAGACG 350
 TATTCTCAAT CACTGGACGT GGTACAGTTG CTTCAGGACG TATCGACCGT 400
 45 GGTGTTGTTC GTGTCAATGA TGAAATCGAA ATCGTTGGTA TCAAAGAAGA 450
 AATCCAAAAA GCAGTTGTTA CTGGTGTGTA AATGTTCCGT AAACAACCTG 500
 ACGAAGGTCT TGCAGGGGAT AACGTTGGTG TGCTTCTTCG TGGTATCCAA 550
 CGTGATGAAA TCGAACGTGG ACAAGTTATC GCTAAACCAG GTTCAATCAA 600
 CCCACACACT AAATTCAAAG GTGAAGTTTA CATCCTTACT AAAGAAGAAG 650
 50 GTGGACGTCA TACTCCATTC TTCAACAACCT ACCGTCCACA GTTCTACTTC 700
 CGTACAACCTG ACGTAACTGG ATCTATCGAA CTTCCACCAG GAACTGAAAT 750
 GGTAATGCCT GGTGATAACG TGACTATCGA CGTTGAGTTG ATCCACCCAA 800
 TCGCCGTTGA ACAAGGTACT ACAT 824

55

2) INFORMATION FOR SEQ ID NO: 226

(i) SEQUENCE CHARACTERISTICS:

60

- (A) LENGTH: 824 bases

(B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus rattii*
 (B) STRAIN: ATCC 19645

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 226

	TGGTGCTATC	CTTGTTAGTAG	CTTCAACTGA	TGGACCAATG	CCGCAAACCTC	50
	GTGAACACAT	CTTGCTTTTCA	CGTCAAGTTG	GTGTTAAATA	CCTTATCGTC	100
15	TTCATGAACA	AGGTTGACTT	GGTTGATGAT	GAAGAATTGC	TTGAATTGGT	150
	TGAAATGGAA	ATCCGTGATC	TTCTTTCAGA	ATACGATTTC	CCAGGTGATG	200
	ACATTCCAGT	TATCCAAGGT	TCAGCCCTTA	AAGCTCTTGA	AGGTGACACT	250
	GAACAAGAAG	ATGTTATCAT	GGAATTGATG	AAAACAGTTG	ATGAGTACAT	300
	CCCAGATCCA	GAACGCGATA	CTGATAAGCC	ATTGCTTCTT	CCAGTCGAAG	350
20	ACGTGTTCTC	AATCACTGGA	CGTGGTACTG	TTGCATCAGG	ACGTATCGAC	400
	CGTGGTACTG	TTAAAGTCAA	TGACGAAGTT	GAAATCGTTG	GTATCCGTGA	450
	TGACATCCAA	AAAGCTGTTG	TTACTGGTGT	TGAAATGTTC	CGTAAACAGC	500
	TTGACGAAGG	TCTTGCTGGT	GATAACGTTG	GTGTACTTCT	TCGTGGTATC	550
	CAACGTGATG	AAATCGAACG	CGGTCAAGTT	CTTGCTAAAC	CAGGTTCAAT	600
25	TCATCCGCAT	ACTAAATTTA	AAGGTGAAGT	TTACATCCTT	ACTAAAGAAG	650
	AAGGCGGACG	TCACACTCCA	TTCTTCAACA	ACTACCGTCC	ACAGTTCTAC	700
	TTCCGTACAA	CTGACGTAAC	TGGTTCAATC	GAATTGCCAG	CAGGTACTGA	750
	AATGGTTATG	CCTGGTGATA	ACGTGACTAT	CGACGTTGAA	TTGATCCACC	800
30	CAATCGCTGT	TGAACAAGGT	ACTA			824

2) INFORMATION FOR SEQ ID NO: 227

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 795 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus sanguinis*
 (B) STRAIN: ATCC 10556

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 227

	TGTTAGTAGCT	TCAACTGACG	GACCAATGCC	ACAAACTCGT	GAGCACATCT	50
50	TGCTTTCACG	TCAGGTTGGT	GTAAACACT	TGATCGTCTT	CATGAACAAA	100
	GTTGACTTGG	TTGACGATGA	AGAATTGCTT	GAATTGGTTG	AAATGGAAAT	150
	CCGTGACCTC	TTGTCAGAAT	ACGACTTCCC	AGGTGACGAT	CTTCCAGTTA	200
	TCCAAGGTTT	AGCTCTTAAA	GCTCTTGAAG	GTGACTCTAA	ATATGAAGAC	250
	ATCATCATGG	AATTGATGGA	CACTGTTGAT	GAGTACATCC	CAGAACCAGA	300
55	ACGCGATACT	GACAAGCCAT	TGCTTCTTCC	AGTCGAAGAC	GTATTCTCAA	350
	TCACTGGTCG	TGGTACAGTT	GCTTCAGGAC	GTATCGACCG	TGGTATCGTT	400
	AAAGTCAACG	ACGAAATCGA	AATCGTTGGT	ATCAAAGAAG	AAATCCAAAA	450
	AGCAGTTGTT	ACTGGTGTTG	AAATGTTCCG	TAAACAGCTT	GACGAAGGTC	500
	TTGCAGGGGA	CAACGTAGGT	GTGCTTCTCT	TGGGTATCCA	ACGTGATGAA	550
60	ATCGAACGTG	GACAAGTTAT	CGCTAAACCA	GGTTCAATCA	ACCCACACAC	600

TAAATTCAAG	GGTGAAGTTT	ATATCCTTAC	TAAAGAAGAA	GGCGGACGTC	650
ACACTCCATT	CTTCAACAAC	TACCGTCCAC	AGTTCTACTT	CCGTACAAC	700
GACGTTACAG	GTTCAATCGA	ACTTCCAGCA	GGTACTGAAA	TGGTAATGCC	750
TGGTGATAAC	GTAACAATCG	ACGTTGAGTT	GATCCACCCA	ATCGC	795

5

2) INFORMATION FOR SEQ ID NO: 228

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 795 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus sobrinus*
- (B) STRAIN: ATCC 33478

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 228

TG	TA	GT	AG	TG	AC	TG	AC	GC	GACCAATGCC	ACAAACTCGT	GAACACATCT	50
25	TG	CT	TT	T	CACG	CCAAGTTGGT	GT	TA	AGAACC	TCATCGTCTT	CATGAACAAG	100
	GT	TG	ACTT	GG	TT	GATGATGA	AGAATTGCTT	GA	ATTGGTTG	AAATGGAAAT		150
	CC	GT	GATCTT	CT	TT	CAGAAT	AC	GATTTCCC	AGGTGACGAC	ATTCTGTG		200
	TT	CA	AGGTTT	AG	CT	CTTAAG	G	CTCTGAAG	GTGATACAGC	TGCCGAAGAC		250
	AA	GATTATGG	AATTGATGGA	CATCGTTGAT	GATTACATTC	CAGAACCAAA						300
30	AC	GC	GATACT	GATAAGCCAT	TGCTTCTCCC	AGTCGAAGAC	GT	ATTCTCAA				350
	TC	ACTGGT	TCG	TGGTACTGTT	GCTTCAGGAC	GTATTGACCG	TGGTACTGTT					400
	AAGGTTA	ACG	ACGAAGTTGA	AATCGTTGGT	ATCCGTGACG	ATATCCAAA						450
	AGCAGTTGTT	ACTGGAGTTG	AAATGTTCCG	TAAGCAATTG	GACGAAGGTC							500
	TTGCTGGAGA	TAACGTTGGT	GTGCTTCTTC	GTGGTATCCA	ACGTGATGAA							550
35	ATTGAACGTG	GTCAAGTATT	GGCTGCACCT	GGTTCAATCC	ACCCACACAC							600
	TAAATTCAAG	GGTGAAGTTT	ACATCCTTTC	TAAAGATGAA	GGTGGACGTC							650
	ACACTCCATT	CTTCAACAAC	TACCGTCCAC	AGTTCTACTT	CCGTACAAC							700
	GACGTA	ACTG	GTTCAATCGA	ATTGCCAGCA	GGTACTGAAA	TGGTTATGCC						750
40	TGGTGATAAC	GTTACTATCG	ACGTTGAATT	GATCCACCCA	ATCGC							795

40

2) INFORMATION FOR SEQ ID NO: 229

45 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 797 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus suis*
- (B) STRAIN: ATCC 43765

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 229

TG	TA	GT	AG	TG	AC	TG	AC	GC	GAGCACATCC	50	
60	TT	CT	TT	T	CACG	TCAGGTTGGT	GT	TAAACACC	TTATCGTCTT	CATGAACAAA	100

```

GTTGACTTGG TTGACGATGA AGAATTGCTT GAGTTGGTTG AAATGGAAAT 150
CCGTGACCTT CTTTCAGAAAT ACGATTTCCC AGGTGATGAT CTTCCAGTTA 200
TCCAAGGTTT AGCTCTTAAA GCTCTTGAAG GTGACTCTAA GTACGAAGAC 250
ATCGTTATGG AATTGATGAA CACTGTTGAT GAGTACATTC CAGAACCAGA 300
5 ACGCGACACT GACAAACCAT TGTTGCTTCC AGTCGAGGAC GTATTCTCAA 350
TCACTGGTCG TGGTACTGTA GCTTCAGGAC GTATCGACCG TGGTACTGTT 400
CGTGTCACG ACGAAATCGA AATCGTTGGT CTTCAAGAAG AAAAATCTAA 450
AGCAGTTGTT ACTGGTGTG AAATGTTCCG TAAACAACCT GACGAAGGTC 500
TTGCCGGCGA TAACGTTGGT GTGCTTCTTC GTGGTGTACA ACGTGATGAA 550
10 ATCGAACGTG GTCAAGTTAT CTCTAAACCA GGTTCATCA ACCCACACAC 600
TAAATTCAA GGTGAAGTTT ACATCCTTAC TAAAGAAGAA GGTGGACGTC 650
ACACTCCATT CTTGACAAAC TACCGTCCAC AGTTCTACTT CCGTACAACCT 700
GACGTAACCT GTTCAATCAA ATTGCCAGAA GGTACTGAAA TGGTAATGCC 750
TGGTGATAAC GTTACTATCG ACGTTGAATT GATCCACCCA ATCGCCG 797
15

```

2) INFORMATION FOR SEQ ID NO: 230

```

20 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 793 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear
25 (ii) MOLECULE TYPE: Genomic DNA
    (vi) ORIGINAL SOURCE:
    (A) ORGANISM: Streptococcus uberis
30 (B) STRAIN: ATCC 19436

```

---(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 230

```

35 TTGTTGTTGC ATCAACTGAT GGACCAATGC CACAACTCG TGAGCACATC 50
CTTCTTTCAC GCCAAGTTGG TGTTAAACAC CTTATCGTTT TCATGAACAA 100
AATCGACCTT GTTGACGATG AAGAATTGCT TGAATTAGTT GAAATGGAAA 150
TCCGTGACCT TCTTTCAGAA TACGATTTCC CAGGTGATGA CCTACCAAGTT 200
ATCCAAGGTT CAGCTCTTAA AGCTCTTGAA GGTGATTCTA AATACGAAGA 250
CATCATCATG GAATTGATGA AAATGTTTGA TGAGTATATT CCAGAACCAG 300
40 AACGTGATAC AGACAAACCA TTACTTCTTC CAGTCGAAGA CGTATTCTCA 350
ATCACAGGTC GTGGTACTGT AGCTTCAGGA CGTATCGATC GTGGTACTGT 400
TCGTGTCAAC GACGAAATTG AAATCGTTGG TATCAAAGAA GAAACTAAAA 450
AAGCAGTTGT TACTGGTGTT GAAATGTTCC GTAAACAACCT TGACGAAGGT 500
CTTGCAGGAG ATAACGTAGG TATCCTTCTT CGTGGTGTTC AACGTGACGA 550
45 AATCGAACGT GGACAAGTTA TTGCTAAACC AGGTTCAATC AACCCACACA 600
CTAAATTCAA AGGTGAAGTT TACATCCTTT CTAAAGATGA AGGTGGACGT 650
CATACTCCAT TCTTCAACAA CTACCGTCCT CAATTCTATT TCCGTACAAC 700
TGACGTAACA GGTTCATCG AACTTCCAGC TGGTACTGAA ATGGTAATGC 750
50 CTGGTGATAA CGTGACAATC AGCGTTGAGT TGATCCACCC AAT 793

```

2) INFORMATION FOR SEQ ID NO: 231

```

55 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 798 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
60 (D) TOPOLOGY: Linear

```


(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus vestibularis*

(B) STRAIN: ATCC 49124

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 231

	TTGTAGTAGC	ATCTACTGAC	GGACCAATGC	CACAAACTCG	TGAGCACATC	50
10	CTTCTTTTAC	GTCAGGTTGG	TGTTAAACAC	CTTATCGTCT	TCATGAACAA	100
	AGTTGACTTG	GTTGACGATG	AAGAATTGCT	TGAATTGGTT	GAAATGGAAA	150
	TCCGTGACCT	TCTTTCAGAA	TACGATTTC	CAGGTGATGA	TATTCCAGTT	200
	ATCCAAGGTT	CAGCTCTTAA	AGCTCTTGAA	GGTGATTCTA	AATACGAAGA	250
	CATCATCATG	GACTTGATGA	ACACTGTTGA	CGAATACATT	CCAGAACCAG	300
15	AACGTGACAC	TGACAAACCA	TTGTTGCTTC	CAGTCGAAGA	CGTATTCTCA	350
	ATCACTGGTC	GTGGTACTGT	TGCTTCAGGA	CGTATCGACC	GTGGTGTTGT	400
	TCGTGTTAAT	GACGAAGTTG	AAATCGTTGG	TCTTAAAGAA	GAAATCCAAA	450
	AAGCAGTTGT	TACTGGTGTA	GAAATGTTCC	GTAACAACACT	TGACGAAGGT	500
	ATTGCCGGAG	ATAACGTCGG	TGTCCTTCTT	CGTGGTATCC	AACGTGATGA	550
20	AATTGAACGT	GGTCAAGTAT	TGGCTGCACC	TGGTTCAATC	AACCCACACA	600
	CTAAATTCAA	AGGTGAAGTT	TACATCCTTT	CTAAAGAAGA	AGGTGGACGT	650
	CACACTCCAT	TCTTCAACAA	CTACCGTCCA	CAGTTCTACT	TCCGTACAAC	700
	TGACGTAACA	GGTTCAATCG	AACTTCCTGC	AGGTACTGAA	ATGGTTATGC	750
25	CTGGTGATAA	CGTGACTATC	GACGTTGAGT	TGATCCACCC	AATCGCCG	798

2) INFORMATION FOR SEQ ID NO: 232

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 829 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tatumella ptyseos*

(B) STRAIN: ATCC 33301

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 232

	GGCGCTATCC	TGGTTGTTGC	TGCAACTGAC	GGCCCTATGC	CTCAGACCCG	50
45	TGAGCACATC	CTGCTGGGCC	GCCAGGTAGG	CGTTCCTTAC	ATCATCGTGT	100
	TCCTGAACAA	ATGTGACATG	GTTGATGATG	AAGAGCTGCT	GGAAGTGGTA	150
	GAAATGGAAG	TCCGTGACCT	GCTGTCACAG	TACGACTTCC	CGGGTGACGA	200
	CACGCCAATC	GTTTCGCGGT	CAGCGCTGAA	AGCACTGGAA	GGTGAAGGCG	250
	AGTGGGAAGA	GAAGATTCTG	GAGCTGGCTG	GCTTCCTGGA	TTCTTACATC	300
50	CCTGAGCCAG	AGCGTGCTAT	CGATCAGCCG	TTCCTGCTGC	CAATCGAAGA	350
	CGTATTCTCA	ATCTCCGGTC	GTGGTACAGT	TGTTACCGGT	CGTGTAAGAGC	400
	GCGGGATCAT	CAAAGTCGGT	GAAGAAGTTG	AGATCGTTGG	TATCAAAGAT	450
	ACTGCGAAAT	CAACCTGTAC	CGGTGTTGAA	ATGTTCCGTA	AACTGCTGGA	500
	CCAGGGTCAG	GCGGGTGAGA	ACGTTGGTGT	TCTGCTGCGT	GGTATCAAGC	550
55	GTGAAGAGAT	CGAACGTGGT	CAGGTTCTGG	CTAAACCAGG	TTCAATCAAA	600
	CCACACACCC	AGTTCGAGTC	AGAAGTTTAT	ATTCTGTCTA	AAGACGAAGG	650
	CGGCCGTCAT	ACTCCGTTCT	TCAAAGGCTA	CCGTCCACAG	TTCTACTTCC	700
	GTACAACCTG	CGTGACCGGA	ACCATCGAAC	TGCCGGAAGG	CGTAGAGATG	750
	GTAATGCCTG	GTGACAACAT	CAAAATGGTT	GTTACCCTGA	TCCATCCAAT	800
60	CGCGATGGAC	GATGGTCTGC	GTTTCGCAA			829

2) INFORMATION FOR SEQ ID NO: 233

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trabulsiella guamensis*
 (B) STRAIN: ATCC 49490

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 233

20	GGCGCAATCC	TGGTAGTAGC	AGCGACTGAC	GGCCCGATGC	CGCAGACTCG	50
	TGAGCACATC	CTGCTGGGTC	GTCAGGTAGG	CGTTCCGTAC	ATCATCGTGT	100
	TCCTGAACAA	ATGCGACATG	GTTGATGACG	AAGAGCTGCT	GGAAGTGGTA	150
	GAGATGGAAG	TTCGTGAACT	GCTGTCTCAG	TACGATTTCC	CGGGCGATGA	200
	CACGCCGATC	GTACGTGGTT	CTGCTCTGAA	AGCGCTGGAA	GGCGACGCAG	250
25	AGTGGGAAGC	GAAAATCATC	GAAC TGCCAG	GTTTCCTGGA	TTCTTACATT	300
	CCGGAACCAG	AGCGTGCGAT	TGACAAGCCG	TTCCTGCTGC	CGATCGAAGA	350
	CGTATTCTCC	ATCTCTGGTC	GTGGTACCGT	TGTTACCGGT	CGTGTAGAGC	400
	GCGGTATCAT	CAAAGTGGGT	GAAGAAGTAG	AAATCGTTGG	TATCAAAGAG	450
	ACTGCGAAGT	CAACCTGTAC	TGGCGTAGAA	ATGTTCCGCA	AACTGCTGGA	500
30	CGAAGGCCGT	GCTGGTGAGA	ACGTAGGTGT	TCTGCTGCGT	GGTATCAAAC	550
	GTGAAGAAAT	CGAACGTGGT	CAGGTACTGG	CTAAGCCGGG	CACCATCAAC	600
	CCGCACACCA	AGTTCGAATC	TGAAGTGATC	ATTCTGTCCA	AAGACGAAGG	650
	CGGCCGTCAC	ACTCCGTTCT	TCAAAGGCTA	CCGTCCGCAG	TTCTACTTCC	700
	GTACAACTGA	CGTGAAGTGC	ACCATCGAAC	TGCCGGAAGG	CGTAGAGATG	750
35	GTAATGCCGG	GCGACAACAT	CAAAATGGTT	GTTACCCTGA	TCCACCCGAT	800
	CGCGATGGAC	GACGGTCTGC	GTTTCGCAA			829

2) INFORMATION FOR SEQ ID NO: 234

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Veillonella parvula*
 (B) STRAIN: ATCC 10790

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 234

55	CGGCGCTATC	TTGGTTGTAT	CCGCAGCTGA	CGGCCCTATG	CCTCAAATCT	50
	GCGAACACAT	CTTGTTGGCT	CGCCAAGTTG	GTGTTCTCTG	AATCGTAGTA	100
	TTCTTGAACA	AAGTCGACAT	GGTTGACGAT	GAAGAATTGA	TCGAATTGGT	150
	AGAAATGGAA	GTTCTGTGAAC	TTCTTTCTTC	CTACGAATTC	CCTGGCGACG	200
60	AAGTACCTAT	CGTTGTAGGT	TCCGCGTTGA	AAGCTTTGGA	AGGCGATGCT	250

CAATATGTAG CTAAAATTGA CGAATTGATG GACGCTGTAG ACTCCTACAT 300
 CCCAACACCA GTTCGTGACA CTGATAAACC ATTCTTGATG CCTGTGGAAG 350
 ATGTTTTTAC AATCACTGGT CGTGGTACAG TAGCAACTGG CCGTGTGAA 400
 CGTGGTCAAG TAAACGTTGG TGATACTGTT GAAGTAGTAG GCTTGAAAGA 450
 5 AAAAGCTGAA CAATACGTAG TAACAGGTCT TGAAATGTTC CGTAAAGTGT 500
 TGGATTCTGC AGTAGCAGGT GACAACGTAG GTGCATTGCT TCGTGGTGT 550
 GATCGTAAAG ACATYGAACG TGGTCAAGTA TTGGCTAAAC CAGGTTCAT 600
 CAACCCACAY ACAAATTCA AAGCAGAAGT ATACGTATTG ACTAAAGAAG 650
 AAGGTGGTCG TCATACTCCA TTCCTCTCCA ACTACCGTCC ACAATTCTAC 700
 10 TTCCGTACAA CAGACGTAAC AGGTGTTGTA AACCTTCCTG AAGGTGTAGA 750
 AATGTGTATG CCTGGCGATA ACGTAACAAT GGAAATCGAA TTGATTACTC 800
 CAATCGCTAT CGAAGAAGGT CTTGC 825

15

2) INFORMATION FOR SEQ ID NO: 235

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Yersinia enterocolitica*
 (B) STRAIN: ATCC 9610

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 235

CGCTATCCTG GTTGGTGGCTG CAACTGATGG CCCAATGCCA CAGACTCGTG 50
 AGCACATCCT GTTGGGTCGT CAGGTGGTGG TTCCTTACAT CATCGTATTC 100
 ATGAACAAAT GTGACATGGT TGACGATGAA GAGCTGCTAG AACTGGTAGA 150
 35 AATGGAAGTG CGCGATCTTC TGTCTACCTA CGATTTCCTA GGCGATGATA 200
 CGCCAGTTGT TCGTGGTTCC GCGCTGAAAG CATTGGAAGG CGAACCTGAG 250
 TGGGAAGCAA AAATTATCGA ACTGGCTGGC TACCTGGATT CTTACATCCC 300
 AGAACCAGAG CGTGCTATCG ATAAGCCGTT CCTGCTGCCA ATCGAAGACG 350
 TATTCTCTAT CTCTGGTCGT GGTACTGTTG TAACGGGTCG TGTAAGCGC 400
 40 GGTATCGTTA AAGTTGGTGA AGAAGTCGAA ATTGTTGGCC TGAAAGATAC 450
 CGTTAAATCT ACTTGACTG GCGTTGAAAT GTTCCGCAA CTGCTGGATG 500
 AAGGCCGTGC AGGTGAGAAC GTTGGTGTTC TGCTGCGTGG TATCAAGCGT 550
 GAAGATATCG AACGTGGTCA AGTTCTTGCT AAACCAGGTT CGATTAAACC 600
 ACACACCAA TTTGAATCAG AAGTTTATAT TCTGAGCAA GATGAAGGTG 650
 45 GTCGCCATAC TCCGTTCTTC AAAGGCTACC GTCCTCAGTT CTAATTCCGT 700
 ACAACTGATG TAACCGGTAC TATTGAACTG CCAGAAGGCG TTGAGATGGT 750
 GATGCCAGGT GATAACATC AAATGATTGT TAACCTGATT GCTCCTATCG 800
 CAATGGATGA CGGCTTGCGC TTTGC 825

50

2) INFORMATION FOR SEQ ID NO: 236

(i) SEQUENCE CHARACTERISTICS:

55 (A) LENGTH: 828 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DN A

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yersinia frederiksenii*
 (B) STRAIN: ATCC 33641

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 236

5
 10
 15
 20
 25

GGCGCGATCC	TGGTTGTTGC	TGCCACTGAT	GGCCCGATGC	CACAGACTCG	50
CGAGCACATT	CTGTTAGGGC	GTCAGGTGGG	TGTTCTTAC	ATCCTGGTCT	100
TCCTGAACAA	ATGTGACATG	GTTGACGACG	AAGAGCTGCT	GGAAGTGGTA	150
GAAATGGAAG	TTCGTGAACT	TCTGTCTCAG	TACGATTTCC	CTGGCGACGA	200
CACTCCAGTT	ATCCGTGGTT	CTGCGCTGAA	AGCGCTGGAA	GGCGAAGCTG	250
AGTGGGAAGC	AAAAATCATC	GAATTGGCTG	AGGCGCTGGA	TAGCTATATT	300
CCACAGCCAG	AGCGTGCGAT	TGATAAACCA	TTCCTGCTGC	CAATCGAAGA	350
CGTATTCTCA	ATCTCTGGCC	TGGTACTGTG	TGTCACCGGT	CGTGTAGAGC	400
GCGGTATCGT	TAAAGTCGGC	GAAGAAGTCG	AAATCGTTGG	TATCATTGAT	450
ACCATCAAGA	CTACCTGTAC	TGGTGTTGAA	ATGTTCCGCA	AATTGCTGGA	500
CGAAGGCCGT	GCGGGTGAGA	ACGTTGGTGT	TCTGCTACGT	GGTACTAAAC	550
GTGATGACGT	ACAACGTGGT	CAGGTATTGG	CAAAACCAGG	TTCTATCAAG	600
CCACACACCA	AATTTGAATC	AGAAGTTTAT	ATTCTGAGCA	AAGATGAAGG	650
TGGTCGCCAT	ACTCCGTTCT	TCAAAGGTTA	TCGTCTCAG	TTCTACTTCC	700
GTACAACTGA	CGTGACCGGT	ACTATCGAAC	TGCCAGAAGG	CGTTGAGATG	750
GTGATGCCAG	GTGATAACAT	TCAAATGATT	GTAAACCTGA	TTGCTCCTAT	800
CGCAATGGAT	GACGGTCTGC	GCTTTGCG			828

2) INFORMATION FOR SEQ ID NO: 237

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 813 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yersinia intermedia*
 (B) STRAIN: ATCC 29909

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 237

45
 50
 55
 60

CTTGGTTGTC	GCTGCAACTG	ATGGTCCTAT	GCCACAGACT	CGCGAGCACA	50
TCCTGCTAGG	TCGTCAGGTG	GGTGTTCCTT	ACATCCTGGT	CTTCCTGAAC	100
AAGTGTGACA	TGGTTGACGA	TGAGGAGTTG	CTGGAATTGG	TAGAAATGGA	150
AGTCCGCGAA	CTTCTGTCTC	AATATGATTT	CCCTGGCGAT	GATACTCCTG	200
TTATCCGTGG	TTCAGCGCTG	AAGGCGTTGG	AAGGCGAGCC	TGAATGGGAA	250
GCAAAAATTA	TCGAATTAGC	TGAGGCGCTG	GATAGTTATA	TTCCACAGCC	300
AGAGCGCGCG	ATTGATAGAC	CATTCTTGCT	GCCAATCGAA	GACGTATTCT	350
CTATCTCAGG	TCGTGGTACA	GTCGTCACCTG	GTCGTGTAGA	GCGTGCGATC	400
GTTAAAGTTG	GCGAAGAAGT	TGAAATCGTT	GGTATTATCG	ATTCCATTAG	450
AACAACATGT	ACTGGCGTTG	AAATGTTCCG	CAAATTGCTG	GACGAAGGCC	500
GCGCGGGTGA	GAACGTTGGT	GTTCTACTGC	GTGGGACTAA	ACGTGATGAC	550
GTACAGCGTG	GTCAGGTATT	AGCTAAGCCA	GGTTCATCA	AGCCACATAC	600
TAAATTCGAA	TCCGAAGTTT	ATATTCTGAG	CAAAGATGAA	GGCGGGCGTC	650
ACACGCCGTT	CTTCAAAGGC	TACCGTCCTC	AGTTCTACTT	CCGTACAACG	700
GATGTAACCG	GTACTATTGA	ATTGCCAGAC	GGCGTTGAGA	TGGTGATGCC	750
AGGTGATAAC	ATTCAAATGA	TTGTTAACCT	GATTGCACCT	ATTGCGATGG	800
ATGATGGTCT	GCG				813

2) INFORMATION FOR SEQ ID NO: 238

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yersinia pestis*
 (B) STRAIN: KIM D27

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 238

```

20  GGAGCGATCT TGGTTGTTGC TGCAACCGAT GGCCCTATGC CGCAGACTCG      50
    TGAGCATATC CTGCTGGGCC GCCAGGTTGG TGTCCCATAC ATTATTGTCT      100
    TCCTGAACAA ATGTGACATG GTTGACGATG AAGAGTTGCT AGAGTTGGTT      150
    GAAATGGAGG TTCGTGAGCT TCTGTCTCAA TACGATTTCC CAGGCGACGA      200
    CACTCCAGTC ATCCGTGGTT CAGCGTTGAA AGCCCTGGAA GGTGACGCTG      250
25  AGTGGGAAGC TAAAATTATC GAGTTGGCAG AAGCTCTGGA TAGCTATATT      300
    CCGCAACCAG AACGCGCTAT TGATAGACCA TTCCTATTGC CAATTGAAGA      350
    CGTATTCTCT ATTTCTGGTC GTGGTACTGT AGTTACTGGT CGTGTAGAAC      400
    GTGGTATTGT TAAGGTCGGC GAAGAAGTTG AAATCGTTGG TATTATCGAT      450
    ACGATTAAAA CAACTTGATC TGGCGTTGAA ATGTTCCGCA AGCTGCTGGA      500
30  TGAAGGCCGT GCTGGTGAAA ATGTTGGTGT TCTGCTGCGT GGTACTAAGC      550
    GTGACGATGT TCAGCGTGGT CAAGTACTGG CGAAACCAGG TTCTATCAAG      600
    CCACACACGA AGTTTGAGTC AGAAGTTTAT ATTCTGAGCA AAGATGAAGG      650
    CGGCCGTCAT ACACCGTTCT TCAAGGGCTA CCGTCCTCAG TTCTACTTCC      700
    GTACAACTGA CGTGACCGGT ACCATTGAGC TGCCAGAAGG CGTTGAAATG      750
35  GTCATGCCTG GTGACAACGT AAACATGGTT GTTAACCTAA TTGCTCCTAT      800
    CGCAATGGAT GATGGTCTGC GCTTCGCAA                                829

```

40 2) INFORMATION FOR SEQ ID NO: 239

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yersinia pseudotuberculosis*
 (B) STRAIN: ATCC 29833

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 239

```

55  TGGAGCGATC TTGGTTGTTG CTGCAACCGA TGGCCCTATG CCGCAGACTC      50
    GTGAGCATAT CCTGCTGGGC CGCCAGGTTG GTGTCCCATA CATTATTGTC      100
    TTCCTGAACA AATGTGACAT GGTGACGAT GAAGAGTTGC TAGAGTTGGT      150
    TGAAATGGAG GTTCGTGAGC TTCTGTCTCA ATACGATTC CCAGGCGACG      200
60  ACACTCCAGT CATCCGTGGT TCAGCGTTGA AAGCCCTGGA AGGTGACGCT      250

```

	GAGTGGGAAG	CTAAAATTAT	CGAGTTGGCA	GAAGCTCTGG	ATAGCTATAT	300
	TCCGCAACCA	GAACGCGCTA	TTGATAGACC	ATTCCCTATTG	CCAATTGAAG	350
	ACGTATTCTC	TATTTCTGGT	CGTGGTACTG	TAGTTACTGG	TCGTGTAGAA	400
	CGCGGTATTG	TTAAGGTCGG	CGAAGAAGTT	GAAATCGTTG	GTATTATCGA	450
5	TACGATTAAA	ACAACCTTGT	CTGGCGTTGA	AATGTTCCGC	AAGCTGCTGG	500
	ATGAAGGCCG	TGCTGGTGAA	AATGTTGGTG	TTCTGCTGCG	TGGTACTAAG	550
	CGTGACGATG	TTCAGCGTGG	TCAAGTACTG	GCGAAACCAG	GTTCTATCAA	600
	GCCACACACG	AAGTTTGTAGT	CAGAAGTTTA	TATTCTGAGC	AAAGATGAAG	650
	GCGGCCGTCA	TACACCGTTC	TTCAAGGGCT	ACCGTCCTCA	GTTCTACTTC	700
10	CGTACAACCTG	ACGTGACCGG	TACCATTGAG	CTGCCAGAAG	GCGTTGAAAT	750
	GGTCATGCCT	GGTGACAACG	TAAACATGGT	TGTTAACCTA	ATTGCTCCTA	800
	TCGCAATGGA	TGATGGT				817

15

2) INFORMATION FOR SEQ ID NO: 240

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 829 bases
20	(B)	TYPE: Nucleic acid
	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

(A)	ORGANISM: <i>Yersinia rohdei</i>
(B)	STRAIN: ATCC 43380

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 240

	TGGCGCGATC	CTGGTTGTTG	CTGCAACTGA	TGGCCCAATG	CCACAGACTC	50
	GCGAGCACAT	CCTGTTGGGT	CGTCAAGTGG	GTGTTCTCTA	CATCTTAGTC	100
	TTCCTGAACA	AGTGTGACAT	GGTTGACGAC	GAAGAGTTGC	TGGAAGTGGT	150
35	TGAAATGGAA	GTTCGTGAGC	TTCTGTCTCA	ATACGATTTC	CCTGGCGATG	200
	AACTCCGGT	TATTCGTGGT	TCCGCGCTGA	AAGCGCTGGA	AGGCGAGGCC	250
	GAGTGGGAAG	CCAAAATTAT	TGAACCTGCT	GAAGCACTGG	ATAGCTACAT	300
	TCCACAGCCA	GAGCGCGCGA	TTGATAAACC	ATTCTTGCTG	CCAATCGAAG	350
	ACGTATTCTC	TATCTCAGGC	CGTGGAACAG	TTGTTACCGG	GCGTGTGAG	400
40	CGCGGTATCG	TCAGAGTGGG	CGAAGAAGTT	GAAATCGTGG	GTATCATCGA	450
	CACCATTAAA	ACCACTTGTA	CCGGTGTGTA	AATGTTCCGC	AAACTGCTGG	500
	ACGAAGGCCG	TGCCGGTGAG	AACGTTGGTG	TTCTGCTGCG	CGGTACTAAA	550
	CGCGATGACG	TGCAACGTGG	TCAAGTGTTG	GCTAAACCAG	GTTCTATTAA	600
	GCCGCATACC	AAATTTGAGT	CAGAAGTTTA	TATTCTGAGC	AAAGATGAAG	650
45	GTGGTCGTCA	TACTCCGTTT	TTCAAAGGTT	ACCGTCCACA	GTTCTACTTC	700
	CGTACAACCTG	ACGTGACCGG	TACCATCGAA	CTGCCAGACG	GTGTTGAGAT	750
	GGTGATGCCA	GGTGATAACA	TTCAAATGAT	TGTTAACCTG	ATTGCGCCTA	800
	TTGCAATGGA	TGACGGTCTA	CGATTGCA			829

50

2) INFORMATION FOR SEQ ID NO: 241

(i) SEQUENCE CHARACTERISTICS:

55	(A)	LENGTH: 804 bases
	(B)	TYPE: Nucleic acid
	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yokenella regensburgei*
 (B) STRAIN: ATCC 35313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 241

5
 10
 15
 20
 25

TGGCGCGATC	CTGGTTGTTG	CTGCGACTGA	CGGCCCGATG	CCGCAGACTC	50
GTGAGCACAT	CCTGCTGGGT	CGTCAGGTAG	GCGTTCCGTA	CATCATCGTG	100
TTCTTGAACA	AATGCGACAT	GGTTGATGAC	GAAGAGCTGC	TGGAAGTGGT	150
AGAAATGGAA	GTTCGTGAAC	TTCTGTCTCA	GTACGATTTC	CCGGGCGACG	200
ACACTCCGAT	CATCCGTGGT	TCTGCTCTGA	AAGCGCTGGA	AGGCGAAGCA	250
GAGTGGGAAG	CTAAAATCGT	TGAGCTGGCT	GGCTTCCTGG	ATTCTTACAT	300
CCCAGAACCA	GTTCGTGCTA	TCGACCTGCC	GTTCTTGCTG	CCGATCGAAG	350
ACGTATTCTC	CATCTCCGGT	CGTGGCACC	TTGTTACCGG	TCGTGTAGAG	400
CGCGGTATCG	TTAAAGTTGG	CGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	450
GACTGCTAAG	TCTACCTGTA	CCGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
ACGAAGGCCG	TGCTGGTGAG	AACGTTGGTG	TTCTGCTGCG	TGGTATCAA	550
CGTGAAGAAA	TCGAACGTGG	TCAGGTACTG	GCTAAGCCGG	GTTCCATCAA	600
GCCGCACACC	AAATTGGAAT	CTGAAGTTTA	TATCCTGTCC	AAAGACGAAG	650
GCGGCCGTCA	TACTCCGTTT	TTCAAAGGCT	ACCGTCCGCA	GTTCTACTTC	700
CGTACAACCT	ACGTGACTGG	TACCATCGAA	CTGCCGGAAG	GCGTAGAGAT	750
GGTAATGCCG	GGCGACAACA	TCAAATGGT	TGTTACCCTG	ATCCACCCGA	800
TCGC					804

2) INFORMATION FOR SEQ ID NO: 242

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 849 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Achromobacter xylosoxidans* subsp. *denitrificans*
 (B) STRAIN: ATCC 15173

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 242

45
 50
 55
 60

TCAGTTCCCC	CGCGATCACA	TGCCCAAGAT	CTACGAAGCG	CTTACTCTGG	50
CCGACGAGGG	TTCTCTCGTT	GCCGAAAAGG	GTCTGACGCT	GGAAGTGCAG	100
CAACAGCTGG	GCGACGGCGT	GGTGCGTACC	ATCGCGCTGG	GCTCCAGCGA	150
CGGCCGTGCG	CGCGGTATGA	AGGTCACCGG	TACGGGCGCG	CCGATCTCGG	200
TGCCGGTCGG	CACCGGCACG	CTGGGCCGCA	TCATGGACGT	GCTGGGTCGT	250
CCCATCGACG	AAGCCGGCCC	GATCCAGCAC	GAAGAAAAGC	GTGGCATTCA	300
CCAGCCGGCT	CCCCGTTTCG	ACGAAGTGTG	GCCGTCGGTG	GAAGTCTGG	350
AAACCGGCAT	CAAGGTTATT	GACCTGGTCT	GCCCGTTTCG	CAAGGGCGGC	400
AAGGTCGGCC	TGTTTCGGCG	CGCCGGCGTG	GGCAAGACCG	TCAACATGAT	450
GGAACATGAT	AACAACATCG	CCAAGCAGCA	CAGCGGCTTG	TCGGTGTTTCG	500
CCGGCGTGGG	CGAGCGTACC	CGCGAAGGCA	ACGACTTCTA	CCACGAAATG	550
GAAGAGTCGA	ACGTTCTGGA	CAAGGTTGCG	ATGGTGTTTCG	GTCAGATGAA	600
CGAACCCCGG	GGCAACCGTC	TGCGCGTGGC	GCTGACCGGC	CTGACCATGG	650
CCGAGAAGTT	CCGCGACGAA	GGCCGCGACA	TCCTGTTCTT	CGTGGAACAAC	700
ATCTACCGCT	ACACCCTGGC	CGGTACGGAA	GTGTCCGCGC	TGCTGGGCCG	750
TATGCCGTCG	GCAGTGGGCT	ACCAGCCAC	GCTGGCCGAA	GAAATGGGCA	800

AGCTGCAAGA GCGCATCACC TCGACCAAGA CCGGCTCGAT CACCTCGAT

849

5 2) INFORMATION FOR SEQ ID NO: 243

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 787 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Acinetobacter baumannii*
 (B) STRAIN: ATCC 19606

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 243

20 TGAAACTACT TTAGAAGTTC AGCAACAAC TGGTGATGGT GTTGTTTCGTA 50
 CCATCGCAAT GGGTTCTACA GAAGGTCTTA AACGTGGTCT TACTGTAACT 100
 AGCACAAACG CACCGATCTC TGTTCCAGTT GGTACAGCCA CTCTTGGCCG 150
 TATCATGGAC GTTTTAGGTC GTCTATCGA TGAAGCAGGT CCTGTTGCGA 200
 25 CTGAAGAACG TTTGCCGATT CACCGTCAAG CGCCTTCTTA TGCTGAACAA 250
 GCAGCTTCTA CTGACCTTTT AGAAACTGGT ATTAAAGTCA TCGACTTACT 300
 TTGCCCCGTTT GCGAAAGGTG GTAAAGTTGG TTTATTTCGGT GGTGCTGGTG 350
 TTGGTAAAC CGTTAACATG ATGGAATTGA TCAACAACAT CGCGAAAGCA 400
 CACTCAGGTT TATCTGTGTT TGCTGGTGTT GGTGAGCGTA CTCGTGAAGG 450
 30 TAATGACTTC TATCACGAAA TGAAAGATTC TAACGTTCTT GACAAAGTAG 500
 CAATGGTCTA CGGTCAGATG AACGAGCCAC CAGGTAACCG TTTACGCGTA 550
 GCGTTAACTG GTTTGACTAT GGCTGAATAC TTCCGTGATG AAAAAAGACGA 600
 AAACGGTAAA GGTCGTGACG TATTATTATT CGTCGACAAC ATCTACCGTT 650
 ATACACTTGC AGGTACTGAA GTATCAGCAT TGTTAGGTCG TATGCCATCT 700
 35 GCGGTAGGTT ACCAACCTAC ACTTGCAGAA GAAATGGGTG TTCTTCAAGA 750
 GCGTATTACA TCTACTAAAT CTGGTTCGAT CACTTCG 787

40 2) INFORMATION FOR SEQ ID NO: 244

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Acinetobacter lwoffii*
 (B) STRAIN: CDCF 3697

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 244

55 GTTCCTAAGA TCTATGACGC TCTCCACGTT GATGGCACTG AAACCTACATT 50
 AGAAGTTCAG CAACAACCTG GTGATGGCGT AGTTCGTACT ATTGCAATGG 100
 GTTCTACTGA AGGCCTTAAG CGTGGTTTGA ACGTAACTAA CACTAACGCG 150
 CCGATTCTG TACCAGTAGG TACAGCGACT CTAGGTCGTA TCATGGACGT 200
 60 TCTTGGTCGC CCAATCGACG AAGCTGGTCC AGTTGCGACT GAAGCGCGTT 250

	TGCCGATTCA	CCGTCAAGCA	CCTTCTTATG	CTGAACAAGC	AGCTTCTACT	300
	GACCTTTTATG	AAACTGGTAT	TAAAGTCATC	GACTTACTTT	GCCCGTTCGC	350
	TAAAGGTGGT	AAAGTTGGTC	TGTTCCGGTGG	TGCCGGTGTT	GGTAAACTG	400
	TAAACATGAT	GGAGTTGATC	AACAACATCG	CTAAAGCGCA	CTCAGGTTTA	450
5	TCTGTATTTCG	CTGGTGTTGG	TGAGCGTACT	CGTGAAGGTA	ATGACTTCTA	500
	TCACGAGATG	AAAGACTCAA	ACGTTCTAGA	CAAAGTAGCA	ATGGTCTACG	550
	GTCAGATGAA	CGAGCCACCG	GGTAACCGTT	TACGCGTAGC	GTTGACTGGT	600
	TTGACCATGG	CTGAGTACTT	CCGTGACGAG	AAAGACGAAA	ACGGCAAAGG	650
	CCGTGACGTA	CTATTGTTTCG	TAGATAACAT	CTACCGTTAT	ACACTAGCAG	700
10	GTACTGAAGT	ATCAGCACTT	CTAGGTCGTA	TGCCGTCTGC	AGTAGGTTAC	750
	CAACCGACAC	TTGCAGAAGA	GATGGGTGTT	CTTCAAGAAC	GTATTACATC	800
	GACTAAGTCT	GGTTCGATTA	CGTCA			825

15

2) INFORMATION FOR SEQ ID NO: 245

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 837 bases
20	(B)	TYPE: Nucleic acid
	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

(A)	ORGANISM: <i>Staphylococcus saprophyticus</i>
(B)	STRAIN: CSG-197

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 245

	CAATGAAGTT	CCAGAAATTA	ACAATGCCTT	AGTCGTAGAC	GTTGAAAGAG	50
	ATGAAGGTAC	AGTATCTCTT	ACATTAGAAG	TGGCATTACA	ACTTGGCGAT	100
	GATGTCGTAC	GTACAATTGC	AATGGATTCT	ACTGATGGTG	TTAAACGTGG	150
35	TACAGAAGTT	CGAGATAGCG	GAGATAGCAT	CAGTGTTCCA	GTTGGTGATG	200
	CTACGTTAGG	ACGTGTGTTT	AATGTTCTTG	GTGATACAAT	TGACTTAGAC	250
	GAGAAGCTTG	ATACTTCTGT	CAAACGTGAT	CCAATTCATA	GAGAAGCACC	300
	TGCATTTCGAT	CAATTATCAA	CAAAAGTTGA	AATCTTAGAA	ACAGGTATTA	350
	AAGTAATTGA	TTACTTTGCA	CCATATATTA	AAGGTGGTAA	AATCGGTTTA	400
40	TTCGGTGGCG	CTGGTGTAGG	TAAACAGTA	TTAATTCAAG	AATTAATTAA	450
	TAATATAGCT	CAAGAACATG	GTGGTATTTC	AGTATTTGCC	GGCGTAGGTG	500
	AACGTACGCG	TGAAGGTAAT	GACTTATACT	ACGAAATGAG	TGATAGTGGT	550
	GTTATTAAGA	AAACAGCTAT	GGTCTTCGGA	CAAATGAATG	AGCCACCTGG	600
	TGCGCGTATG	CGTGTTGCTT	TATCAGGCTT	AACAATGGCT	GAACACTTCC	650
45	GTGATGTACA	AGGACAAGAT	GTTTTACTAT	TTATTGATAA	CATATTCAGA	700
	TTTACGCAAG	CTGGTTCAGA	AGTATCAGCA	CTATTAGGTC	GTATGCCATC	750
	AGCCGTTGGT	TATCAACCTA	CCCTTGCTAC	TGAAATGGGT	CAATTACAAG	800
	AACGTATTAC	ATCAACAAC	AAAGGATCTG	TAACGTC		837

50

2) INFORMATION FOR SEQ ID NO: 246

(i) SEQUENCE CHARACTERISTICS:

55	(A)	LENGTH: 851 bases
	(B)	TYPE: Nucleic acid
	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

350

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Alcaligenes faecalis*

(B) STRAIN: ATCC 15554

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 246

5
10
15
20
25

TTCCCCCGCG	ACAGCATCCC	TAAAGTCTAC	GAAGCATTGA	CGCTCGTTGA	50
CGAAAGTTTCG	GCTTTCGCAG	AAAAAGGCCT	GACTTTTGAA	GTACAGCAAC	100
AATTGGGTGA	CGGTGTAGTT	CGCACCATCG	CCATGGGTTC	CAGCGACGGC	150
CTGCGCCGCG	GTATGGAAGT	GGCCGGTTTCG	GGCGCTCCCA	TCTCCGTTCC	200
CGTGGGTGTC	GGCACCCCTGG	GTCGCATTAT	GGACGTTCTG	GGTCGCCCTA	250
TTGACGAAGT	CGGTCCTATT	CAGTCCGACG	AGCGTCGCGC	CATTCAACCAG	300
CCTGCGCCTA	CTTTCGACGA	ACTGTCGCCT	TCCGTAGAGC	TGCTGGAAAC	350
CGGTATTAAA	GTGATTGACC	TGGTTTGCCC	GTTTCGCCAAG	GGTGGTAAGG	400
TTGGTCTGTT	CGGTGGTGCC	GGTGTGGGCA	AGACCGTGAA	CATGCTGGAG	450
CTGATCAACA	ACATCGCCAA	GGCACACAGC	GGTCTGTCCG	TGTTTGCCCG	500
TGTGGGTGAG	CGTACCCGTG	AAGGTAACGA	CTTCTACCAC	GAAATGGCCG	550
ATGCTGGCGT	TATCCAGATG	GACAACCTGA	GCGAGTCCAA	AGTGGCCATG	600
GTGTTTCGGTC	AGATGAACGA	ACCTCCAGGC	AACCGTCTGC	GTGTGGCACT	650
GTCCGGCCTG	ACCATGGCCG	AGAAGTTCCG	TGACGAAGGC	CGTGACATCC	700
TGTTCTTTGT	GGACAACATC	TACCGCTACA	CGCTGGCCCG	TACAGAAGTG	750
TCCGCTCTGC	TGGGTCGTAT	GCCTTCCGCA	GTGGGTTACC	AGCCTACGCT	800
GGCCGAGGAA	ATGGGTAAGC	TGCAAGAGCG	CATTACCTCC	ACCAAGACCG	850
G					851

2) INFORMATION FOR SEQ ID NO: 247

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 846 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bacillus anthracis*

(B) STRAIN: 4229

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 247

45
50
55
60

GATGGCGGAA	AGCTACCAGA	AATCTACAAC	GCCCTTACGG	TAAAACAGAG	50
CAACGAAAAC	GGAACAAGCA	TTAACTTAAC	ATTTGAAGTT	GCACTTCATT	100
TAGGTGATGA	CACAGTTCGT	ACAGTTGCAA	TGCTTTCCAC	AGATGGACTT	150
GTTTCGTGGCA	CAGAAGTAGA	AGATACTGGT	AAAGCAATCT	CTGTACCAGT	200
TGGTGATGCA	ACACTTGGTC	GTGTATTTAA	CGTATTAGGT	GATGCAATTG	250
ACTTAGATGG	TGAGGTTCCCT	GCGGATGTAC	GTCGTGATCC	AATTCACCGT	300
CAAGCACCTG	CATTCGAAGA	ATTATCTACT	AAAGTAGAAA	TTCTTGAAAC	350
TGGTATTAAA	GTAAGTACT	TACTTGCTCC	TTACATTAAG	GGTGGTAAGA	400
TCGGTCTATT	CGGTGGTGCC	GGTGTAGGTA	AAACGGTATT	AATTCAGGAA	450
TTAATCAATA	ACATCGCACA	AGAACACGGT	GGTATCTCTG	TATTCGCTGG	500
TGTAGGTGAG	CGTACTCGTG	AGGGTAATGA	CTTATACCAC	GAAATGAGCG	550
ATTCTGGCGT	AATTAAGAAA	ACTGCGATGG	TATTCGGACA	AATGAACGAG	600
CCACCTGGAG	CACGTCAACG	TGTTGCGTTA	ACAGGTTTAA	CAATGGCTGA	650
GCATTTCCGT	GATGAGCAAG	GACAAGATGT	ACTTCTGTTC	ATCGATAATA	700
TCTTCCGTTT	CACGCAAGCA	GGTTCTGAAG	TATCTGCCCT	TCTTGGCCGT	750
ATGCCATCTG	CGGTAGGTTA	CCAACCAACA	CTTGCAACAG	AAATGGGTCA	800

ATTACAAGAG CGTATTACAT CTACAAATAA AGGGTCTATC ACGTCT

846

5 2) INFORMATION FOR SEQ ID NO: 248

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 810 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus cereus*
 (B) STRAIN: ATCC 14579

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 248

20 CCAGAAATCT ACAATGCCCT TACGGTAAAA CAAAGCAACG AAAACGGAAG 50
 CATGAACTTA ACATTTGAAG TTGCACTTCA TTTAGGTGAT GATACAGTTC 100
 GTACAGTTGC GATGTCTTCC ACAGATGGAC TTGTTCTGTTG CACAGAAGTA 150
 GAAGATACTG GTAAAGCAAT CTCTGTACCA GTTGGTGATG CAACACTTGG 200
 25 ACGTGTATTC AACGTATTAG GTGATGCAAT TGAAGTAGAT GGTGAACTTC 250
 CTGCGGATGT ACACCGTGAT CCAATTCACC GTCAAGCACC TGCATTCGAA 300
 GAATTATCTA CTAAAGTAGA AATTCCTGAA ACTGGTATTA AAGTAGTAGA 350
 CTTACTTGCT CCTTACATTA AGGGTGGTAA GATCGGCCTA TTCGGTGGTG 400
 CCGGCGTAGG TAAAACAGTA TTAATTCAGG AGTTAATCAA TAACATCGCA 450
 30 CAAGAGCACG GTGGTATCTC TGTATTCGCT GGTGTAGGTG AGCGTACTCG 500
 TGAGGGTAAT GACTTATACC ACGAAATGAG CGATTCTGGC GTAATCAAGA 550
 AAAGTGCAT GGTATTCGGA CAAATGAACG AGCCACCTGG AGCACGTCAA 600
 CGTGTTCAT TAACAGGTTT AACAAATGGCT GAGCATTTCC GTGATGAGCA 650
 AGGACAAGAC GTACTTCTGT TCATCGATAA CATCTTCCGT TTCACGCAAG 700
 35 CGGGTTCTGA AGTATCTGCC CTTCTTGGTC GTATGCCATC TGCGGTAGGT 750
 TACCAACCAA CACTTGCAAC AGAAATGGGT CAATTACAAG AGCGTATTAC 800
 ATCTACAAAT 810

40 2) INFORMATION FOR SEQ ID NO: 249

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 944 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacteroides distasonis*
 (B) STRAIN: ATCC 8503

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 249

CTTTGATTAT GGGACAGAAG AAACAGTAAC CCTCCCCCGT ATCCACGACG 50
 CCATGGAGAT TTCCCGCCCA AACGGAAAGA TCTTGATCGT CGAAGTTCAG 100
 CAACACATCG GGGAAAACAC CGTCCGTACC GTAGCGATGG ATACGACCGA 150
 60 CGGATTGAGA CGAGGCATGG AGGCCGTGTC ATACGGAATG CCCATCACCA 200

	TGCCGACCGG	CGACCAAGTC	AAAGGACGTT	TAATGAATGT	CACCGGCGAC	250
	CCTATCGATG	GCATGGCCCA	GCTTACTAAA	GACGGGGCTC	TTCCCATCCA	300
	TCGTGAGCCT	CCTAAATTCT	AGGATCTGAC	AACGACCCAA	GAGGTCTTGT	350
	ACACGGGTAT	TAAAGTAATC	GATTTATTGG	AACCTTACGC	CAAAGGAGGC	400
5	AAGATCGGAC	TTTTCGGAGG	AGCCGGAGTC	GGCAAAACGG	TATTGATCAT	450
	GGAATTGATC	AACAACATCG	CAAAGAAAAA	CAACGGATTTC	TCCGTCTTCG	500
	CCGGTGTGGG	TGAACGTACA	CGTGAAGGAA	ATGACCTATT	GCGTGAAATG	550
	ATCCAATCCG	GTGTCATCCG	ATACGGCGAG	GAGTTTAAGA	AGAGTATGGA	600
	GGCAGGCAAC	TGGGACTTGT	CGAAGATCGA	TTACGATGAA	TTGGCTAAGT	650
10	CGCAGGTAC	CTTGGTATTC	GGGCAGATGA	ACGAACCGCC	GGGCGCCCGC	700
	TCGTCCGTGG	CCTTATCCGG	TTTGACGATC	GCCGAATCCT	TCCGTGACAA	750
	AGCCTCTGAG	GGAGAAAGAA	AAGATATATT	ATTCTTCATC	GATAATATCT	800
	TCCGTTTCAC	CCAAGCCGGT	TCCGAGGTTT	CCGCCTTGCT	GGGGCGTATG	850
	CCTTCCGCCG	TAGGTTACCA	ACCGACATTG	GCCACGGAAA	TGGGAGCTAT	900
15	GCAAGAGCGT	ATCACTTCAA	CCAAGAAGGG	CTCCATCACC	TCCG	944

2) INFORMATION FOR SEQ ID NO: 250

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 939 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacteroides ovatus*
 (B) STRAIN: ATCC 8483

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 250

35	TTGAGGGTAC	GGATGCAGAA	TTGGTGCTGC	CAAGCATCCA	CGACGCACTG	50
	GAGATAAAGA	GGCCAAACGG	CAAAATACTG	GTTGTAGAAG	TTGAGCAACA	100
	TATCGGCGAA	AATACGGTGC	GTACCGTAGC	GATGGACAGT	ACTGACGGAC	150
	TTGAGAGAGG	CATGAAAGTG	TATCCCACCG	GAGGCCCGAT	CACGATGCCG	200
	ATTGGCGAAC	AGATTAAAGG	ACGACTGATG	AACGTAGTCG	GTGATTTCGAT	250
40	CGACGGTATG	AAAGGACTCG	ACCGCAAAGG	TGCATATTCC	ATTCATCGCG	300
	ACCCCCCTAA	GTTTGAGGAT	TTGACTACTG	TGCAAGAGGT	GCTCTTCACA	350
	GGTATCAAAG	TGATCGACCT	GCTCGAACCG	TATGCCAAAG	GTGGTAAAT	400
	CGGTTTGTTT	GGCGGTGCCG	GTGTAGGAAA	GACTGTATTG	ATTCAGGAAC	450
	TTATCAATAA	TATCGCCAAG	AAACATAATG	GATTCTCTGT	ATTGCGCGGA	500
45	GTAGGTGAAC	GTACCCGTGA	AGGTAACGAC	TTGCTGCGCG	AAATGATTGA	550
	ATCCGGTGTA	ATCCGTTACG	GCGAAGCATT	CAAAGAAGGA	ATGGAGAAAG	600
	GTCACGGGGA	TCTTTTCAAA	GTGGATTATA	ACGAACGGGA	GAAATCGCAA	650
	GTGTCTCTGA	TTTTTCGGTCA	GATGAACGAG	CCTCCGGGCG	CACGTGCCTC	700
	TGTGGCATTG	TCCGGACTGA	CGGTGGCGGA	ATCTTTCCGC	GACGCAGGAA	750
50	AAGAAGGTGA	GAAACGCGAT	ATTCTGTTCT	TTATTGATAA	TATCTTCCGT	800
	TTCACGCAAG	CAGGTTTACA	AGTGTCCGCC	CTTTTGGGAC	GTATGCCCTC	850
	CGCTGTTGGT	TACCAGCCCA	CGTTGGCTAC	GGAAATGGGT	GCGATGCAGG	900
	AACGTATCAC	GTCTACCCGC	AAAGGTTCTA	TCACCTCCG		939

55

2) INFORMATION FOR SEQ ID NO: 251

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 833 bases

60

(B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Leclercia adecarboxylata*
 (B) STRAIN: ATCC 23216

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 251

	CGAATTCCCT	CAGGATGCCG	TACCGCGCGT	GTACGATGCT	CTTGAGGTTC	50
	AGAATGGTAA	TGAGAGCCTG	GTGCTGGAAG	TTCAGCAGCA	GCTCGGCGGC	100
15	GGTATTGTGC	GTACCATCGC	CATGGGTTC	TCCGACGGTC	TGCGTCGTGG	150
	TCTGGAAGTT	AAAGACCTCG	AGCACCCAAT	CGAAGTACCA	GTAGGTAAAG	200
	CAACCTGGG	CCGTATCATG	AACGTCCTGG	GTCAGCCGAT	CGACATGAAA	250
	GGCGACATCG	GCGAAGAAGA	GCGTTGGGCT	ATCCACCGTT	CAGCACCTTC	300
	CTATGAAGAG	CTGTCCAGCT	CTCAGGAAC	GCTGGAAACC	GGCATCAAAG	350
20	TTATCCACCT	GATGTGTCCG	TTCCGGAAGG	GCGGTAAAGT	TGGTCTGTTC	400
	GGCGGTGCGG	GTGTAGGTAA	AACCGTAAAC	ATGATGGAGC	TGATCCGTAA	450
	CATCGCGATC	GAGCACTCCG	GTTACTCCGT	GTTTGCAGGC	GTGGGTGAGC	500
	GTACTCGTGA	GGGTAACGAC	TTCTACCACG	AAATGACCGA	CTCCAACGTT	550
	CTGGACAAAG	TATCCCTGGT	TTACGGCCAG	ATGAACGAGC	CACCAGGAAA	600
25	CCGTCTGCGC	GTTGCGCTGA	CCGGCCTGAC	CATGGCTGAG	AAGTTCCGTG	650
	ACGAAGGTCG	TGACGTACTG	CTGTTCGTTG	ACAACATCTA	CCGTTACACC	700
	CTGGCCGGTA	CGGAAGTATC	CGCACTGCTG	GGTCGTATGC	CATCAGCAGT	750
	AGGCTACCAG	CCGACCCTGG	CGGAAGAGAT	GGGTGTTCTG	CAGGAACGTA	800
	TCACCTCTAC	CAAAACCGGT	TCTATCACCT	CCG		833

30

2) INFORMATION FOR SEQ ID NO: 252

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 819 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Stenotrophomonas maltophilia*
 (B) STRAIN: CDC F3338

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 252

	GTGTACGACG	CACTGAAGGT	GGAAAACACC	GAGATCACCC	TCGAAGTCCA	50
50	GCAGCAGCTG	GGCGACGGCG	TGGTGCGTAC	CATCGCCCTC	GGTTCCACCG	100
	ACGGCCTGAA	GCGCAACCTG	GTTGCCGTCA	ACACCGGCCG	TGGCATCTCG	150
	GTGCCGGTCG	GCGCCGGCAC	CCTGGGCGCG	ATCATGGACG	TGCTGGGCGG	200
	TCCGATCGAC	GAAGCCGGCC	CGGTCGCTGC	CAGCGACAAC	TGGGAAATCC	250
	ACCGCGCTGC	GCCGTCGTAT	GAAGACCAGT	CCCCGGCCAC	CGAGCTGCTG	300
55	GAAACCGGCA	TCAAGGTCAT	CGACCTGATG	TGCCCGTTTC	CCAAGGGCGG	350
	CAAGGTCGGC	CTGTTCTGGC	GCGCCGGCGT	CGGCAAGACC	GTCAACATGA	400
	TGGAACATGAT	CAACAACATC	GCCAAGGCGC	ACAGCGGCCT	GTCCGTGTTC	450
	GCCGGCGTGG	GTGAGCGTAC	CCGTGAGGGC	AACGACTTCT	ACCACGAGAT	500
	GAAGGACTCC	AACGTCCTGG	ACAAGGTGGC	GATGGTGTAC	GGCCAGATGA	550
60	ACGAGCCGCC	GGGCAACCGT	CTGCGCGTCG	CCCTGACCGG	CCTGACCATG	600

	GCCGAGTACT	TCCGCGATGA	GAAGGACGAA	AACGGCAAGG	GCAAGGACGT	650
	CCTGCTGTTC	GTCGACAACA	TCTACCGCTA	CACCCTGGCC	GGTACCGAAG	700
	TGTCGGCACT	GCTGGGCCGC	ATGCCGTCCG	CGGTGGGTTA	CCAGCCGACC	750
	CTGGCCGAGG	AAATGGGCGT	CCTGCAGGAG	CGCATCACCT	CGACCAAGAA	800
5	TGGTTCGATC	ACCTCGATC				819

2) INFORMATION FOR SEQ ID NO: 253

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 864 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bartonella henselae*
 (B) STRAIN: ATCC 49882

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 253

25	AGTTTGAAGG	CCCTTTGCCA	AATATTCTCA	ATGCATTAGA	AACAGATAAT	50
	TTGGGCAATC	GGCTAGTTTT	AGAAGTTGCT	CAGCATTTGG	GTGAAAATAC	100
	CGTGCGTACC	ATTGCCATGG	ATACTACCGA	TGGTCTTGTC	CGTGGTCAAA	150
	AAGTTTTTGA	TACAGGAACA	CAGATCAGTG	TTCCCGTGGG	AGAAGCAACA	200
	CTTGGTCGTA	TTATGAATGT	GATTGGAGAG	CCGGTTGATA	ATGTTGGCCC	250
30	AATTGCTACA	AGCAAAACCC	GTTCCATTCA	CCAAGAGGCT	CCTGAATATG	300
	TGGAGCAATC	AACCGCATCA	GAAATCCTTG	TGACTGGTAT	TAAAGTCGTT	350
	GATCTGTTAG	CTCCTTATTC	TAAAGGGGGG	AAGGTTGGTT	TGTTTGGAGG	400
	TGCCGGTGTT	GGTAAAACCG	TTCTCATTAT	GGAGCTTATC	AACAATATTG	450
	CAAAGGCGCA	TGGTGGCTAT	TCAGTGTTTG	CCGGTGTTGG	TGAACGTACA	500
35	CGTGAGGGAA	ATGATCTTTA	TTATGAAATG	ATCGAAAGCC	GTGTGAATGT	550
	GAATCCAAAA	GACAACAATG	GTTCAACAGA	AGGATCAAAA	TGTGCACTCG	600
	TTTATGGGCA	AATGAATGAA	CCACCAGGGG	CGCGTGCACG	TGTGGCTCTT	650
	TCAGGATTGA	CCATTGCAGA	AAGTTTCCGT	GATGAGGGAC	AAGATGTTTT	700
	GTTCTTCGTA	GATAATATT	TCCGTTTTAC	GCAAGCAGGC	GCTGAAGTGT	750
40	CAGCTCTTTT	AGGGCGTATT	CCTTCTGCTG	TAGGGTATCA	GCCAACTTTG	800
	GCAACTGATA	TGGGGGCTTT	GCAAGAGCGT	ATTACCAGTA	CAAGAACAGG	850
	CTCTATTACC	TCTG				864

2) INFORMATION FOR SEQ ID NO: 254

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 866 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bifidobacterium adolescentis*
 (B) STRAIN: ATCC 15703

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 254

TTCCCGGTGG GCCACCTGCC CGACATTAC AATGCACTTA CCGTTGAACT 50
 GKCCAACACC GGYGTCCACG AASAGGGCGA GACCACCAAG AAGATCACCC 100
 TTGMGGTTGA ACAGCATCTT GGCGATTCCA CCGTGCGTAC CGTCGCTCTG 150
 5 AAGCCGACTG ACGGCCTTGT GCGTGGCGCC ACCGTGTATG ACACCGGCGG 200
 CCCGATCTCT GTGCCGGTTG GCGATGTCAC CAAGGGCCAC GTATTGACG 250
 TGTCCGGCAA CATCCTCAAC AAGAAGGCCG ACAGAGCCGT TAAGGTTACC 300
 GAACGTTGGT CTATCCACCG TAACCCGCCG GCATTGACC AGCTGGAGTC 350
 CAAGACCCAG ATGTTGAAA CCGGTATCAA GGTCATCGAT TTGCTGACCC 400
 10 CGTATGTGCA GGGCGGCAAG ATCGGTCTGT TCGGCGGCGC AGGCGTCGGC 450
 AAGACCGTGC TGATCCAGGA AATGATTGAG CGTGTGGCTC AGAACCACGG 500
 CCGTGTGTCC GTGTTGCGAG GCGTCGGCGA GCGTACCCGT GAGGGTAACG 550
 ATCTGATCGG CGAAATGGAC GAAGCCGGCG TGCTCGAGAA GACCGCACTG 600
 GTCTTCGGCC AGATGGATGA GCAGCCGGGT ACCCGTCTGC GCGTGCCGCT 650
 15 GACCGCACTG ACCATGGCAG AGTACTTCCG TGACGTACAG AATCAGGACG 700
 TGCTGTGTT CATCGATAAC ATCTTCCGTT TCACCCAGGC TGGTTCCGAG 750
 GTGTCCACCC TGCTCGGCCG TATGCCGTCC GCAGTGGGCT ACCAGCCGAA 800
 CCTGGCCGAT GAGATGGGCG CGCTGCAGGA GCGAATCACT TCGACCCGTG 850
 GACACTCCAT CACCTC 866
 20

2) INFORMATION FOR SEQ ID NO: 255

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 842 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

35 (A) ORGANISM: *Brucella abortus*
 (B) STRAIN: S2308

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 255

40 AAGGCCAGCT GCCGCTGATC CTGAACGCGC TTGAAGTGGA CAATCAGGGC 50
 CATCGTCTGG TTCTCGAAGT TGCCCAGCAC CTCGGCGAAG ACACCGTGCG 100
 CACCATCGCC ATGGACGCGA CCGAAGGTCT CGTTCGCGGT CAGGAAGCAC 150
 GCGACACTGG CGAACCGATC ATGGTGCCGG TCGGCGTCGA AACGCTTGGC 200
 CGCATCATGA ACGTCATCGG CGAGCCGGTT GACGAAGCAG GCCCCATCAA 250
 45 GACCAAGGCA ACCCGCGCCA TCCACCAGAA CGCGCCGGAA TATATCGAAC 300
 AGTCGACCGA AGCCGAAATT CTGGTCACGG GCATCAAGGT CGTCGACCTT 350
 CTGGCGCCTT ACGCCAAGGG CGGCAAGATC GGCCTCTTCG GCGGTGCAGG 400
 CGTCGGCAAG ACCGTTCTCA TCATGGAACT CATCAACAAC GTCGCCAAGG 450
 CGCACGGCGG TTATTCCGTG TTCGCAGGCG TCGGTGAGCG TACCCGTGAG 500
 GGCAACGACC TTTACCACGA AATGATCGAG TCGGGCGTGA ACAAGCTCGG 550
 50 CGGCGGCGAA GGCTCCAAGG CAGCCCTCGT TTACGGCCAG ATGAACGAAC 600
 CCCCGGGTGC CCGCGCCCGC GTTGCCCTTT CCGGTCTGAC GGTGCTGAA 650
 AACTTCCGTG ACCAGGGCCA GGACGTTCTG TTCTTCGTGG ACAACATCTT 700
 CCGCTTCACG CAGGCAGGTT CGGAAGTGTC GGCTCTTCTC GGCCGTATTC 750
 CTTCCGCTGT GGGTTATCAG CCGACGCTGG CAACCGACAT GGGCGCCATG 800
 55 CAGGAACGCA TCACCACGAC GACCAAGGGT TCGATCACCT CG 842

2) INFORMATION FOR SEQ ID NO: 256

60

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 833 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cedecea davisae*
 (B) STRAIN: ATCC 33431

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 256

```

15  CGAGTTCCTT CAGGACGGCG TACCGCGCGT TKATGATGCG CTTGAAGTAC      50
    AAAATAACAG CGAGCAGCTG GTGCTGGAAG TTCAGCAGCA GCTCGGCGGC      100
    GGTATCGTGC GTACCATCGC TATGGGTTCT TCCGACGGTC TCGTTCGTGG      150
    TCTGGAAGTT AAAGACCTCG AGCACCCGAT CGAAGTCCCG GTAGGTAAAG      200
    CGACCCTTGG CCGTATCATG AACGTGCTGG GTCAGCCGAT CGACATGAAA      250
    GCGGATATCG GCGAAGAAGA CCGTTGGGCT ATTCACCGCG CTGCACCTTC      300
    CTATGAAGAG CTGTCCAGCT CTCAGGAAC TCTGGAACC GGCATCAAAG      350
    TAATCGACCT TATCTGTCCG TTCGCTAAGG GCGGTAAAGT AGGTCTGTTC      400
    GGTGGTGC GGCTGGGTAA AACCGTAAAC ATGATGGAGC TTATCCGTAA      450
    CATCGCGATC GAGCACTCCG GCTACTCCGT GTTTGCGGGC GTGGGTGAGC      500
    G TACTCGTGA GGGTAACGAC TTCTATCACG AAATGACCGA CTCCAACGTT      550
    CTGGACAAAG TTGCCCTGGT TTACGGCCAG ATGAACGAGC CACCGGGTAA      600
    CCGTCTGCGC GTAGCGCTGA CCGTCTGAC CATCGCGGAG AAATTCCGTG      650
    ACGAAGGTCG TGACGTTCTG CTGTTCTGTTG ATAACATCTA CCGTTACACC      700
    CTGGCCGGTA CTGAAGTATC CGCGCTGCTG GGTCTGATGC CTTCTGCGGT      750
30  AGGTTACCAG CCAACTCTGG CGGAAGAGAT GGGTGTCTT CAGGAGCGTA      800
    TTACCTCCAC CAAGACCGGT TCCATCACCT CCG                               833
  
```

35 2) INFORMATION FOR SEQ ID NO: 257

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cedecea lapagei*
 (B) STRAIN: ATCC 33432

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 257

```

50  TTCCCTCAGG ACGGCGTACC GCGCGTATAT GACGCGCTTG AGGTACAGAA      50
    TAACAGCGAG AAGCTGGTGC TGGAAGTTCA GCAGCAGCTC GCGGCGGTA      100
    TCGTACGTAC CATCGCAATG GGTCTTCCG ACGGTCTGCG TCGTGGTCTG      150
    GAAGTGAAAG ACCTCGAGCA CCCGATCGAA GTCCCGGTAG GTAAAGCGAC      200
55  TCTGGGTCTG ATCATGAACG TGCTGGGTCA GCCAATTGAT ATGAAAGGCG      250
    ACATCGGCGA AGAAGATCGT TGGGCGATTC ACCGCGCAGC ACCTTCCTAT      300
    GAAGAGCTGT CCAGCTCTCA GGAAGTGTG GAAACCGGCA TCAAAGTTAT      350
    CGACCTGATT TGTCCGTTCT CTAAGGGCGG TAAAGTTGGT CTGTTCTGGT      400
    GTGCGGGCGT AGGTAAAACC GTAAACATGA TGGAGCTGAT CCGTAACATC      450
60  GCGATCGAGC ACTCCGGTTA CTCCGTGTTT GCAGGCGTGG GTGAGCGTAC      500
  
```


	TCGTGAGGGT	AACGACTTCT	ACCACGAGAT	GACCGACTCC	AACGTTCTGG	550
	ACAAAGTTGC	ACTGGTTTAC	GGCCAGATGA	ACGAGCCGCC	AGGTAACCGT	600
	CTGCGCGTAG	CGCTGACCGG	TCTGACCATC	GCGGAGAAAT	TCCGTGACGA	650
	AGGCCGTGAC	GTTCTGCTGT	TCGTGCGATAA	CATCTATCGT	TATACCCTGG	700
5	CCGGTACAGA	AGTTTCTGCA	CTGCTGGGTC	GTATGCCATC	TGCGGTAGGT	750
	TATCAGCCTA	CTCTGGCAGA	AGAGATGGGT	GTTCTTCAGG	AGCGTATTAC	800
	CTCCACCAAG	ACCGGTTCCA	TCACTTCCG			829

10

2) INFORMATION FOR SEQ ID NO: 258

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 830 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cedecea neteri*
- (B) STRAIN: ATCC 33855

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 258

	TCCCTCAGGA	CGGCGTACCG	CGCGTTTATG	ACGCGCTTGA	GGTACAGAAC	50
	AACAATGAGA	AGCTGGTGCT	GGAAGTTCAG	CAGCAGCTCG	GCGGCGGTAT	100
	CGTGCGTACC	ATCGCAATGG	GTTCTTCCGA	CGGTCTGCGT	CGTGGTCTGG	150
30	TAGTAACAGA	CCTCGAGCAC	CCGATCGAAG	TCCCGGTAGG	TAAAGCGACC	200
	CTTGGEEGTA	TCATGAACGT	GCTGGGTCAG	CCGATCGACA	TGAAAGGCGA	250
	CATCGGCGAA	GAAGACCGTT	GGGCGATTCA	CCGCGCAGCA	CCTTCCTACG	300
	AAGAGCTGTC	CAGCTCTCAG	GAATTGCTGG	AAACCGGCAT	CAAAGTTATC	350
	GACCTGATTT	GTCCGTTTCG	TAAGGGCGGT	AAAGTAGGTC	TGTTCCGGTGG	400
35	TGCGGGCGTA	GGTAAAACCG	TAAACATGAT	GGAGCTGATC	CGTAACATTG	450
	CGATCGAGCA	CTCCGGTTAT	TCCGTGTTTG	CGGGCGTGGG	TGAGCGTACT	500
	CGTGAGGGTA	ACGACTTCTA	CCACGAAATG	ACCGACTCCA	ACGTTCTGGA	550
	TAAAGTAGCA	CTGGTTTACG	GCCAGATGAA	CGAGCCACCA	GGTAACCGTC	600
	TGCGCGTAGC	GCTGACCGGT	CTGACCATCG	CGGAAAAATT	CCGTGACGAA	650
40	GGCCGCGACG	TTTTGCTGTT	CGTTGATAAC	ATCTACCGTT	ATACCCTGGC	700
	CGGTACCGAA	GTATCTGCAC	TGCTGGGTCG	TATGCCTTCT	GCGGTAGGTT	750
	ATCAGCCAAC	TCTGGCAGAA	GAGATGGGTG	TTCTTCAGGA	GCGTATTACC	800
	TCCACCAAGA	CCGGTTCTAT	CACCTCCGTA			830

45

2) INFORMATION FOR SEQ ID NO: 259

(i) SEQUENCE CHARACTERISTICS:

50

- (A) LENGTH: 931 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Chryseobacterium meningosepticum*
- (B) STRAIN: CDC B7681

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 259

```

5   TTTCAGGAAG TAGAGGAACT ACCAAACATT TATGACGCAC TTGAAGTTGT      50
    CAGAGAAGGC CAGAAAGGTC TGATCTTAGA AGTTGAACAA CACATCGGTG      100
    AGGATACAGT GAGATGTATC GCTATGGATG CAACAGACGG ACTTCAAAGA      150
10  GGACAATCTG TAATAGGACA TGGAAGACAA ATTACTATGC CTATTGGTGA      200
    AGAAGTAAAT GGTAGATTGT TCAACGTGGT AGGAGATGCT ATCGACGGAC      250
    TTCAGGAATT ATCTAAAGAC AATGGTTTGC CAATCCACAG AGAAGCACCT      300
    AAATTTCGATC AGTTATCAAC TTCTGCTGAA GTACTATATA CAGGTATCAA      350
15  AGTAATCGAC CTTATCGAGC CTTATGCAAA AGGTGGTAAA ATTGGTTTGT      400
    TCGGTGGTGC TGGTGTAGGT AAAACAGTAT TGATCCAGGA ATTGATTAAT      450
    AACATTGCTA AAGGACACGG TGGTCTTCT GTATTTCGCAG GAGTAGGTGA      500
    GAGAACAAGA GAAGGAAATG ACCTTCTTCG TGAGATGTTA GAGTCTGGTA      550
    TTATTAAATA TGGTGACGAA TTCATGCATT CTATGGAGAA CGGTGGATGG      600
20  GATCTTTCTA AAGTTGACAG TGAGTTGATG AAAGAGTCTA AAGCTGCTTT      650
    CGTTTTTCGGA CAGATGAACG AGCCACCAGG TGCAAGAGCA CGTGTAGCCC      700
    TTTCTGGTCT TACTTTAGCT GAATACTACC GTGATGGTGG CGAAAGCGGA      750
    CAAGGTAGAG ACGTTCCTTT CTTCTAGTAG AACATCTTCC GTTTTACACA      800
    GGCTGGTTCT GAGGTGTCTG CACTTCTAGG TCGTATGCCT TCAGCGGTAG      850
25  GTTACCAACC AACTCTAGCT TCTGAGATGG GTGCAATGCA GGAGAGAATT      900
    ACTTCAACTA AAAACGGATC TATTACATCT G                               931

```

25 2) INFORMATION FOR SEQ ID NO: 260

(i) SEQUENCE CHARACTERISTICS:

```

30  (A) LENGTH: 726 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

```

    (A) ORGANISM: Citrobacter amalonaticus
    (B) STRAIN: ATCC 25405

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 260

```

40  GTATCGTACG TACCATCGCA ATGGGTTCTT CCGACGGTCT GCGTCGTGGT      50
    CTGGAAGTCA AAGACCTCGA GCACCCGATC GAAGTCCCGG TAGGTAAAGC      100
    AACCCTGGGT CGTATCATGA ACGTCCTGGG TCACCCGATC GACATGAAAG      150
    GCGATATCGG TGAAGAAGAG CGTTGGGCTA TCCACCGCGC AGCACCGTCC      200
45  TATGAAGAGC TGTCCAGCTC TCAGGAACTG CTGGAAACCG GTATCAAAGT      250
    TATCGACCTG ATGTGTCCGT TCGCGAASGG CGGTAAAGTG GGTCTGTTCTG      300
    GTGGTGCGGG TGTAGGTAAA ACCGTAAACA TGATGGAGCT TATCCGTAAC      350
    ATCGCGATCG AGCACTCCGG TTA CTCCGTG TTTGCGGGCG TAGGTGAACG      400
    TACTCGTGAG GGTAACGACT TCTACCACGA AATGACCGAC TCCAACGTTT      450
50  TGGATAAAGT ATCCCTGGTA TATGGCCAGA TGAACGAGCC GCCGGGAAAC      500
    CGTCTGCGCG TTGCACTGAC CGGTCTGACC ATGGCAGAGA AATTCCGTGA      550
    CGAAGGTCGT GACGTACTGC TGTTCTGTCG TAACATCTAT CGTTACACCC      600
    TGGCCGGTAC GGAAGTTTCC GCACTGCTGG GTCGTATGCC ATCAGCGGTA      650
    GGTACCAGC CGACCCTGGC GGAAGAGATG GGTGTTCTGC AGGAACGTAT      700
55  CACTTCTACC AAAACCGGTT CTATCA                               726

```

2) INFORMATION FOR SEQ ID NO: 261

60

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 812 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter braakii*
 (B) STRAIN: ATCC 43162

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 261

```

15  GCCGTACCGC  GCGTGTACGA  TGCTCTTGAG  GTTATGAATG  GTAAAGAGAG      50
    CCTGGTGCTG  GAAGTTCAGC  AGCAGCTCGG  CGGCGGTATC  GTACGTACCA      100
    TCGCCATGGG  TTCTTCCGAC  GGTCTGCGTC  GTGGTCTGGA  AGTTAAAGAT      150
    CTCGAGCACC  CGATCGAAGT  CCCGGTAGGT  AAAGCAACTC  TGGGTCGTAT      200
    CATGAACGTC  CTGGGTCACC  CGATCGACAT  GAAAGGCGAT  ATCGGTGAAG      250
20  AAGAGCGTTG  GGCTATCCAC  CGCGCGGCAC  CTTCCCTATGA  AGAGCTGTCC      300
    AGCTCTCAGG  AACTGCTGGA  AACC GG CATC  AAAGTTATCG  ACCTGATGTG      350
    TCCGTTGCTG  AAGGGCGGTA  AAGTTGGTCT  GTTCGGTGGT  GCGGGTGTAG      400
    GTAAAACCGT  AAACATGATG  GAGCTGATCC  GTAACATCGC  GATCGAACAC      450
    TCCGGTTACT  CCGTGTTTGC  GGGCGTGGGT  GAACGTAATC  GTGAGGGTAA      500
25  CGACTTCTAC  CACGAAATGA  CCGACTCCAA  CGTTCTGGAT  AAAGTATCCC      550
    TGGTATATGG  CCAGATGAAC  GAGCCGCCGG  GAAACCGTCT  GCGCGTTGCT      600
    CTGACCGGTC  TGACCATGGC  AGAGAAGTTC  CGTGACGAAG  GTCGTGACGT      650
    TCTGCTGTTT  GTTGATAACA  TCTATCGTTA  CACCCTGGCC  GGTACAGAAG      700
    TATCCGCTCT  GCTGGGTCGT  ATGCCATCAG  CGGTAGGCTA  CCAGCCGACC      750
30  CTGGCGGAAG  AGATGGGTGT  TCTTCAGGAA  CGTATCACCT  CTACCAAAC      800
    CGGTTCTATC  AC
  
```

35 2) INFORMATION FOR SEQ ID NO: 262

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 811 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter koseri*
 (B) STRAIN: ATCC 27156

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 262

```

50  GCGCGTGTA  GACGCCCTTG  AGGTGCAGAA  TGGTAATGAA  CATCTGGTG      50
    TGGAAGTTCA  GCAGCAGCTC  GGTGGCGGTA  TCGTACGTAC  CATCGCCATG      100
    GGTTCTTCCG  ACGGCCTGCG  TCGTGGTCTG  GATGTGAAAG  ACCTTGAGCA      150
    CCCGATCGAA  GTCCCGGTAG  GTAAAGCAAC  GCTGGGTCGT  ATCATGAACG      200
55  TACTGGGCGA  ACCAGTAGAC  ATGAAAGGCG  AGATCGGTGA  AGAAGAGCGT      250
    TGGGCTATCC  ACCGTGCGGC  ACCGTCCTAC  GAAGAGTTGT  CAAACTCTCA      300
    GGAAC TGCTG  GAAACCGGTA  TCAAAGTTAT  CGACCTGATG  TGCCCGTTCTG      350
    CGAAGGGCGG  TAAAGTGGGT  CTGTTCCGGT  GTGCGGGTGT  AGGTAAAACC      400
    GTAAACATGA  TGGAGCTGAT  CCGTAACATC  GCGATCGAAC  ACTCCGGTTA      450
60  CTCCGTGTTT  GCGGGCGTAG  GTGAACGTAC  TCGTGAGGGT  AACGACTTCT      500
  
```

5 ACCACGAAAT GACCGACTCC AACGTTATCG ACAAAGTATC CCTGGTTTAC 550
 GGCCAGATGA ACGAGCCGCC GGGAAACCGT CTGCGCGTTG CGCTGACCGG 600
 CCTGACCATG GCGGAGAAAT TCCGTGACGA AGGTCGTGAC GTTCTGCTGT 650
 TCGTCGACAA CATCTACCGT TACACCCTGG CCGGTACGGA AGTATCCGCA 700
 CTGCTGGGTC GTATGCCCTT AGCGGTAGGT TACCAGCCGA CCCTGGCGGA 750
 AGAGATGGGT GTTTTGCAGG AACGTATCAC CTCCACCAA ACCGGTTCTA 800
 TCACCTCCGT A 811

10

2) INFORMATION FOR SEQ ID NO: 263

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 816 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Citrobacter farmeri*
 (B) STRAIN: ATCC 51112

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 263

30 GATGCCGTAC CGCGCGTGTA CGATGCTCTT GAGGTTATGA ATGGTAAAGA 50
 GAGTCTGGTG CTGGAAGTTC AGCAGCAGCT CGGCGGCGGT ATCGTACGTA 100
 CCATCGCGAT GGGTTCTTCC GACGGTCTGC GTCGTGGTCT GGAAGTAAAA 150
 GACCTCGAAC ACCCGATCGA AGTCCCAGTA GGTAAAGCAA CTCTGGGTCTG 200
 TATCATGAAC GTCCTGGGTC ACCCGATCGA CATGAAAGGC GATATCGGTG 250
 AAGAAGAGCG TTGGGCTATC CACCGCGCAG CGCCATCCTA TGAAGAGCTG 300
 TCCAGCTCTC AGGAACTGCT GGAAACCGGT ATCAAAGTTA TCGACCTGAT 350
 GTGTCCGTTT GCGAAGGGCG GTAAAGTCGG TCTGTTTCGGT GGTGCGGGTG 400
 35 TAGGTAAAC CGTAAACATG ATGGAAGTCA TCCGTAACAT CGCGATCGAG 450
 CACTCCGGTT ACTCCGTGTT TGCGGGCGTA GGTGAACGTA CTCGTGAGGG 500
 TAACGACTTC TACCACGAAA TGACCGATTC CAACGTTCTG GATAAAGTAT 550
 CCCTGGTATA TGGCCAGATG AACGAGCCGC CGGGAAACCG TCTGCGCGTT 600
 GCGCTGACCG GTCTGACCAT GGCAGAGAAA TTCCGTGACG AAGGTCGTGA 650
 40 CGTACTGCTG TTCGTGCGATA ACATCTATCG TTACACCCTG GCCGGTACGG 700
 AAGTATCCGC ACTGCTGGGC CGTATGCCAT CAGCGGTAGG CTACCAGCCA 750
 ACCCTGGCGG AAGAGATGGG TGTTCCTGCAG GAACGTATCA CTTCTACCAA 800
 AACCGGTTCT ATTACC 816

45

2) INFORMATION FOR SEQ ID NO: 264

(i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 819 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Citrobacter freundii*
 (B) STRAIN: ATCC 8090

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 264

```

5  AGGATGCCGT ACCGCGCGTG TACGATGCTC TTGAGGTTAT GAATGGTAAA 50
   GAGAGCCTGG TGCTGGAAGT TCAGCAGCAG CTCGGCGGCG GTATCGTACG 100
   TACCATCGCC ATGGGTTCTT CTGACGGTCT GCGTCGTGGT CTGGAAGTTA 150
   AAGACCTCGA GCACCCGATC GAAGTCCCGG TAGGTAAAGC AACGCTGGGT 200
   CGTATCATGA ACGTTCCTGG TCACCCGATC GACATGAAAG GCGATATCGG 250
   TGAAGAAGAG CGTTGGGCTA TCCACCGTGC AGCACCTTCC TACGAAGAGC 300
   TGTCAAGCTC TCAGGAACTG CTGGAAACCG GTATCAAAGT TATCGACCTG 350
10 ATGTGTCCGT TCGCTAAGGG CGGTAAAGTT GGTCTGTTCG GTGGTGCGGG 400
   TGTAGGTAAA ACCGTAAACA TGATGGAGCT GATCCGTAAC ATCGCGATCG 450
   AACACTCCGG TTA CTCCGTG TTTGCGGGCG TAGGTGAACG TACTCGTGAG 500
   GGTAACGACT TCTACCACGA AATGACCGAC TCCAACGTTT TGGACAAAGT 550
   ATCCCTGGTA CATGGCCAGA TGAACGAGCC GCCTGGAAC CGTCTGCGTG 600
15 TTGCGCTGAC CGGTCTGACC ATGGCTGAGA AGTTCCTGTA CGAAGGTCTG 650
   GACGTTCTGC TGTTCGTTGA TAACATCTAT CGTTACACCC TGGCCGGTAC 700
   AGAAGTATCT GCACTGCTGG GTCGTATGCC ATCAGCGGTA GGCTACCAGC 750
   CGACCTGGC GGAAGAGATG GGTGTTCTGC AGGAACGTAT CACCTCCACC 800
   AAAACCGGTT CTATCACCT 819
20

```

2) INFORMATION FOR SEQ ID NO: 265

```

25 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 822 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear
30

```

```

(ii) MOLECULE TYPE: Genomic DNA

```

(vi) ORIGINAL SOURCE:

```

35 (A) ORGANISM: Citrobacter koseri
    (B) STRAIN: ATCC 27028

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 265

```

40 GATGCCGTAC CGCGCGTGTA CGACGCCCTT GAGGTGCAGA ATGGTAATGA 50
   ACATCTGGTG CTGGAAGTTC AGCAGCAGCT CCGTGCGGCT ATCGTACGTA 100
   CCATCGCCAT GGGTTCTTCC GACGGCCTGC GTCGTGGTCT GGATGTGAAA 150
   GACCTTGAGC ACCCGATCGA AGTCCCGGTA GGTAAAGCAA CGCTGGGTCTG 200
   TATCATGAAC GTACTGGGCG AACCAGTAGA CATGAAAGGC GAGATCGGTG 250
   AAGAAGAGCG TTGGGCTATC CACCGTGCGG CACCGTCCTA CGAAGAGTTG 300
45 TCAAACCTCT AGGAACTGTT GGAAACCGGT ATCAAAGTTA TCGACCTGAT 350
   GTGTCCGTTT GCGAAGGGCG GTAAAGTGGG TCTGTTCCGT GGTGCGGGTG 400
   TAGGTAAAAC CGTAAACATG ATGGAGCTGA TCCGTAACAT CGCGATCGAA 450
   CACTCCGGTT ACTCCGTGTT TCGGGGCGTA GGTGAACGTA CTCGTGAGGG 500
   TAACGACTTC TACCACGAAA TGACCGACTC CAACGTTATC GACAAAGTAT 550
50 CCTTGGTTTA CGGCCAGATG AACGAGCCGC CGGGAAACCG TCTGCGCGTT 600
   GCGCTGACCG GCCTGACCAT GCGGAGAGAA TTCCGTGACG AAGGTCGTGA 650
   CGTTCTGCTG TTCGTCGACA ACATCTACCG TTACACCCTG GCCGGTACGG 700
   AAGTATCCGC ACTGCTGGGT CGTATGCCTT CAGCGGTAGG TTACCAGCCG 750
   ACCCTGGCGG AAGAGATGGG TGTTTTGCAG GAACGTATCA CCTCCACCAA 800
55 AACCGGTTCT ATCACCTCCG TA 822

```

2) INFORMATION FOR SEQ ID NO: 266

60

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 820 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter sedlakii*
 (B) STRAIN: ATCC 51115

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 266

```

15  GATGCCGTAC CGCGCGTGTA CGACGCCCTT GAGGTACAGA ATGGTAATGA      50
    GCGTCTGGTG CTGGAAGTTC AGCAGCAGCT CGGTGGCGGT ATTGTACGTA      100
    CCATCGCCAT GGGTTCCTTC GACGGTCTGC GTCGTGGTCT GGAAGTAAAA      150
    GACCTTGAGC ACCCGATCGA AGTCCCGGTA GGTAAGCAA CGCTGGGTCG      200
    TATCATGAAC GTACTGGGCG AACCAGTAGA CATGAAAGGC GACATCGGTG      250
20  AAGAAGAGCG TTGGGCTATC CACCGTGCCG CGCCGTCCTA TGAAGAGTTG      300
    TCTAACTCTC AGGAAGTGTG GGAAACCGGC ATCAAAGTTA TCGACCTGAT      350
    GTGTCCGTTT GCGAAGGGCG GTAAAGTCGG TCTGTTCCGGT GGTGCGGGCG      400
    TAGGTAAAAC CGTAAACATG ATGGAGCTGA TCCGTAACAT CGCGATCGAG      450
    CACTCCGGTT ACTCTGTGTT TGCGGGCGTG GGTGAACGTA CTCGTGAGGG      500
25  TAACGACTTC TACCACGAAA TGACCGACTC CAACGTTATC GACAAAGTAT      550
    CCCTGGTGTA CGGCCAGATG AACGAGCCGC CTGGAAACCG TCTGCGCGTC      600
    GCACTGACCG GTCTGACCAT GGCTGAGAAG TTCCGTGACG AAGGTCGTGA      650
    CGTTCTGCTG TTCGTCGATA ACATCTATCG TTACACCCTG GCCGGTACGG      700
    AAGTATCCGC ACTGCTGGGT CGTATGCCTT CAGCGGTAGG TTATCAGCCG      750
30  ACTCTGGCGG AAGAGATGGG TGTTCTGCAG GAACGTATCA CCTCAACCAA      800
    AACCGGTTCT ATCACCTCCG
  
```

35 2) INFORMATION FOR SEQ ID NO: 267

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 806 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter werkmanii*
 (B) STRAIN: ATCC 51114

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 267

```

50  GCCGTACCGC GCGGTGACGA TGCTCTTGAG GTTATGAATG GTAAAGAGAG      50
    CCTGGTGCTG GAAGTTCAGC AGCAGCTCGG CGGCGGTATC GTACGTACCA      100
    TCGCCATGGG TTCTTCCGAC GGTCTGCGTC GTGGTCTGGA AGTTAAAGAC      150
    CTTGAGCACC CGATCGAAGT CCCGGTAGGT AAAGCAACCC TGGGTCGTAT      200
55  CATGAACGTC CTGGGTCATC CGATCGACAT GAAAGGCGAT ATCGGTGAAG      250
    AAGAGCGTTG GGCTATCCAC CGCGCAGCAC CTACCTATGA AGAACTGTCC      300
    AGTTCTCAGG AACTGCTGGA AACCGGCATC AAAGTTATCG ACCTGATGTG      350
    TCCGTTCCGG AAGGGCGGTA AAGTTGGTCT GTTCGGTGGT GCGGGTGTAG      400
    GTAAAACCGT AAACATGATG GAGCTGATCC GTAACATCGC GATCGAACAC      450
60  TCCGGTTACT CAGTGTTTGC GGGCGTTGGT GAACGTACTC GTGAGGGTAA      500
  
```

	CGACTTCTAC	CACGAAATGA	CCGACTCCAA	CGTTCTGGAC	AAAGTATCCC	550
	TGGTATATGG	CCAGATGAAC	GAGCCGCCGG	GAAACCGTCT	GCGCGTTGCG	600
	CTGACCGGTC	TGACCATGGC	TGAGAAAGTTC	CGTGACGAAG	GTCGTGACGT	650
	TCTGCTGTTC	GTTGATAACA	TCTATCGTTA	CACCCTGGCC	GGTACTGAAG	700
5	TATCTGCACT	GCTGGGTCGT	ATGCCATCAG	CGGTAGGCTA	CCAGCCAACC	750
	CTGGCGGAAG	AGATGGGTGT	TCTGCAGGAA	CGTATCACCT	CTACCAAAC	800
	CGGTTTC					806

10

2) INFORMATION FOR SEQ ID NO: 268

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 810 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter youngae*
- (B) STRAIN: ATCC 29935

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 268

	GCCGTACCGC	GCGTGACGA	TGCTCTTGAG	GTTATGAATG	GTAAAGAGAG	50
	CCTGGTGCTG	GAAGTTCAGC	AGCAGCTCGG	CGGCGGTATC	GTACGTACCA	100
	TCGCCATGGG	TTCTTCCGAC	GGTCTGCGTC	GTGGTCTGGA	AGTTAAAGAC	150
30	CTCGAGCACC	CGATCGAAGT	CCCGGTAGGT	AAAGCAACGC	TGGGTCGTAT	200
	CATGAACGTT	CTGGGTCACC	CGATCGACAT	GAAAGGCGAT	ATCGGAGAAG	250
	AAGAGCGTTG	GGCTATTCAC	CGCGCAGCAC	CTTCCTATGA	AGAGCTGTCC	300
	AGCTCTCAGG	AACTGCTGGA	AACCGGCATC	AAAGTTATCG	ACCTGATGTG	350
	TCCGTTTCGT	AAGGGCGGTA	AAGTTGGTCT	GTTTCGGTGGT	GCGGGTGTAG	400
35	GTAAACCGT	AAACATGATG	GAGCTTATTC	GTAACATCGC	GATCGAGCAC	450
	TCCGGTTACT	CTGTGTTTGC	GGGTGTAGGT	GAACGTACTC	GTGAGGGTAA	500
	CGACTTCTAC	CACGAAATGA	CCGATTCCAA	CGTTCTGGAT	AAAGTATCCC	550
	TGGTTTATGG	CCAGATGAAC	GAGCCGCCGG	GAAACCGTCT	GCGCGTTGCG	600
	CTGACCGGTC	TGACCATGGC	TGAGAAATTC	CGTGACGAAG	GTCGTGACGT	650
40	ACTGCTGTTC	GTCGATAACA	TCTATCGTTA	TACCCTGGCC	GGTACGGAAG	700
	TATCCGCACT	GCTGGGTCGT	ATGCCATCAG	CGGTAGGTTA	CCAGCCGACC	750
	CTGGCGGAAG	AGATGGGTGT	TCTGCAGGAA	CGTATCACTT	CTACCAAAC	800
	CGGTTCTATC					810

45

2) INFORMATION FOR SEQ ID NO: 269

(i) SEQUENCE CHARACTERISTICS:

50

- (A) LENGTH: 827 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium innocuum*
- (B) STRAIN: ATCC 14501

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 269

```

5   TTGAGAACGG AGATTTGCCG CAGCTATTGA CCGCTATTGA AATTCCTCTG      50
    AAAGACAGTG AATCTCTGAT TGTCGAAGTT GCTCAGCATA TCGGTGATGA      100
    ACGTGTCCGC TGTATCGCTA TGGGCGGTAC AGATGGTCTG GTTCGTGGAA      150
    TGGAAAGCCAT TGATACAGGA TCCGCAATCC GTGTACCGGT GGGAAAAGAA      200
    ATTCTGGGAA GAATGTTCAA TGTCCTCGGA CGTGAAATTG ATGGTCTGGG      250
    ACCTGTAGGA ACGGATAACA CACTGCCGAT CCACAGACAG GCACCGGGCT      300
    TTGAGGAGCA GCAGACATCC GCAGAAATGC TGGAAACAGG AATTAAGGTC      350
10  ATTGACCTGT TATGTCCATA TTCCAAGGGT GGTAAGATTG GTTTGTTTGG      400
    TGGTGCGGGA GTAGGTAAAA CCGTACTGAT TCAGGAGCTG ATTCATAATA      450
    TCGCCAAGGA ACATGGTGGA ATGTCCGTCG TTACCGGTGT AGGGGAGAGA      500
    ACCCGTGAAG GAAACGACAT GTATCATGAA ATGAAGGACA GCGGTGTCCT      550
    TGATAAGACC GTACTGGTTT ACGGACAGAT GAATGAATCA CCGGGTGCCA      600
15  GAATGCGTGT CGGTCTGACC GGGCTGACGA TGGCGGAATA TTTCCGTGAT      650
    CACGACCATC AGGATGTATT GCTGTTTATT GATAATATTT TCCGTTTTAC      700
    CCAGGCGGGA AGTGAAGTAA GTGCCCTGCT GGGACGTATG CCAAGTGCAG      750
    TAGGCTATCA GCCGACACTT GCGACAGAAA TGGGACAGCT GCAGGAGCGC      800
    ATTACATCCA CGAAGGATGG TTCCATT                                827
20

```

2) INFORMATION FOR SEQ ID NO: 270

```

25  (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 829 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear
30

```

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

```

35  (A) ORGANISM: Clostridium perfringens
    (B) STRAIN: ATCC 13124

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 270

```

40  GCAAATGATG AACTTCCTAA TATATTTAAT GCAATACACA TAAAAATGGA      50
    CGATGGAAAA ATCTTAGTTT GTGAGGTAGA GCAACACGTA GGAGACGATA      100
    TAGTTAGAAC TATAGCTATG GAAGCTACTG AAGGACTAAG AAGAGGTGTA      150
    GAAGCTGTTG ATACAGGAGC ACCTATATCA GTACCAGTTG GTGAATGCGT      200
    ATTAGGAAGA ATATTTAACG TATTAGGTAA ACCACTAGAT AGTGGAGCTG      250
    AAGTTAATAA CGAAGAAAAA TATCCAATTC ATAGACCAGC TCCATCATTT      300
45  GAAGAACAAT CAGTTGTTCC TCAAATGTTT GAGACAGGAA TAAAGGTTAT      350
    CGACCTTTTA GCACCTTACC AAAGAGGGGG AAAAATCGGT CTATTTGGAG      400
    GTGCAGGTGT TGGTAAAACA GTTCTTATCC AAGAGCTTAT AAACAACATA      450
    GCTAAAGAGC ACGGTGGACT TTCTGTATTC ACAGGAGTTG GAGAAAGATC      500
    AAGAGAAGGT AATGACCTTT ACTATGAAAT GATGGAATCA GGAGTTATAA      550
50  AAAATACAGC ATTAGTATTT GGACAAATGA ACGAACCACC TGGAGCAAGA      600
    ATGAGAGTTG CTTTAACAGG ACTTACTATG GCTGAGTACT TCAGAGACCA      650
    AGGTCAAGAC GTGTTATTAT TCATAGATAA CATATTCAGA TTCTCACAAG      700
    CTGGATCAGA GGTTTCAGCT TTATTAGGAA GAATACCATC AGCTGTTGGT      750
    TACCAACCAA CTCTTGCTAC AGAGATGGGA GCTCTTCAAG AGAGAATCAC      800
55  ATCAACTACC CATGGATCAA TTACATCAG                                829

```

2) INFORMATION FOR SEQ ID NO: 271

60

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 271

TTGTCCACGT TGGATRTCTT CA

22

2) INFORMATION FOR SEQ ID NO: 272

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 818 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Corynebacterium diphtheriae*
 (B) STRAIN: ATCC 27010

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 272

30	CCCCGCGTGGC	GAGCTGCCGG	CACTGTACAA	CGCGTTGACT	GTCGAGGTCA	50
	CCCTCGAGGC	AGTCGCTAAG	ACCATTACCC	TTGAGGTTGC	CCAGCACTTG	100
	GGCGACAACC	TCGTTCCGCG	CGTGTCCATG	GCCCCCTACCG	ACGGCCTCGT	150
	CCGTGGTGCT	GTTGTGACCG	ACTCGGGCAA	GCCAATCTCC	GTGCCAGTTG	200
35	GCGACGTTGT	TAAAGGCCAC	GTTTCAACG	CACTGGGCGA	TTGCTTGGAT	250
	GAGCCAGGTC	TCGGCCGCGA	TGGTGAGCAG	TGGGGAATTC	ACCGCGATCC	300
	ACCACCATTC	GATCAGCTCG	AAGGTAAGAC	CGAAATCCTC	GAGACCGGTA	350
	TTAAGGTCAT	CGACTTGCTC	ACCCCTTACG	TTAAGGGCGG	CAAGATTGGT	400
	CTGTTCGGTG	GTGCAGGTGT	GGGTAAGACC	GTGCTCATCC	AGGAGATGAT	450
40	CACTCGTATT	GCTCGCGAGT	TCTCCGGTAC	CTCCGTCTTC	GCTGGCGTTG	500
	GTGAGCGTAC	CCGTGAGGGC	ACCGACCTCT	TCCTCGAAAT	GGAAGAAATG	550
	GGCGTTCTTC	AGGACACCGC	TCTCGTGTTC	GGCCAGATGG	ACGAGCCACC	600
	AGGAGTCCGT	ATGCGCGTTG	CTCTGTCCGG	TCTGACCATG	GCGGAGTACT	650
	TCCGCGATGT	TCAGCACCAG	GACGTGCTTC	TGTTTCATCGA	TAACATTTTC	700
45	CGTTTCACCC	AGGCCGGTTC	CGAGGTTTCG	ACCCTTCTTG	GTCGTATGCC	750
	TTCCGCCGTG	GGTTACCAGC	CAACCTTGGC	TGACGAGATG	GGTGTCTCTC	800
	AGGAGCGTAT	TACCTCTA				818

2) INFORMATION FOR SEQ ID NO: 273

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 833 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium pseudodiphtheriticum*
 (B) STRAIN: ATCC 10700

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 273

```

CGATGCCTGC TCTGTACAAC GCGCTGACTG TCGAGGTCAC CCTCGAGGCA    50
GTCGCCAAGA CCATCACGCT TGAGGTTGCA CAGCACCTCG GCGATAACCT    100
GATCCGGACC ATTGCGTTGG CACCTACGGA CCGTCTCGTC CGTGGCGCTG    150
10 AGGTTATCGA CACTGGTAAG CCAATTACTG TTCCCGTCGG CGATGCCGTC    200
AAAGGACACG TCTTCAATGC GCTCGGTGAG TGTTTGACG AACCAGGATT    250
GGGCCGCGAC GCGGAACAGT GGGGAATCCA CCGCGATCCG CCACCATTCTG    300
ATGCGCTGGA GGGCAAACCC GAGATTCTGG AGACTGGAAT CAAGGTTATC    350
GACCTCCTTA CCCCTTACGT TAAGGGTGGC AAAATTGGTC TGTTCCGGTGG    400
15 CGCCGGCGTC GGCAAGACCG TTCTTATCCA GGAAATGATC ACTCGTATCG    450
CTCGTAACTT CTCCGGTACT TCCGTGTTCC CCGGCGTCGG TGAGCGTACC    500
CGTGAGGGTA CTGACCTGTT CCTGGAAATG GAAGAGATGG GCGTGTTGCA    550
AGACACCGCC CTTGTCTTCG GTCAAATGGA CGAACCACCA GGGGTTTCGTA    600
TGCGCGTGCG CTTGTCTGGT CTAACCATGG CTGAATATTT CCGCGACGTT    650
20 CAAAACCAGG ACGTTTTGTT GTTCATTGAC AACATCTTCC GTTTTACTCA    700
GGCAGGTTCC GAGGTTTCCA CGCTGTTGGG CCGTATGCCT TCCGCCGTGG    750
GTTATCAGCC AACATTGGCT GATGAGATGG GTGTTTTCGA GGAACGGATT    800
ACCTCTACAC GTGTAAGTC AATTACTTCC CTG                        833

```

25

2) INFORMATION FOR SEQ ID NO: 274

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 417 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium ulcerans*
 (B) STRAIN: NCTC 8665

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 274

```

CCGTGCTCAT CCAGGAGATG ATCACCCGTG TGGCCCGCAA CTTCGGCGGC    50
ACCTCTGTGT TCGCCGGCGT CCGCGAGCGC ACCCGTGAGG GCAACGACCT    100
45 CTGGGTCGAG ATGGACGAGG CCGACGTGCT CAAGGACACC GCCCTGGTGT    150
TCGGCCAGAT GGACGAGCCG CCGGGAACCC GTCTGCGCGT GGCCCTGTCC    200
GCGCTGACCA TGGCGGAGTA CTTCCGCGAT GTGCAGAACC AGGACGTGCT    250
GCTGTTTCATC GACAACATCT TCCGCTTCTC CCAGGCCGGC TCCGAGGTCT    300
CCACCCTGCT GGGCCGCATG CCTCCGCGG TGGGCTACCA GCCGAACCTG    350
50 GCGGACGAGA TGGGTGTGCT GCAGGAGCGC ATCACCTCGA CTCGCGGCCA    400
CTCCATCACC TCGATGC                        417

```

55 2) INFORMATION FOR SEQ ID NO: 275

(i) SEQUENCE CHARACTERISTICS:

- 60 (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Corynebacterium urealyticum*
(B) STRAIN: ATCC 43042

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 275

```

10 GGGCAGCAGC CAGCACTATT CAACGCGCTG CACGTCGAGG TTGACCTCGA      50
   GGCAGTTGCG AAGACCATTA CCCTGGAGGT CGCACAGCAC CTGGGTGACA      100
   ACCTGGTGCG CACCGTCTCC ATGGCCCCGA CCGACGGCCT GGTCCGCGGT      150
   GCAGAGGTGA AGGACACCGG TAAGCCGATC TCTGTGCCAG TCGGCGATGT      200
15 TGTC AAGGGG CACGTCTTCA ACGCCCTGGG CGACTGCCTG GATGAGCCAG      250
   GTCTCGGCCG CGACGGCGAG CAGTGGGGCA TCCACCGCGA GCCACCGGCA      300
   TTCGACGAGC TCGAGGGTAA GACCGAGATC CTGGAGACCG GCGTTAAGGT      350
   CATCGACCTG CTGACCCCTT ACGTCAAGGG CGGCAAGATT GGCCTCTTCG      400
   GTGGTGCAGG TGTGGGTAAG ACCGTCTCTG TTCAGGAGAT GATTACCCGT      450
20 ATCGCCCGCG AGTTCTCCGG TACCTCCGTG TTCGCCGGCG TCGGCGAGCG      500
   TACCCGTGAG GGTACGGACC TCTTCCTCGA GATGGAGGAG ATGGGCGTGC      550
   TCCAGGACAC CGCGCTGGTG TTCGGTCAGA TGGATGAGCC GCCGGGAGTC      600
   CGTATGCGCG TGGCTCTGTC CGGTCTGACC ATGGCGGAGT ACTTCCGCGA      650
   TGTT CAGGGC CAGGACGTGC TGCTGTTCAT CGACAACATC TTCCGTTTCA      700
25 CCCAGGCAGG TTCTGAGGTC TCCACGCTGC TCGGCCGCAT GCCGTCCGCA      750
   GTGGGTTACC AGCCGACCTT GGCTGACGAG ATGGGTGTTT TGCAGGAGCG      800
   CATTACCTCC ACGAAGGGTA AGTCCATTAC CTCCC                      835

```

30 2) INFORMATION FOR SEQ ID NO: 276

(i) SEQUENCE CHARACTERISTICS:

```

35 (A) LENGTH: 818 bases
   (B) TYPE: Nucleic acid
   (C) STRANDEDNESS: Double
   (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Coxiella burnetii*
(B) STRAIN: Nine Mile phase II

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 276

```

   CCCGTCACGC TGTCCCGAAA GTGTACGATG CTTTGCAGGT GGATGAAAAT      50
   AATTTAACGC TCGAAGTCCA ACAGCAACTC GGGGACGGTG TCGTGCGCAC      100
   AATTGCCATG GGCAGCACTG AGGGCTTAAA ACGCGATATC GCCGTAAAAA      150
50 ATACGGAAAA ACCGATTGAA GTTCCCGTAG GAAAAGAAAC TTTAGGTCGT      200
   ATCATGAACG TGCTGGGTGA GCCGATCGAT GAGTTAGGTC CCATTAATTC      250
   AAAAGAAAAA CTCCCTATTC ATCGTCCTGC GCCGAGCTTT ATTGAGCAAT      300
   CTGGCGCTAC CGAATTATTA GAAACCGGTA TTAAAGTGGT CGATTTGCTT      350
   TGCCCTTTTG CTAAGGGAGG CAAAGTGGGT CTTTTTGGAG GCGCGGGCGT      400
55 TGGAAAAACG GTTAATATGA TCGAATTAAT CCGTAATATC GCCATTGAAC      450
   ACAGCGGTTA TTCTGTTTTT GCGGGTGTGG GAGAAAGAAC GCGAGAAGGC      500
   AATGATTTTT ATCATGAAAT GAAAGAATCC AATGTCTTGG ATAAAGTGGC      550
   GTTGGTGTAC GGACAAATGA ACGAGCCGCC AGGGAACCGC TTGCGGGTGG      600
   GTTTGACGGG GCTTACGCTG GCGGAAGCCT TCCGTGACGA AGGACGCGAC      650
60 GTTCTGTTAT TTATCGATAA TATCTTTCGT TACACTTGG CAGGGGTTGA      700

```

AGTCTCTGCC CTCCTCGGTC GGATGCCATC GGCTGTGGGT TATCAGCCGA	750
CGTTGGCCGA AGAGATGGGG GCCCTGCAAG AACGCATTAC TTCCACTAAA	800
AAAGGGTCCA TTACGTCG	818

5

2) INFORMATION FOR SEQ ID NO: 277

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Edwardsiella hoshinae*
 (B) STRAIN: ATCC 33379

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 277

TTCCCGCAGG ACGCCGTGCC GAAGGTGTAT AACGCACTGG AAGTAAAAGG	50
CGGTGCCACG AAAC TGGTAC TGGAAGTGCA GCAGCAGCTG GGTGGCGGCG	100
25 TAGTTCGCTG CATCGCGATG GGCTCTTCCG ACGGTCTGCG CCGTGGGCTA	150
GAGGTTGAAG ACCAAGACCA TCCGATCGAG GTTCCTGTTG GCAAGGCGAC	200
TCTGGGCCGT ATCATGAACG TACTGGGTGA TCCGGTCGAC ATGAAGGGCG	250
AGATCGGTGA AGAAGAGCGT TGGGCTATCC ATCGTGCTGC ACCGAGCTAT	300
GAAGATCTGT CTAAC TCTCA GGAAC TGCTG GAGACCGGCA TTAAGGTTAT	350
30 CGACCTGATT TGCCCGTTCC GTAAAGGCGG TAAAGTGGGC CTGTTCCGTG	400
GGGCCGGTGT GGGTAAGACC GTTAACATGA TGGAGCTTAT CCGTAACATC	450
GCTATCGAGC ACTCCGGTTA CTCAGTCTTC GCCGGTGTGG GTGAGCGTAC	500
CCGTGAGGGT AACGACTTCT ACCACGAGAT GACCGATTCC AACGTATTGG	550
ATAAAGTTTC TCTGGTGAT GGTCAGATGA ACGAGCCACC GGGAAACCGT	600
35 CTGCGCGTGG CGCTGACCGG TCTGACCATG GCGGAGAAAT TCCGTGATGA	650
AGGTCGTGAT GTACTGTTGT TCATCGATAA CATCTACCGT TATACCTTGG	700
CCGGTACTGA AGTCTCCGCT CTGCTGGGCG GTATGCCGTC GGCGGTAGGT	750
TATCAGCCGA CTCTGGCGGA GGAAATGGGG GTGCTGCAAG AGCGTATTAC	800
CTCCACTAAG ACCGGGTCCA TCACCTCTG	829
40	

2) INFORMATION FOR SEQ ID NO: 278

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 809 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 50 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Edwardsiella tarda*
 55 (B) STRAIN: ATCC 15947

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 278

GCCGTGCCGA AGGTGTATAA CGCACTGGAA GTAAAAGGCG GTGCCACGAA	50
60 ACTGGTACTG GAAGTGCAGC AGCAGCTGGG TGGCGGCGTC GTTCGCTGCA	100

	TCGCGATGGG	CTCCTCCGAC	GGTCTGCGCC	GTGGGCTGGT	GGTTGAAGAC	150
	CAAGACCATC	CGATCGAGGT	TCCGGTCCGT	AAGGCGACCC	TGGGCCGTAT	200
	CATGAACGTA	CTGGGTGATC	CGGTGACAT	GAAGGGCGAG	ATCGGCGAAG	250
	AAGAGCGTTG	GGCTATCCAC	CGCGCGGCGC	CGAGCTATGA	AGATCTGTCC	300
5	AACTCTCAGG	AGCTGCTGGA	GACCGGCATC	AAGGTTATCG	ACCTGATTTG	350
	CCCGTTCGCC	AAAGGCGGTA	AAGTTGGCCT	GTTCGGTGGT	GCCGGTGTGG	400
	GTAAGACCGT	TAACATGATG	GAGCTTATCC	GTAACATCGC	TATCGAGCAC	450
	TCCGGTTACT	CCGTATTTGC	CGGTGTAGGC	GAGCGTACCC	GTGAGGGTAA	500
	CGACTTCTAC	CACGAGATGA	CCGACTCCAA	CGTATTGGAT	AAAGTTTCTC	550
10	TGGTATACGG	CCAGATGAAT	GAGCCGCCGG	GAAACCGTCT	GCGTGTGGCG	600
	TTGACCGGTC	TGACCATGGC	GGAGAAATTC	CGTGATGAAG	GTCGCGATGT	650
	GTTGTTGTTT	ATCGATAACA	TTTATCGTTA	TACCTTGGCT	GGTACCGAAG	700
	TTTCTGCTCT	GCTGGGTCGT	ATGCCGTCGG	CGGTAGGTTA	TCAGCCGACC	750
	CTGGCGGAAG	AGATGGGTGT	GTTGCAAGAG	CGTATCACCT	CAACGAAGAC	800
15	GGGCTCTAT					809

2) INFORMATION FOR SEQ ID NO: 279

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 840 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Eikenella corrodens*
 (B) STRAIN: ATCC 23834

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 279

35	TTTCCGCGTA	CCGCCATTCC	GCGTGTTTAC	GATGCACTCA	AACTGGTTGA	50
	TACTGATTTG	ACGCTGGAAG	TACAGCAGCA	GCTTGGTGAC	GGCGTTGTCC	100
	GTACCATTGC	GATGGGTAGT	ACAGACGGTT	TGAAACGTGG	CTTGGCTGTG	150
	CAAAATACTG	GTGCACCGAT	TACTGTGCCG	GTGGGGAAAG	CCACCCTAGG	200
	CCGCATCATG	GACGTTCTGG	GCAACCCCGT	GGACGAACAA	GGTCCGATCG	250
40	GTTCTGACCA	AACCCGTGCT	ATTCATCAAT	TTGCACCTAA	GTTTCGACGAA	300
	CTCTCCAGCA	CTACCGAATT	GTTGGAAACA	GGCATTAAAG	TGATCGATTT	350
	GCTTTGTCCG	TTTGCTAAAG	GTGGTAAAGT	GGGTCTGTTT	GGCGGTGCCG	400
	GTGTGGGCAA	AACCGTGAAC	ATGATGGAGC	TGATTAACAA	CATTGCCAAA	450
	GCGCACAGTG	GTCTTTCCGT	ATTCGCCGGT	GTGGGTGAGC	GTACTCGTGA	500
45	AGGTAACGAC	TTCTACCACG	AAATGAAAGA	CTCCAACGTG	TTGGATAAAG	550
	TGGCAATGGT	GTATGGCCAG	ATGAACGAGC	CGCCTGGTAA	CCGCTTGCGT	600
	GTTGCTCTAA	CTGGTTTGTC	GATGGCTGAA	TACTTCCGTG	ACGAAAAAGA	650
	CGAAAACGGC	AAAGGCCGTG	ACGTATTATT	CTTTGTGGAT	AATATCTACC	700
	GCTATACTCT	GGCGGGTACC	GAAGTGTCGG	CTCTGCTTGG	CCGTATGCCT	750
50	TCTGCTGTGG	GTTATCAGCC	AACTTTGGCT	GAAGAAATGG	GTCGTTTGCA	800
	GGAGCGTATT	ACCTCCACCC	AAACTGGTTC	CATTACCTCT		840

55 2) INFORMATION FOR SEQ ID NO: 280

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 803 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double

60

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter agglomerans*
 (B) STRAIN: ATCC 27989

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 280

```

10  GCCGTACCAC GAGTGTACGA TGCAC TTGAG GTAAAGAATG GTGAAGAGCG      50
    TCTGGTGCTG GAAGTTCAGC AACAGCTCGG CGGTG GCGTT GTACGTACCA      100
    TCGCAATGGG TTCTTCTGAT GGTCTGCGTC GTGGTCTGGA AGTAACGGAC      150
    CTGGCTCACC CGATCGAAGT CCCGGTAGGT AAAGCAACAC TGGGTCGTAT      200
15  CATGAACGTA CTGGGCGAAC CAGTAGACAT GAAAGGCGAC ATCGGTGAAG      250
    AAGAGCGTTG GCGGATCCAC CGTGCAGCAC CGTCTACGA AGAGTTGTCA      300
    AACTCTCAGG AACTGCTGGA AACC GG TATC AAAGTTATCG ACCTGATGTG      350
    TCCGTTTCGCT AAGGGCGGTA AAGTGGGTCT GTTCGGTGGT GCGGGTGTAG      400
    GTAAAACCGT AAACATGATG GAGCTTATTC GTAACATCGC GATCGAGCAC      450
20  TCCGGTTACT CTGTGTTTGC GGGCGTAGGT GAACGTACTC GTGAGGGTAA      500
    CGACTTCTAC CACGAAATGA CCGACTCCAA CGTTATCGAC AAAGTATCCC      550
    TGGTGTATGG TCAGATGAAC GAGCCGCCGG GAAACCGTCT GCGCGTTGCG      600
    CTGACCGGTC TGACCATGGC TGAGAAAGTTC CGTGACGAAG GTCGTGACGT      650
    ACTGTTGTTC GTTGACAACA TCTACCGTTA CACCCTGGCC GGTACGGAAG      700
25  TATCCGCACT GCTGGGCCGT ATGCCTTCTG CGGTAGGTTA TCAGCCGACG      750
    CTGGCGGAAG AGATGGGCGT TCTGCAGGAA CGTATCACCT CCACCAAAAC      800
    CGG                                     803
  
```

30 2) INFORMATION FOR SEQ ID NO: 281

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 833 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter amnigenus*
 (B) STRAIN: ATCC 33072

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 281

```

    CGAATTCCCT CAGGATGCCG TACCGCGCGT GTACGATGCT CTTGAGGTAC      50
    AGAATGGTAA CGAGAGTCTG GTGCTGGAAG TTCAGCAGCA GCTCGGTGGT      100
    GGTATCGTAC GTACTATCGC CATGGGTTCT TCCGACGGTC TGCGTCGTGG      150
50  TCTGGCTGTT AAAGATCTCG AACACCCGAT CGAAGTCCCG GTAGGTAAAG      200
    CAACACTGGG TCGTATCATG AACGTTTTGG GTCAACCAAT CGACATGAAA      250
    GGCGACATCG GTGAAGAAGA CCGTTGGGCA ATCCACCGTG CAGCACCTTC      300
    CTATGAAGAG CTGTCTAGCT CTCAGGAACT GCTGGAAACC GGCATCAAAG      350
    TTATCGACCT GATGTGTCCG TTCGCTAAGG GCGGTAAAGT TGGTCTGTTC      400
55  GGCGGTGCGG GCGTGGGTAA AACTGTAAAC ATGATGGAGC TGATCCGTAA      450
    CATCGCGATC GAGCACTCCG GTTACTCCGT GTTTGCAGGC GTGGGTGAGC      500
    GTACTCGTGA GGGTAACGAC TTCTACCACG AAATGACCGA TTCCAACGTT      550
    CTGGATAAAG TATCCCTGGT TTATGGCCAG ATGAACGAGC CACCAGGAAA      600
    CCGTCTGCGC GTTGCGCTGA CCGGTCTGAG TATGGCTGAG AAGTTCCGTG      650
60  ACGAAGGTCTG TGACGTACTG CTGTTCTGAG ATAACATCTA CCGTTACACC      700
  
```

CTGGCCGGTA	CTGAAGTATC	TGCGCTGCTG	GGCCGTATGC	CTTCAGCGGT	750
AGGTTACCAG	CCGACCCTGG	CGGAAGAGAT	GGGCGTTCTG	CAGGAACGTA	800
TCACTTCTAC	CAAAACCGGT	TCTATCACCT	CCG		833

5

2) INFORMATION FOR SEQ ID NO: 282

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 810 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter asburiae*
 (B) STRAIN: ATCC 35953

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 282

GCCGTACCAC	GCGTGACGA	CGCGCTTGAG	GTACAGAATG	GTAACGAGAG	50
CCTGGTGCTG	GAAGTTCAGC	AGCAGCTCGG	CGGCGGTATC	GTGCGTACCA	100
TCGCGATGGG	TTCTTCCGAC	GGTCTGCGTC	GTGGTCTGGA	AGTCAAAGAC	150
CTTGAGCACC	CGATCGAAGT	CCCGGTAGGT	AAAGCAACAC	TGGGTCGTAT	200
CATGAACGTA	TTGGGTCAAC	CAATCGACAT	GAAAGGCGAC	ATCGGTGAAG	250
AAGAGCGTTG	GGCTATCCAC	CGCGCGGCAC	CTTCCTACGA	AGAGCTGTCC	300
AGCTCTCAGG	AAC TGCTGGA	AACCGGTATC	AAAGTTATCG	ACCTGATGTG	350
TCCGTTTCGG	AAGGGCGGTA	AAGTCGGTCT	GTTTCGGTGGT	GCGGGTGTTG	400
GTAAAACCGT	AAACATGATG	GAGCTGATCC	GTAACATCGC	GATCGAGCAC	450
TCCGGTTACT	CCGTGTTTGC	GGGCGTAGGT	GAACGTACTC	GTGAGGGTAA	500
CGACTTCTAC	CACGAAATGA	CCGACTCCAA	CGTTCTGGAC	AAAGTATCCC	550
TGGTTTACGG	CCAGATGAAC	GAGCCACCAG	GAAACCGTCT	GCGCGTTGCG	600
CTGACCGGTC	TGACGATGGC	TGAGAAGTTC	CGTGATGAAG	GCCGTGACGT	650
TCTGCTGTTT	GTTGATAACA	TCTATCGTTA	CACCCTGGCC	GGTACGGAAG	700
TATCTGCACT	GCTGGGTCGT	ATGCCTTCAG	CGGTAGGTTA	CCAGCCTACG	750
CTGGCGGAAG	AGATGGGTGT	TCTTCAGGAA	CGTATCACCT	CTACCAAAC	800
CGGTTCTATC					810

2) INFORMATION FOR SEQ ID NO: 283

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 811 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter cancerogenus*
 (B) STRAIN: ATCC 35317

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 283

GCCGTACCGC	GCGTGACGA	TGCTCTTGAG	GTACAGAATG	GTAACGAGAG	50
CCTGGTGCTG	GAAGTTCAGC	AGCAGCTCGG	CGGCGGTATC	GTACGTACTA	100

```

TCGCCATGGG TTCTTCCGAC GGTCTGCGTC GTGGTCTGGA AGTAAAAGAC 150
CTTGAGCACC CGATCGAAGT CCCGGTAGGT AAAGCAACAC TGGGTCGTAT 200
CATGAACGTA TTGGGTCAAC CAATCGACAT GAAAGGCGAC ATCGGTGAAG 250
AAGAGCGTTG GGCTATCCAC CGCGCAGCAC CTTCTACGA AGAGCTGTCC 300
5 AGCTCTCAGG AACTGCTGGA AACC GG CATC AAAGTTATCG ACCTGATGTG 350
TCCGTTTCGCG AAGGGCGGTA AAGTCGGTCT GTTCGGTGGT GCGGGTGTAG 400
GTAAAACCGT AAACATGATG GAGCTGATCC GTAACATCGC GATCGAGCAC 450
TCCGGTTATT CCGTGTTTGC GGGCGTGGGT GAACGTACTC GTGAGGGTAA 500
CGACTTCTAC CACGAAATGA CCGACTCCAA CGTTCTGGAT AAAGTATCCC 550
10 TGGTGTACGG CCAGATGAAC GAGCCACCAG GAAACCGTCT GCGCGTTGCG 600
CTGACCGGCC TGACCATGGC TGAGAAGTTC CGTGACGAAG GTCGTGACGT 650
ACTGCTGTTC GTTGATAACA TCTACCGTTA CACCCTGGCC GGTACCGAAG 700
TATCTGCACT GCTGGGTCGT ATGCCTTCAG CGGTAGGTTA TCAGCCTACG 750
CTGGCGGAAG AGATGGGTGT TCTTCAGGAA CGTATCACCT CAACCAAAAC 800
15 CGGTTCTATC A 811

```

2) INFORMATION FOR SEQ ID NO: 284

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter cloacae*
 (B) STRAIN: ATCC 13047

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 284

```

35 GCCGTACCAC GCGTGTACGA CGCGCTTGAG GTACAGAATG GTAACGAGAG 50
CCTGGTGCTG GAAGTTCAGC AGCAGCTCGG CGGCGGTATC GTGCGTACCA 100
TCGCGATGGG GTCTTCCGAC GGTCTGCGTC GTGGTCTGGA AGTTAAAGAC 150
CTTGAGCACC CGATCGAAGT CCCGGTAGGT AAAGCAACAC TGGGTCGTAT 200
CATGAACGTA TTGGGTCAGC CAATCGACAT GAAAGGCGAC ATCGGTGAAG 250
40 AAGAGCGTTG GGCTATCCAC CGCGCGGCAC CTTCTACGA AGAGCTGTCC 300
AGCTCTCAGG AACTGCTGGA AACC GG TATC AAAGTTATCG ACCTGATGTG 350
TCCGTTTTCG AAGGGCGGTA AAGTTGGTCT GTTCGGTGGT GCGGGTGTAG 400
GTAAAACCGT AAACATGATG GAGCTGATCC GTAACATCGC GATCGAGCAC 450
TCCGGTTACT CCGTATTTGC GGGCGTAGGT GAACGTACTC GTGAGGGTAA 500
45 CGACTTCTAC CACGAAATGA CCGACTCCAA CGTTCTGGAC AAAGTATCCC 550
TGTTTTACGG CCAGATGAAC GAGCCACCAG GAAACCGTCT GCGCGTTGCG 600
CTGACTGGTC TGACGATGGC TGAGAAGTTC CGTGACGAAG GCCGTGACGT 650
TCTGCTGTTC GTTGATAACA TCTACCGTTA CACCCTGGCC GGTACCGAAG 700
TATCTGCACT GCTGGGTCGT ATGCCTTCAG CGGTAGGTTA TCAGCCTACG 750
50 CTGGCGGAAG AGATGGGTGT TCTTCAGGAA CGTATCACCT CTACCAAAAC 800
CGGTTCTATC ACTTCCG 817

```

55 2) INFORMATION FOR SEQ ID NO: 285

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 766 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterobacter gergoviae*

(B) STRAIN: ATCC 33028

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 285

10
 AATGAGAGCC TGGTGCTGGA AGTTCAGCAG CAGCTCGGCG GCGGTATCGT 50
 GCGTACCATC GCAATGGGTT CTTCTGACGG TCTGCGTCGC GGTCTGGAAG 100
 TTAAAGATCT CGAACATCCG ATCGAAGTCC CGGTAGGTAA AGCGACCCTC 150
 GGCCGTATTA TGAACGTGCT GGGTCAGCCG GTTGATATGA AAGGCGATAT 200
 15 CGGCGAAGAA GAGCGTTGGG CGATCCACCG CGCTGCGCCG TCCTATGAAG 250
 AGCTCTCCAG CTCTCAGGAA CTGCTGGAAA CCGGTATCAA GGTAATGGAC 300
 CTGATTTGCC CGTTCGCGAA GGGCGGTAAA GTCGGTCTGT TCGGCGGTGC 350
 GGGCGTTGGT AAAACCGTAA ACATGATGGA GCTGATCCGT AACATCGCGA 400
 TCGAGCACTC CGGCTACTCC GTGTTTGCGG GCGTGGGTGA ACGTACTCGT 450
 20 GAGGGTAACG ACTTCTACCA CGAAATGACC GACTCCAACG TTATCGACAA 500
 AGTATCCCTG GTGTACGGCC AGATGAACGA GCCGCCGGGA AACCCTCTGC 550
 GCGTGGCGCT GACCGGTCTG ACCATGGCTG AGAAATTCCG TGACGAAGGT 600
 CGTGACGTTT TGCTGTTCTG CGATAACATC TACCGCTATA CCCTCGCCGG 650
 TACTGAAGTA TCCGCACTGC TGGGCCGTAT GCCTTCTGCA GTAGGTTACC 700
 25 AGCCGACGCT GCGGGAAGAG ATGGGTGTTT TGCAGGAACG TATCACCTCC 750
 ACCAAAACCG GTTCTA 766

30 2) INFORMATION FOR SEQ ID NO: 286

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 805 bases

(B) TYPE: Nucleic acid

35 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterobacter hormaechei*

(B) STRAIN: ATCC 49162

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 286

45
 GCCGTACCAC GCGTGACGA CGCGCTTGAG GTACAGAATG GTAACGAGAG 50
 CCTGGTGCTG GAAGTTCAGC AGCAGCTCGG CGGCGGTATC GTGCGTACCA 100
 TCGCCATGGG TTCTTCCGAC GGTCTGCGTC GTGGTCTGGA AGTGAAAGAC 150
 CTTGAGCACC CGATCGAAGT CCCGGTAGGT AAAGCAACGC TGGGTCGTAT 200
 50 CATGAACGTA TTGGGTCAGC CAATCGACAT GAAAGGCGAC ATCGGTGAAG 250
 AAGAGCGTTG GGCTATCCAC CGCGCGGCAC CTTCTTACGA AGAGCTGTCC 300
 AGCTCTCAGG AACTGCTGGA AACCGGCATC AAAGTTATCG ACCTGATGTG 350
 TCCGTTTGCG AAGGGCGGTA AAGTTGGTCT GTTCGGTGGT GCGGGTGTAG 400
 GTAAAACCGT AAACATGATG GAGCTGATCC GTAACATCGC GATCGAGCAC 450
 55 TCCGGTTACT CCGTGTTTGC GGGCGTGGGT GAACGTACTC GTGAGGGTAA 500
 CGACTTCTAC CACGAAATGA CCGACTCCAA CGTTCTGGAC AAAGTATCCC 550
 TGGTTTACGG CCAGATGAAC GAGCCACCAG GAAACCGTCT GCGCGTTGCG 600
 CTGACTGGCC TGACGATGGC TGAGAAGTTC CGTGACGAAG GCCGTGACGT 650
 TCTGCTGTTT GTCGATAACA TCTACCGTTA CACCCTGGCC GGTACGGAAG 700
 60 TATCTGCACT GCTGGGTCGT ATGCCTTCAG CCGTAGGTAA TCAGCCAACG 750

CTTGCGGAAG AGATGGGTGT TCTTCAGGAA CGTATCACCT CGACCAAAC
CGGTT

800
805

5

2) INFORMATION FOR SEQ ID NO: 287

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 791 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter sakasaki*
(B) STRAIN: ATCC 29544

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 287

	TACGACGCCC	TTGAGGTAAC	GAATGGTAAT	GAGCGTCTGG	TGCTGGAAGT	50
	CCAGCAGCAG	CTCGGCGGCG	GTATCGTACG	TACCATCGCG	ATGGGCTCTT	100
	CCGACGGTCT	GCGTCGCGGT	CTGCCTGTTG	CAGACCTTGA	GCACCCGATC	150
25	GAAGTGCCCG	TAGGTAAAGC	GACGCTGGGT	CGTATCATGA	ACGTCCTGGG	200
	TCAGCCTATC	GACATGAAAG	GCGACATCGG	CGAAGAAGAG	CGTTGGGCGA	250
	TTCATCGCGC	GGCGCCGTCC	TATGAAGAGC	TGTCCAGCTC	TCAGGAAGTG	300
	CTGGAACCG	GCATCAAAGT	TATCGACCTG	ATGTGTCCGT	TCGCGAAGGG	350
	CGGTAAAGTC	GGTCTGTTCG	GTGGTGACAG	TGTAGGTAAA	ACCGTAAACA	400
30	TGATGGAGCT	TATTCGTAAC	ATCGCGATTG	AGCACTCCGG	TTACTCCGTG	450
	TTTGCGGGCG	TGGGCGAACG	TACCCGTGAA	GGTAACGACT	TCTACCACGA	500
	AATGACCGAC	TCCAACGTAC	TGGATAAAGT	ATCCCTGGTG	TACGGCCAGA	550
	TGAACGAGCC	GCCGGGAAAC	CGTCTGCGCG	TTGCGCTGAC	CGGCCTGACC	600
	ATGGCTGAGA	AATTCCGTGA	CGAAGGTCGT	GACGTTCTGC	TGTTTCGTCGA	650
35	CAACATCTAC	CGTTACACCC	TGGCCGGTAC	TGAAGTATCC	GCACTGCTGG	700
	GCCGTATGCC	TTCAGCGGTA	GGTTATCAGC	CGACCCTGGC	GGAAGAGATG	750
	GGTGTCTGTC	AGGAGCGTAT	CACCTCCACC	AAAACCGGTT	C	791

40

2) INFORMATION FOR SEQ ID NO: 288

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 839 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus avium*
(B) STRAIN: ATCC 14025

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 288

	TTTCTTTAGA	TCAATCCTTA	CCAGACATCA	ACAATGCGTT	GATTGTTTAC	50
	AAAAAAGATA	AAACAAAAGT	TGTTCTTGAA	GTTGCTTTGG	AACTTGGTGA	100
	TGGTGTATC	CGCACAATCG	CTATGGAGGC	TACTGATGGA	TTGCAACGTG	150
60	GAATGGAAGT	TGTCGATACT	GGCAAATCAA	TCTCCGTTCC	TGTAGGTAAA	200

	GATACTCTAG	GTCGTGTGTT	TAACGTATTA	GGTGAAACGA	TTGATAAAGA	250
	AGCACCTTTT	CCAGAAGATG	CAGAAAGAAG	CGGCATTCAT	AAAAAGGCGC	300
	CTGCTTTTGA	AGACCTTAGT	ACAAGTAACG	AGATTTTGGA	AACAGGGATC	350
	AAGGTTATCG	ACTTATTAGC	CCCTTATTTA	AAAGGTGGGA	AAGTCGGACT	400
5	ATTCCGTGGT	GCCGGTGTTG	GTAAAACCGT	TTTGATCCAA	GAATTAATTC	450
	ATAATATCGC	CCAAGAACAC	GGTGGTATTT	CAGTGTTTAC	CGGTGTTGGG	500
	GAACGTACTC	GTGAAGGGAA	CGACCTTTAT	TATGAAATGA	AAGACTCTGG	550
	CGTTATTGAG	AAAACAGCCA	TGGTGTTCCG	ACAAATGAAC	GAGCCGCCTG	600
	GTGCACGTAT	GCGTGTTGCC	TTGACTGGTT	TGACATTAGC	TGAATATTTT	650
10	CGTGATGAAG	AAGGACAAGA	TGTGTTGCTA	TTTATTGACA	ACATCTTCCG	700
	CTTTACTCAA	GCCGGATCAG	AAGTTTCTGC	CTTATTAGGA	CGTATGCCAT	750
	CAGCCGTTGG	GTATCAACCA	ACTTTGGCAA	CTGAAATGGG	GCAATTACAA	800
	GAACGAATCA	CTTCAACCAA	AAAAGGTTCG	ATCACTTCA		839

15

2) INFORMATION FOR SEQ ID NO: 289

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 847 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus casseliflavus*
 (B) STRAIN: ATCC 25788

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 289

	TTCTCTCTAG	ACCAATCATT	ACCAGATATC	AACAATGCGT	TGATTGTTTA	50
	CAAAAAAGAT	GAGCAGAAAA	CAAAAGTTGT	GTTAGAAGCT	GCCTTAGAAC	100
35	TTGGCGACGG	CGTTATCCGT	ACGATTGCCA	TGGAATCAAC	AGATGGCTTA	150
	CAACGAGGAA	TGGAAGTAAT	CGATACAGGC	GCCTCCATTT	CTGTTCCAGT	200
	TGGGACAGAA	ACCTTAGGAC	GGGTGTTTAA	TGTCTTAGGG	GACACCATCG	250
	ATTTAGAAGC	GCCGTTCCTT	GAAGAAGCAC	CCCGCAGTGG	GATTCACAAA	300
	AAAGCACCTG	ACTTTGATGA	ATTGTCAACA	AGTACGGAGA	TCCTTGAAAC	350
40	TGGGATCAAA	GTTATCGATT	TGTTAGCCCC	TTATTTAAAA	GGGGGGGAAAG	400
	TTGGACTTTT	CGGTGGTGCC	GGTGTGTTGT	AAACCGTCTT	GATCCAAGAA	450
	TTGATCCACA	ACATCGCCCC	AGAGCATGGT	GGGATCTCTG	TCTTCACAGG	500
	TGTTGGTGAA	CGGACACGTG	AAGGAAATGA	CCTTTATAAT	GAAATGAAAG	550
	AATCTGGCGT	TATCGAAAAA	ACAGCCATGG	TGTTTGGACA	AATGAACGAA	600
45	CCACCAGGTG	CTCGGATGCG	GGTAGCCTTG	ACTGGTTTGA	CATTAGCCGA	650
	GTACTTCCGT	GATGTGGAAG	GACAAGACGT	GCTCTTGTTT	ATCGATAATA	700
	TCTTCCGCTT	CACTCAAGCA	GGTTCTGAAG	TATCTGCCTT	ACTAGGTCGG	750
	ATGCCGTCTG	CCGTTGGGTA	TCAGCCAACA	TTAGCAACTG	AGATGGGGCA	800
	ATTACAAGAA	CGGATCACAT	CGACGAAGAA	AGGTTCCGTT	ACGTCTA	847

50

2) INFORMATION FOR SEQ ID NO: 290

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 845 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus durans*
 (B) STRAIN: ATCC 19432

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 290

	TTTCTTTTGA	CCAATCCTTA	CCAGATATCA	ACAACGCTTT	AGTTGTTTAT	50
10	AAAAATGATG	AGAAGAAATC	GAAAGTTGTT	CTTGAAACAG	CGCTAGAATT	100
	AGGTGACGGT	GTCATCCGTA	CAATCGCGAT	GGAATCAACA	GATGGTTTAC	150
	AACGCGGAAT	GGAAGTCATT	GATACAGAAA	AAGCAATTTC	TGTACCAGTG	200
	GGTAAAGAAA	CGTTAGGTCG	TGTATTCAAT	GTATTAGGAG	ATACGATCGA	250
	TTTATCTGCA	CCTTTCCAG	AAGATGCAAA	ACGTAGCGAA	ATCCATAAAA	300
15	AAGCACCAAA	CTTTGATGAG	TTAAGTACAA	GTACTGAGAT	CCTTGAAACT	350
	GGGATCAAAG	TTATTGACTT	GCTTGCTCCT	TACTTAAAG	GTGGGAAAGT	400
	TGGATTATTC	GGTGGTGCCG	GTGTAGGTAA	AACTGTATTG	ATCCAAGAAT	450
	TGATCCATAA	TATCGCTCAA	GAACACGGTG	GTATTTCTGT	ATTTACTGGT	500
	GTTGGTGAAC	GTACACGTGA	AGGTAATGAC	CTTTATTATG	AAATGAAAGA	550
20	TTCAAGGAGTT	ATTGAAAAAA	CAGCCATGGT	GTTTGGTCAA	ATGAACGAAC	600
	CACCAGGTGC	ACGTATGCGT	GTTGCCTTGA	CTGGTTTGAC	GATTGCTGAA	650
	TACTTCCGTG	ATGTTGAAGG	GCAAGACGTG	CTATTGTTTA	TTGATAATAT	700
	TTTCCGTTTC	ACTCAAGCCG	GTTCAGAAAGT	TTCTGCCCTA	TTAGGTCGTA	750
	TGCCTTCTGC	CGTTGGGTAC	CAACCAACGC	TAGCAACAGA	AATGGGTCAA	800
25	TTACAAGAAC	GGATCACTTC	AACGAAAAAA	GGTTCAATCA	CTTCA	845

2) INFORMATION FOR SEQ ID NO: 291

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 840 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecalis*
 (B) STRAIN: ATCC 29212

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 291

45	TTAGATCAAT	CCTTACCCGA	TATTAACAAC	GCTTTAGTCG	TTTATAAAAA	50
	TGGCGAAGCA	AAACAAAAAG	TAGTACTTGA	AGTCGCTTTA	GAAC TAGGTG	100
	ATGGAGTGAT	TCGTTCTATC	GCCATGGAAT	CGACAGATGG	TTTACAACGT	150
	GGAATGGAAG	TTATCGATAC	AGGAAAATCA	ATTTCAAGTC	CTGTTGGTAA	200
	AGATACATTA	GGTCGTGTGT	TTAACGTTTT	AGGAGACACA	ATTGACTTAG	250
50	AAGCGCCATT	CCCTGCAGAT	GCTGAACGTA	GTGGGATTCA	TAAAAAAGCG	300
	CCAGCATTTG	ATGAATTAAG	TACCAAGTAAT	GAAATTTTAG	AAACAGGGAT	350
	TAAAGTTATT	GACTTATTAG	CACCTTATCT	AAAAGGTGGT	AAAGTCGGAC	400
	TTTTTCGGTGG	TGCCGGTGTT	GGTAAAACCG	TCCTTAATTCA	AGAATTAATT	450
	CATAATATTG	CCCAAGAACA	TGGAGGGATT	TCCGTCTTTA	CTGGTGTTGG	500
55	TGAACGGACA	CGTGAAGGGA	ACGATCTGTA	CTATGAAATG	AAAGATTCAG	550
	GCGTTATTGA	AAAAACAGCC	ATGGTTTTTG	GTCAAATGAA	CGAACC GCCA	600
	GGTGCACGGA	TGCGTGTTGC	CTTAAC TGGG	TTAACGATTG	CTGAATATTT	650
	CCGTGATGTG	GAAGGACAAG	ACGTGCTATT	ATTTATTGAT	AACATTTTCC	700
	GTTTCACCCA	AGCCGGTTCA	GAAGTTTCTG	CCCTTTTAGG	TCGGATGCCG	750
60	TCAGCCGTTG	GTTACCAACC	AACCTTAGCG	ACTGAAATGG	GACAATTACA	800

AGAACGGATT ACTTCAACGA AAAAAGGATC AATTACCTCT

840

5 2) INFORMATION FOR SEQ ID NO: 292

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*
 (B) STRAIN: ATCC 19434

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 292

20 TTTCTTTAGA CCAATCCTTA CCAGATATCA ACAACGCATT AGTTGTTTAT 50
 AAAAATGACG AAAATAAATC AAAAGTTGTT CTTGAAGCAG CGTTAGAATT 100
 AGGGGACGGA GTGATCCGGA CCATTGCGAT GGAATCAACA GATGGTTTAC 150
 AAAGAGGAAT GGAAGTCATT GATACAGGCA AAGCAATCTC TGTTCCCTGTA 200
 25 GGTAAGAAA CATTAGGTCG CGTATTCAAC GTACTAGGAG ATACGATCGA 250
 TTTAGAAACA CCTTTCCAG AAGATGCGGA AAGAAGCGAA ATTCATAAAA 300
 AAGCACCAGC CTTTGACGAA TTAAGTACAA GTACAGAAAT TTTGGAAACA 350
 GGGATCAAAG TTATCGATTT GCTTGCCCCA TATTTAAAAG GTGGGAAAGT 400
 CGGACTATTC GGTGGTGCCG GTGTTGGTAA AACCGTACTG ATCCAAGAAC 450
 30 TGATCCATAA TATCGCCCAA GAACATGGTG GTATTTCTGT ATTTACCGGT 500
 GTAGGTGAAC GTACTCGTGA AGGTAATGAC TTGTATTATG AAATGAAAGA 550
 TTCAGGAGTT ATCGAAAAAA CAGCCATGGT GTTCGGACAA ATGAACGAAC 600
 CACCAGGTGC ACGTATGCGT GTTGCTTTGA CTGGTTTGAC GATTGCGGAA 650
 TATTTCCGTG ATGTAGAAGG TCAAGATGTA CTGTTGTTTA TCGACAACAT 700
 35 TTTCCGTTTC ACTCAAGCTG GATCTGAAGT ATCAGCCTTG TTAGGACGGA 750
 TGCCTTCTGC GGTGTTGTTAT CAACCAACAT TGGCAACAGA AATGGGTCAA 800
 TTGCAAGAAC GTATCACATC TACGAAAAAA G 831

40 2) INFORMATION FOR SEQ ID NO: 293

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 826 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus gallinarum*
 (B) STRAIN: ATCC 49573

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 293

60 CCTTACCAGA TATCAACAAT GCGTTGATCG TTTACAAAAA AGACGAGAAA 50
 AAAACAAAAG TAGTATTGGA AGCCGCTTTA GAACTAGGGG ATGGTGTGAT 100
 CCGCACCATC GCAATGGAAT CTACAGACGG TTTGCAACGA GGAATGGAAG 150
 TCATCGATAC CGGTGCCTCA ATCTCTGTCC CTGTAGGAAC AGATACTCTA 200

	GGCCGAGTAT	TTAATGTACT	AGGCGATACT	ATCGACTTGG	AAGCACCATT	250
	CCCAGAAGAT	GCCAAACGTA	GTGGCATCCA	CAAAAAAGCC	CCAGATTTTCG	300
	ATGAATTGTC	AACAAGTACA	GAAATCCTTG	AAACTGGGAT	CAAAGTTATC	350
5	GATTTATTAG	CTCCTTACTT	AAAAGGTGGT	AAAGTCGGCT	TGTTTCGGTGG	400
	TGCCGGTGTT	GGTAAAACCG	TATTGATTCA	AGAATTGATT	CACAATATCG	450
	CTCAAGAGCA	TGGGGGAATT	TCAGTATTTA	CCGGTGTGTTG	CGAACGGACG	500
	CGTGAAGGTA	ATGACTTGTA	TTATGAAATG	AAAGAATCAG	GCGTTATCGA	550
	AAAGACAGCC	ATGGTTTTTCG	GTCAAATGAA	TGAACCACCA	GGTGCCCGGA	600
10	TGCGGGTTGC	TTTGACTGGT	TTGACCATTG	CTGAGTATTT	CCGTGACGTT	650
	GAAGGACAAG	ATGTGCTCTT	GTTTATCGAT	AATATTTTCC	GTTTCACACA	700
	AGCGGGTTCT	GAAGTATCTG	CCTTGTTAGG	CCGGATGCCA	TCAGCCGTTG	750
	GTTATCAACC	AACTCTAGCA	ACTGAAATGG	GTCAATTACA	AGAACGAATC	800
	ACTTCTACGA	AAAAAGGATC	TGTAAC			826

15

2) INFORMATION FOR SEQ ID NO: 294

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 846 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus saccharolyticus*

(B) STRAIN: ATCC 43076

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 294

	TTTCTTTGGA	CCAATCCTTA	CCAGACATCA	ACAATGCGTT	GGTGGTCTAT	50
	AAAAAGAATG	ATGAAAAAAC	AAAAGTGGTA	CTTGAAACAG	CTTTAGAACT	100
35	TGGTGATGGT	GTCGTACGTA	CGATTGCTAT	GTCGTCAACA	GACGGTTTGC	150
	AACGTGGGAT	GGAAGTCATC	GATACAGGAG	CATCAATTTC	TGTTCCCTGTT	200
	GGGAAAGAGA	CATTAGGACG	TGTATTTAAC	GTTTATAGGG	AGACTATCGA	250
	CTTAGATGGT	CCATTCCCAG	AAGAAGTAGC	ACGAGATGGT	ATTCATAAAA	300
	AGGCACCTGA	TTTTGATGAA	TTAAGTACAA	GTACGGAGAT	TCTTGAAACA	350
40	GGGATTAAAG	TAATCGATTT	ATTAGCGCCT	TACTTAAAAG	GTGGGAAAGT	400
	TGGTTTATTC	GGTGGTGCCG	GTGTAGGTAA	AACGGTATTA	ATTCAAGAAT	450
	TGATTAACAA	TATTGCGCAA	GAACATGGTG	GTATTTTCAGT	ATTTGCGGGT	500
	GTTGGTGAGC	GTACTCGTGA	AGGAAATGAC	CTTTATTATG	AAATGAAAGA	550
	GTCGGGCGTT	ATTGAGAAAA	CAGCGATGGT	TTTTGGACAA	ATGAACGAAC	600
45	CACCAGGTGC	ACGTATGCGA	GTTGCTTTAA	CTGGTTTAAC	CATTGCAGAA	650
	TACTTCCGTG	ATGTTGAAGG	ACAAGATGTA	TTACTATTTA	TTGATAACAT	700
	TTTCCGTTTT	ACTCAAGCTG	GTTCAGAAGT	TTCAGCTTTA	TTAGGACGTA	750
	TGCCTTCAGC	GGTAGGGTAT	CAACCGACAT	TAGCAACAGA	AATGGGACAA	800
50	TTACAAGAAC	GTATTACGTC	AACGAAAAAA	GGCTCAATTA	CATCAA	846

2) INFORMATION FOR SEQ ID NO: 295

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 803 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

60

(ii)MOLECULE TYPE: Genomic DNA

(vi)ORIGINAL SOURCE:

(A) ORGANISM: *Escherichia fergusonii*

(B) STRAIN: ATCC 35469

(xi)SEQUENCE DESCRIPTION: SEQ ID NO: 295

10	GCCGTACCGC	GCGTGTACGA	TGCTCTTGAG	GTGCAAAATG	GTAATGAGCG	50
	TCTGGTGTCTG	GAAGTTCAGC	AGCAGCTCGG	CGGTGGTATC	GTGCGTACCA	100
	TCGCAATGGG	GTCTCCGAC	GGTCTGCGTC	GCGGTCTGGA	TGTAAAAGAC	150
	CTCGAACACC	CGATCGAAGT	CCCGGTAGGT	AAAGCGACTC	TGGGCCGTAT	200
	CATGAACGTA	CTGGGTGAAC	CGGTGACAT	GAAAGGCGAG	ATCGGTGAAG	250
	AAGAGCGTTG	GGCGATTAC	CGCGCAGCAC	CTTCCTACGA	AGAGCTGTCA	300
15	AACTCTCAGG	AACTGCTGGA	AACCGGTATC	AAAGTTATCG	ACCTGATGTG	350
	TCCGTTCGCT	AAGGGCGGTA	AAGTCGGTCT	GTTCGGTGGT	GCGGGTGTAG	400
	GTAAACTGT	AAACATGATG	GAGCTTATTC	GTAACATCGC	GATCGAGCAC	450
	TCCGGTTACT	CTGTGTTTGC	GGGCGTAGGT	GAACGTACTC	GTGAGGGTAA	500
	CGACTTCTAC	CACGAAATGA	CTGACTCCAA	CGTTATCGAC	AAAGTATCCC	550
20	TGGTATATGG	CCAGATGAAC	GAGCCGCCGG	GAAACCGTCT	GCGCGTTGCA	600
	CTGACCGGCC	TGACCATGGC	TGAGAAATTC	CGTGACGAAG	GTCGTGACGT	650
	TCTGCTGTTT	GTTGACAACA	TCTATCGTTA	CACCCTGGCC	GGTACGGAAG	700
	TATCCGCACT	GCTGGGCCGT	ATGCCTTCAG	CGGTAGGTTA	TCAGCCGACT	750
	CTGGCGGAAG	AGATGGGCGT	TCTTCAGGAA	CGTATCACCT	CCACCAAAC	800
25	TGG					803

2) INFORMATION FOR SEQ ID NO: 296

(i)SEQUENCE CHARACTERISTICS:

(A) ~~LENGTH: 822 bases~~

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii)MOLECULE TYPE: Genomic DNA

(vi)ORIGINAL SOURCE:

(A) ORGANISM: *Escherichia hermannii*

(B) STRAIN: ATCC 33650

(xi)SEQUENCE DESCRIPTION: SEQ ID NO: 296

45	GATGCCGTAC	CGCGCGTGTA	CGATGCTCTT	GAGGTGCAAA	ATGGTGATGA	50
	GCGTCTGGTG	CTGGAAGTGC	AGCAGCAGCT	CGGCGGCGGT	ATCGTGCGTA	100
	CCATCGCAAT	GGGTTCTTCC	GACGGTCTGC	GTCGTGGTCT	GACTGTGCTC	150
	GACCTCGAGC	ACCCGATCGA	AGTCCCGGTA	GGTAAAGCGA	CCC'TGGGCCG	200
	TATCATGAAC	GTGCTGGGTC	AGCCGATCGA	CATGAAAGGC	GATATCGGTG	250
50	AAGAAGAGCG	TTGGGCGATT	CACCGCGCGG	CGCCGTCCTA	TGAAGAGCTG	300
	TCCAGCTCTC	AGGAAC'TGCT	GGAAACCGGC	ATCAAAGTTA	TCGACCTGAT	350
	GTGTCCGTTT	GCGAAGGGCG	GTAAAGTCGG	TCTGTTTCGGT	GGTGCGGGCG	400
	TAGGTAAAAC	CGTAAACATG	ATGGAGCTGA	TCCGTAACAT	CGCGATCGAG	450
	CACTCCGGTT	ACTCTGTGTT	TGCGGGCGTG	GGTGAACGTA	CTCGTGAGGG	500
55	TAACGACTTC	TACCATGAAA	TGACCGACTC	CAACGTTCTG	GACAAAGTAT	550
	CCCTGGTTTA	CGGCCAGATG	AACGAACCGC	CGGGAAACCG	TCTGCGCGTT	600
	GCACTGACCG	GCCTGACCAT	GGCTGAGAAA	TTCCGTGACG	AAGGTCGTGA	650
	CGTTCTGTTG	TTCGTGACAA	ACATCTACCG	TTACACCCTG	GCCGGTACTG	700
	AAGTATCCGC	ACTGCTGGGC	CGTATGCCTT	CTGCGGTAGG	TTACCAGCCG	750
60	ACCCTGGCGG	AAGAGATGGG	CGTTCTGCAG	GAGCGTATCA	CCTCCACCAA	800

AACCGGTTCT ATCACCTCCG TA

822

5 2) INFORMATION FOR SEQ ID NO: 297

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 808 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia vulneris*
 (B) STRAIN: ATCC 33821

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 297

20 CCGAACGTGT ACGACGCCCT CGAAGTGACA AATGGTAATG AGCGTCTGGT 50
 GCTGGAAGTT CAGCAGCAGC TCGGCGGCGG TATCGTACGT ACCATCGCTA 100
 TGGGTTCTTC CGACGGTCTG CGTCGTGGTC TGGAAAGTTCA GGACCTCGAG 150
 CACCCGATCG AAGTGCCGGT AGGTAAAAGCG ACCCTGGGTC GTATCATGAA 200
 25 CGTACTGGGT CAGCCGATCG ATATGAAAGG CGACATCGGT GAAGAAGAGC 250
 GTTGGGCTAT TCACCGTGCA GCACCGTCCT ATGAAGAGCT CTCCAGCTCT 300
 CAGGAACTGC TGGAAACCGG CATCAAGGTT ATCGACCTGA TGTGTCCGTT 350
 CGCCAAGGGC GGTAAAGTCG GCCTGTTCGG CGGCGCGGGC GTGGGTAAAA 400
 CCGTAAACAT GATGGAGCTG ATCCGTAACA TCGCGATCGA GCACTCCGGT 450
 30 TACTCCGTGT TTGCAGGCGT GGTGAGCGT ACTCGTGAGG GTAACGACTT 500
 CTACCCAGAG ATGACCGGCT CCAACGTTCT GGACAAAGTA TCCCTGGTGT 550
 ACGGCCAGAT GAACGAGCCG CCGGGAAACC GTCTGCGCGT GGCCTGACC 600
 GGCCTGACCA TGGCTGAGAA GTTCCGTGAC GAAGGTCGTG ACGTTCTGCT 650
 GTTCGTTGAC AACATCTATC GTTACACCCT GGCCGGTACG GAAGTATCTG 700
 35 CACTGCTGGG CCGTATGCCT TCAGCGGTAG GTTACCAGCC GACGCTGGCG 750
 GAAGAGATGG GCGTTCCTGCA GGAGCGTATC ACCTCCACCA AAACCGGTTT 800
 TATCACCT 808

40 2) INFORMATION FOR SEQ ID NO: 298

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 843 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Eubacterium lentum*
 (B) STRAIN: ATCC 43055

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 298

TTTCCCCCTG ATCAGCTGCC GGCGATTAC AACCGCTGA CGGTTGATGC 50
 CAAGACCCTG GCGGGCGACT TGCACCTCGT GCTCGAGGTC GAGACGCACC 100
 TGCCGGGCAA CCTTGTCGCG TCGGTGGCCA TGAGCTCGAC GGACGGTCTC 150
 60 GTCCGCGGCC TCGAGGTCGT CGACACGGGC AACCCGATCA TGATGCCCGT 200


```

GGGTCCCGAG ACCCTGGGTC GCATCTGGAA CGTCATGGGC GAGCCCGTCG 250
ACGAGAAGCC GATGCCCCGAG GTGAAGGGCT ACATGCCCAT CCACCGTCCG 300
GCTCCGGACT ACGACGAGCT GTCCACCACC ACCGAGATCT TCGAGACCGG 350
CATCAAGGCC ATCGACCTCG TCGAGCCCTT CGTCAAGGGC GGCAAGACGG 400
5 GTCTGTTCGG CGGCGCCGCG GTGGGCAAGA CGGTTATCAT CCAGGAGCTC 450
ATCAACAACC TGGCCCAGGA GCACGGCGGC ACGTCGGTGT TCACGGGCGT 500
GGGCGAGCGT ACCCGCGAGG GTACCGACCT CTACCTGGAG ATGAGCGACT 550
CGGGCGTCAT CAACAAGACC TGCCTCGTGT ACGGTCAGAT GAACGAGCCT 600
CCGGGAGCGC GTCTGCGCGT GGGTCTCGCG GGCCTCACCAG AGGCGGAGTA 650
10 CTTCCGCGAT CAGGGCCAGG ACGTGCTTCT GTTCGTGGAC AACATCTTCC 700
GCTTCACGCA GGCCGGCTCC GAGGTGTCCG CTCTGCTGGG CCGCATGCCC 750
TCTGCCGTGG GTTACCAGCC GACGCTGGCA ACCGAGATGG GCGACCTGCA 800
GGAGCGCATC ACGTCGACGT CCACCGGCTC CATCACGTCC GTG 843

```

15

2) INFORMATION FOR SEQ ID NO: 299

(i) SEQUENCE CHARACTERISTICS:

```

20 (A) LENGTH: 829 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

```

(A) ORGANISM: Ewingella americana
(B) STRAIN: ATCC 33852

```

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 299

```

TCCCTCAGGA TGCAGTACCG AACGTGTACA ATGCTCTTGA GGTAGAAAAC 50
GGTGCCTCCA AACTGGTTCT GGAAGTTCAG CAACAGTTAG GCGGCGGCGT 100
35 TGTTTCGTTGT ATCGCAATGG GTACCTCAGA CGGCCTTCGT CGCGGTCTGA 150
AAGTGAACAA CCTGGAACAC CCAATTGAAG TTCCGGTTGG TAAAGCGACT 200
CTGGGTCGTA TCATGAACGT ATTGGGTGAA CCAATCGACA TGAAAGGTGA 250
AATCGGCGAA GAAGAACGTC GTGCAATTCA CCGTCCAGCG CCTTCTTATG 300
AAGAGCTGGC TAACTCCCAA GAATTGCTGG AAACCGGTAT CAAAGTTATG 350
40 GACCTGATGT GTCCGTTTCG TAAGGGCGGT AAAGTCGGTC TGTTCGGTGG 400
TGCGGGTGTT GTAAAAC TGTAACATGAT GGAGCTGATC CGTAACATCG 450
CGATCGAGCA CTCCGGTTAC TCAGTGTGTTG CAGGCGTGGG TGAGCGTACT 500
CGTGAGGGTA ACGACTTCTA CCACGAAATG ACTGACTCCA ACGTTATCGA 550
CAAAGTTTCC CTGGTCTATG GTCAGATGAA TGAGCCACCA GGTAACCGTC 600
45 TGCGCGTTGC ACTGACCGGC CTGACCATGG CGGAGAAATT CCGTGATGAA 650
GGTCGTGACG TACTGCTGTT CGTTGACAAC ATTTACCGTT ACACCCTGGC 700
AGGTACCGAA GTGTCCGCAC TTCTGGGCCG TATGCCATCG GCGGTAGGTT 750
ATCAGCCAAC GCTGGCGGAA GAGATGGGTG CTCTGCAAGA GCGTATCACC 800
50 TCTACCAAAA GTGGTTCTAT CACCTCCGT 829

```

50

2) INFORMATION FOR SEQ ID NO: 300

(i) SEQUENCE CHARACTERISTICS:

```

55 (A) LENGTH: 805 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear
60

```

(ii)MOLECULE TYPE: Genomic DNA

(vi)ORIGINAL SOURCE:

(A) ORGANISM: *Francisella tularensis*
(B) STRAIN: LVS

(xi)SEQUENCE DESCRIPTION: SEQ ID NO: 300

	AACACGCCTA	AAGTATATGA	TGCTTTAAAT	GTAGTAGAAG	CTGGTTTAGT	50
10	ATTAGAAGTT	CAGCAACAAA	TTGGTGATGG	CGTAGTTCGT	ACAATTGCTA	100
	TGGGATCTAG	TGATGGTCTT	AGACGTGGTA	TGGAAGTTAA	GAACACAAAT	150
	GCGCCTATTT	CTGTTCCAGT	TGGACATGGC	ACACTTGGAC	GTATCATGAA	200
	TGTTTTAGGT	GAACCAATTG	ATGAAGCTGG	TCCAATTGAA	TATACTGAGA	250
	AAAGATCTAT	CCATCAAGCT	CCTCCTGCAT	ATGATGAGTT	AGCATTAAGT	300
15	ACAGAAATAT	TAGAAACAGG	TATCAAAGTA	GTTGACCTTA	TTTGTCCATT	350
	TGCTAAGGGC	GGTAAAGTTG	GTTTATTTGG	CGGTGCAGGT	GTTGGTAAAA	400
	CTGTAACGAT	GATGGAACCT	ATCAACAATA	TTGCAAAAGA	ACATAGTGGC	450
	TACTCTGTAT	TTTCCGGTGT	TGGTGAAAGA	ACTCGTGAAG	GTAATGACTT	500
	CTACTATGAG	ATGAAATATT	CTAATGTATT	GGATAAAGTA	TCATTAGTAT	550
20	ATGGTCAGAT	GAATGAGCCG	CCTGGAAACA	GATTAAGAGT	AGCTCTTAGT	600
	GGCTTAACAA	TAGCAGAAGG	ATTCCGTGAT	GAAAAGCGTG	ATGTTTTGAT	650
	GTTTATCGAT	AACATCTATC	GTTATACATT	AGCAGGTACA	GAGGTATCGG	700
	CGCTACTTGG	TCGTATGCCA	TCTGCTGTGG	GTTATCAGCC	AACGCTTGCA	750
	GCTGAGATGG	GTGCTTTACA	GGAGCGTATT	ACATCTACTA	AGACAGGATC	800
25	TATTA					805

2) INFORMATION FOR SEQ ID NO: 301

(i)SEQUENCE CHARACTERISTICS:

(A) LENGTH: 825 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii)MOLECULE TYPE: Genomic DNA

(vi)ORIGINAL SOURCE:

(A) ORGANISM: *Fusobacterium gonidiaformans*
(B) STRAIN: ATCC 25563

(xi)SEQUENCE DESCRIPTION: SEQ ID NO: 301

45	GACGAATTGC	CAAAAATATA	CAATGCATTA	AAGGTGCAAG	TTGGAGAAAA	50
	AGAACTTGTA	TTGGAAGTGC	AACAACATTT	GGGAAATAAT	GTTGTGAGAA	100
	CAGTAGCGAT	GGACTCAACA	GATGGATTGC	TTCGAGGAAT	GGAAGTAATG	150
	GATACCGGAG	CACCGATTAC	TGTTCCAGTA	GGGAAGGCGG	TTTTAGGAAAG	200
	AATATTGAAT	GTTTTGGGAG	AGCCTGTGGA	TCAAAAAGGG	CCTGTGGAAA	250
50	CAGAAGAATA	TTTACCTATC	CATAGAGAAG	CACCAAAATT	TGAAGAACAA	300
	GAAACAGTAA	CAGAAATTTT	TGAAACAGGA	ATTAAAGTCA	TAGATTTGTT	350
	AGCCCCTTAT	ATCAAAGGAG	GAAAGACAGG	TCTATTCGGT	GGAGCCGGAG	400
	TAGGGAAAAC	AGTTTTAATT	ATGGAATTAA	TTAATAACAT	TGCAAAGGGC	450
	CACGGAGGAA	TTTCTGTGTT	TGCAGGAGTT	GGAGAAAGAA	CAAGAGAAGG	500
55	AAGAGATTTA	TACAACGAAA	TGACAGAGTC	CGGAGTTTGT	AATAAGACCT	550
	CGTTGGTGTA	TGGTCAAATG	AATGAGCCGC	CCGGAGCAAG	ACTTCGTGTG	600
	GCGTTGACAG	GATTAAACGGT	TGCTGAAAAC	TTTAGAGATA	AAGAAGGGCA	650
	AGATGTATTG	TTGTTTATCG	ACAATATCTT	CCGTTTCACA	CAAGCAGGAT	700
	CAGAAGTATC	GGCTCTATTG	GGAAGAATTC	CATCGGCAGT	AGGATATCAA	750
60	CCGAACCTAG	CGACAGAAAT	GGGAACCTTA	CAAGAAAGAA	TTACTTCTAC	800

AAAATCAGGA TCTATCACTT CGGTA

825

5 2) INFORMATION FOR SEQ ID NO: 302

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 806 bases
 (B) TYPE: Nucleic acid
 10 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Fusobacterium necrophorum* subsp. *necrophorum*
 (B) STRAIN: ATCC 25286

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 302

20 ACAATGCATT AAAGGTACAG GTGGGAGAAA GGGAACTTGT GTTGGGAAGTG 50
 CAGCAACATT TAGSAAATAA TGTTGTCAGA ACAGTAGCAA TGGATTCAAC 100
 AGACGGATTA CTTCGGGGAA TGGAAGTGAG AGATACAGGA GTTCCCATT 150
 CTGTTCCGGT AGGAAAGGCG GTTTTGGGAA GAATATTAAA TGTCTTAGGG 200
 25 GAGCCTGTGG ACGAAAAGG TCCGATAGAG ACAGAAGAAT ATTTACCAAT 250
 ACATAGAGAA GCACCGAAAT TTGAAGAACA GGAAACGGTG ACAGAAATTT 300
 TTGAAACAGG AATTAAAGTC ATTGATTGTG TAGCTCCTTA TATTAAAGGA 350
 GGAAAAACAG GCCTATTCGG AGGAGCCGGA GTAGGAAAAA CCGTTTTGAT 400
 TATGGAAGTG ATCAATAATA TTGCAAAAGG TCATGGAGGA ATTTCTGTTT 450
 30 TTGCAGGAGT TGGAGAAAGA ACGAGAGAGG GAAGAGATCT ATACAACGAA 500
 ATGACAGAGT CCGGAGTTTT GAATAAAACT TCTTTGGTAT ATGGGCAAAT 550
 GAATGAGCCG CCCGGAGCAA GACTTCGAGT GGCTTTAACC GGACTTACTG 600
 TTGCCGAAAA TTTCAGAGAT AAAGAGGGAC AGGATGTCTT ATTGTTTATT 650
 GACAATATTT TCCGTTTCAC ACAAGCAGGT TCGGAAGTAT CGGCACTTTT 700
 35 GGGGAGAATT CCTTCTGCAG TGGGATATCA ACCGAAC TTG GCGACAGAAA 750
 TGGGAAGCTT ACAAGAAAGA ATTACTTCTA CAAAATCCGG TTCTATCACT 800
 TCCGTG 806

40 2) INFORMATION FOR SEQ ID NO: 303

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 821 bases
 45 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Fusobacterium nucleatum* subsp. *polymorphum*
 (B) STRAIN: ATCC 10953

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 303

GATGAATTGC CTGCAATATA TAATGCTTTA AAAGTAAAT TAGAAGATAA 50
 GGAAGTTGTT CTAGAAGTTG AACACATCT TGGTAACAAT GTTGTAAAGAA 100
 CTGTTGCTAT GGATTCAACT GATGGATTAA AAAGAGGAAT GGAAGTTATA 150
 60 GATACAGGTA AACCAATTAC AGTACCAGTT GGTAAAGCTG TTCTTGGTAG 200

AATATTAAAT GTTTTAGGAG AACCTGTTGA TAATCAAGGT CCTATAAATG 250
 CTGAAACATT TTTACCTATT CATAGAGAAG CACCAGAATT TGATGACTTA 300
 GAAACTGAAA CTGAAATATT TGAAACAGGA ATAAAAGTTA TAGACTTATT 350
 AGCACCATAT ATTAAAGGTG GAAAAATAGG ATTATTTGGT GGAGCTGGAG 400
 5 TAGGAAAAAC AGTTTTAATA ATGGAACCTA TCAACAACAT TGCAAAAGGA 450
 CATGGAGGAA TTTCAGTTTT TGCAGGAGTT GGAGAAAGAA CAAGAGAAGG 500
 TAGAGACTTA TATGGTGAAA TGACTGAATC AGGAGTTATC ACAAAAACAG 550
 CTCTTGTTTA TGGACAAATG AATGAGCCAC CTGGAGCAAG ACTTAGAGTT 600
 GCATTAACAG GGCTTACTGT TGCAGAAAAC TTTAGAGATA AAGATGGGCA 650
 10 AGATGTTCTT CTATTTATAG ATAATATATT TAGATTTACA CAAGCAGGTT 700
 CAGAAGTTTC AGCTTTACTT GGAAGAATAC CATCAGCTGT TGGATATCAA 750
 CCAAACCTAG CAACTGAAAT GGGTGCTTTA CAAGAAAGAA TAACATCTAC 800
 AAAATCTGGT TCAATTACAT C 821

15

2) INFORMATION FOR SEQ ID NO: 304

(i) SEQUENCE CHARACTERISTICS:
 20 (A) LENGTH: 864 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Gardnerella vaginalis*
 (B) STRAIN: ATCC 49145

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 304

TTCCCAGTTG GCTATCTTCC AGATATTTAT AATGCTCTCA AGGTTGATAT 50
 CAACACCGTT GGAAACACGG AGGGAGATAC CGTCCACGAG ATTACATTGG 100
 35 AAGTTGAGCA GCACCTTGTT GATTCAACTG TGCGAGCAGT GGCACCTAAG 150
 CCTACGGACG GCTTGGTCCG TGGTGCTTTA GTGCGAGATA CTGGTGGCCC 200
 AATTTCTGTG CCTGTTGGAG ATGTTACAAA AGGTCACGTT TTTGACGTAA 250
 CTGGTAACAT TTAAACGCT AAACCAGGCG AAAACATTGA GGTGACCGAG 300
 CGCTGGCCAA TCCACCGCAA CCCACCTGCT TTCGATCAGC TTGAGTCTAA 350
 40 GACTCAAAATG TTTGAAACAG GCATTAAGGT TATCGATTTG CTTACGCCCTT 400
 ACGTTCAGGG CGGAAAGATT GGTCTGTTCC GTGGTGCAGG CGTTGGTAAA 450
 ACTGTGTTGA TTCAGGAGAT GATTACGCG GTTGACAGA ACCACGGCGG 500
 TGTGTCTGTG TTTGCTGGCG TTGGCGAACG TACTCGTGAG GGTAACGATT 550
 TGATTGGCGA AATGGCTGAG GCTGGCGTTT TGGAGAAAAC AGCGCTTGTC 600
 45 TTTGGTTCAGA TGGATGAGCC TCCTGGGACT CGTCTTCGTG TGCCTCTTAC 650
 TGCTTTGACT ATGGCTGAGT ATTTCCGTGA TGTTTCAGAA CAGGATGTGT 700
 TGCTGTTTAT CGACAACATC TTCCGCTTTA CTCAGGCAGG TTCTGAGGTT 750
 TCCACGTTGC TTGGTCGTAT GCCTTCTGCA GTTGGTTATC AGCCAACTT 800
 GCGGATGAA ATGGGTGCGT TGCAGGAGCG CATTACTTCT ACGCGCGGTC 850
 50 ATTCTATTAC GTCG 864

2) INFORMATION FOR SEQ ID NO: 305

55

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 848 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 60 (D) TOPOLOGY: Linear

(ii)MOLECULE TYPE: Genomic DNA

(vi)ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Gemella haemolysans*
 (B) STRAIN: ATCC 10379

(xi)SEQUENCE DESCRIPTION: SEQ ID NO: 305

10	TCGAATCAGG	GCATATGCCA	AATCTATTAA	ACGCTTTAGA	AGTTTACATA	50
	GAAAAAGGCG	ATGGGAAAAA	AGAAAAATTA	GTTCTTGAAG	TTTCTCTTGA	100
	AATTGGTGAT	AACGTAGTAA	GAACAATCGC	TATGTCATCT	ACTGATGGAT	150
	TAAATAGGGG	AGCAGAAGTA	GTAGATACAG	GAGCACCAAT	TACAGTTCCT	200
	GTAGGTAAC	ACACATTAGG	TCGTGTGTTC	AACGTATTAG	GTGAAGCAGT	250
15	TGACCACGGT	GAAGAAGCAG	GAGCAGAAGT	TCGTAAAGAT	TCAATTCACA	300
	AAGAAGCTCC	AACATTTCGAT	GAATTATCAA	CTCACGTTGA	GGTTCCTGAA	350
	ACAGGTATTA	AAGTTATCGA	CTTACTTGCA	CCATATATTA	AAGGTGGTAA	400
	AATCGGTCTT	TTCCGTTGGT	CGGGAGTTGG	TAAAACGGTT	CTTATCCAAG	450
	AATCTATCAA	CAACGTTGCG	CAACAACACG	GTGGATTATC	AGTATTCACA	500
20	GGTGTAGGTG	AGCGTACTCG	TGAAGGAAAT	GACTTATACT	ATGAAATGAA	550
	AGATTCTGGT	GTTATTAAAC	AAACAGCCAT	GGTATTCGGA	CAAATGAACG	600
	AACCACCAGG	TGCTCGTATG	CGTGTAGCAT	TAACAGGATT	AACAATGGCG	650
	GAATACTTCC	GTGATGAAGA	AGGACAAGAC	GTGCTTCTAT	TCATCGATAA	700
	CATTTTCCGT	TTCACACAAG	CAGGTTCTGA	GGTTTCTGCG	TTATTAGGAC	750
25	GTATGCCATC	AGCCGTTGGT	TACCAACCAA	CACTTGCTAC	AGAGATGGGA	800
	CGTTTACAAG	AACGTATAAC	ATCAACTAAA	AAAGGTTCTG	TTACATCT	848

30 2) INFORMATION FOR SEQ ID NO: 306

(i)SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 848 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii)MOLECULE TYPE: Genomic DNA

40 (vi)ORIGINAL SOURCE:

- (A) ORGANISM: *Gemella morbillorum*
 (B) STRAIN: ATCC 27824

(xi)SEQUENCE DESCRIPTION: SEQ ID NO: 306

45	TCGAATCAGG	GCATATGCCT	AATCTACTAA	ACGCTTTAGA	AGTTTATATA	50
	GAAAAAGGCG	ATGGAAAAAA	AGAAAAATTA	GTTCTTGAAG	TTTCTCTTGA	100
	AATCGGGGAT	AATGTCGTAA	GAACTATTGC	GATGTCATCT	ACTGATGGAT	150
	TAAACAGAGG	GGCAGAAGTA	GTTGATACTG	GAGCGCCAAT	TACAGTGCCA	200
50	GTAGGTAAC	ATACATTAGG	ACGTGTGTTC	AACGTATTAG	GTGAAGCAGT	250
	TGACCACGGA	GAAGAAGCTG	GAGCAGAAGT	TCAAAAAGAA	TCTATTCATA	300
	AAGAAGCTCC	AACTTTCGAA	GAATTATCAA	CACATGTTGA	GGTATTAGAA	350
	ACAGGTATTA	AAGTTATCGA	CCTTCTTGCA	CCATATATTA	AAGGTGGTAA	400
	GATTGGACTA	TTCCGTTGGT	CTGGAGTTGG	GAAAACAGTT	CTTATCCAAG	450
55	AAC TTATTA	CAACGTAGCA	CAACAACACG	GAGGACTTTC	AGTATTTACT	500
	GGGGTAGGTG	AACGTACTCG	TGAGGGTAAC	GACTTGTA	ATGAAATGAA	550
	AGACTCTGGA	GTTATTAATA	AAACTGCCAT	GGTATTTGGT	CAAATGAATG	600
	AGCCACCAGG	TGCACGTATG	CGTGTTGCCT	TAACAGGATT	AACAATGGCA	650
	GAGTACTTCC	GTGATGAAGA	AGGACAAGAC	GTACTATTAT	TTATCGATAA	700
60	TATCTTCCGT	TTCACACAAG	CAGGGTCTGA	GGTATCTGCA	TTATTAGGGC	750

GTATGCCTTC	AGCCGTTGGA	TATCAACCAA	CTCTTGCAAC	AGAAATGGGA	800
CGTCTTCAAG	AACGTATTAC	ATCAACTAAA	AAAGGATCTG	TTACATCT	848

5

2) INFORMATION FOR SEQ ID NO: 307

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 813 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Haemophilus ducreyi*
 (B) STRAIN: DSM 8925

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 307

GATGCAGTAC	CAAAAGTATA	TGATGCTTTA	AAAGTTGAAT	CAGGTTTAAC	50
CTTAGAAGTT	CAACAACAAT	TAGGTGGTGG	TTTAGTACGT	TGTATCGCAT	100
TAGGTACCTC	AGATGGTTTA	AAGCGTAGCT	TAAAGGTTGT	AAATACAGGT	150
25 AACCCTATTC	AAGTTCCTGT	AGGCACTAAA	ACATTAGGCC	GTATTATGAA	200
TGTATTAGGC	GAACCAATTG	ATGAAAAAAG	ACCTATTAGC	GAAGAAGCTC	250
GTTGGGATAT	TCATCGTGCG	GCTCCAAATT	ATGAAGAACA	GTCAAATAGT	300
ACTGAATTAC	TTGAAACCGG	TATCAAAGTT	ATTGACTTAA	TTTGTCCATT	350
TGCAAAAGGT	GGTAAAGTCG	GCTTATTTGG	TGGAGCTGGT	GTAGGTAAAA	400
30 CCGTTAATAT	GATGGAATTG	ATCCGTAATA	TTGCTATTGA	GCACTCAGGT	450
TATTCGGTTT	TTGCTGGTGT	AGGTGAGCGT	ACTCGTGAAG	GTAATGATTT	500
TTATCATGAA	ATGACGGATT	CTAATGTATT	AGATAAAGTA	TCACTAGTAT	550
ATGGTCAAAT	GAATGAACCA	CCAGGTAACC	GCCTACGTGT	TGCGTTAACA	600
GGTTTAACTA	TGGCTGAAAA	ATTCCGTGAT	GAAGGTCGTG	ATGTATTATT	650
35 TTTCGTAGAT	AATATTTATC	GTTATACTTT	AGCCGGTACA	GAAGTTTCTG	700
CTTTATTAGG	CCGTATGCCA	TCAGCGGTAG	GTTATCAACC	AACCCTTGCA	750
GAAGAAATGG	GTGTATTACA	AGAACGTATT	ACCTCAACTA	AAACTGGTTC	800
AATCACGGCA	GTA				813

40

2) INFORMATION FOR SEQ ID NO: 308

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 826 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Haemophilus haemolyticus*
 (B) STRAIN: ATCC 33390

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 308

TGAATTTCCA	CAAGATGCAG	TGCCAAAAGT	TTACGATGCA	TTAAAAGTTG	50
AATCAGGTTT	AACACTTGAG	GTGCAACAAC	AATTAGGTGG	CGGTGTGGTA	100
60 CGTTGTATCG	CATTAGGTGC	TTCTGACGGT	TTAAAACGTG	GTTTAAAAGT	150

```

AGAAAACACG AATGATCCGA TTCAAGTACC GGTAGGCACA AAAACCCTTG 200
GTCGTATCAT GAATGTATTG GGTGAACCAA TTGACGAACA AGGTCCAATC 250
GGTGAAGAAG AGCGTTGGGC TATCCATCGT TCTGCACCAA GCTATGAAGA 300
ACAATCAAAC AGTACGGAAT TATTAGAGAC TGGTATCAAA GTTATCGACT 350
5 TAATTTGTCC ATTCGCAAAA GGTGGTAAAG TTGGTCTATT CGGTGGTGCG 400
GGTGTAGGTA AAACCGTTAA CATGATGGAA TTAATCCGTA ACATCGCGAT 450
CGAGCACTCA GGTACTCCG TATTTGCGGG TGTAGGTGAA CGTACTCGTG 500
AAGGTAACGA CTTCTATCAT GAAATGAAAG ATTCTAACGT ATTAGATAAA 550
GTATCTTTGG TTTATGGTCA GATGAATGAG CCACCAGGTA ACCGTTTACG 600
10 TGTTGCGTTA ACTGGTTTAA CCATGGCAGA AAAATTCCGC GATGAAGGTC 650
GTGATGTATT ATTCTTCGTG GATAATATCT ATCGTTATAC CCTTGCTGGT 700
ACGGAAGTAT CTGCGTTATT AGGTCGTATG CCATCTGCGG TAGGTTACCA 750
ACCAACTCTT GCTGAAGAAA TGGGTGTGTT ACAAGAACGT ATCACTTCAA 800
CCAAAACAGG TTCTATTACA TCTGTA 826
15

```

2) INFORMATION FOR SEQ ID NO: 309

```

20 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 809 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear
25 (ii) MOLECULE TYPE: Genomic DNA
    (vi) ORIGINAL SOURCE:
    (A) ORGANISM: Haemophilus parahaemolyticus
30 (B) STRAIN: ATCC 10014
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 309

```

```

35 GATGCAGTAC CAAAAGTATA TGATGCGTTA AAAGTTGAAT CAGGTTTAAC 50
GCTTGAAGTT CAACAACAAT TAGGCGGTGG CTTAGTGCGC TGTATCGCAT 100
TAGGTACGTC TGATGGTTTA AAACGTGGCT TAAAAGTAGA AAATACAGGC 150
AACCCAATTG AAGTGCCAGT GGGCACTAAA ACCCTTGGTC GTATTATGAA 200
CGTATTGGGT GAGCCGATTG ACGAAAAAGG TCCTATCGGT GAAGAAGCAC 250
GCTGGGCAAT CCACCGTGCA GCACCAAGCT ACGAAGAGCA ATCAAATAGC 300
40 ACGGAATTAC TCGAAACAGG TATCAAAGTT ATCGACTTAA TCTGCCCATT 350
CGCAAAAAGG GGTAAAGTTG GTTTATTTGG TGGTGCAGGT TAGGTAAAAA 400
CCGTAAATAT GATGGAGTTA ATCCGTAACA TCGCGATCGA ACACTCTGGT 450
TACTCTGTAT TTGCAGGGGT AGGTGAGCGT ACTCGTGAAG GTAATGACTT 500
CTACCACGAA ATGACAGACT CTAACGTATT AGATAAAGTA TCGTTAGTGT 550
45 ATGGTCAAAT GAACGAACCA CCAGGTAACC GTTTACGCGT AGCTTTAACA 600
GGCTTAACCA TGGCGGAAAA ATTCGCGGAT GAAGGTCGTG ACGTATTATT 650
CTTCGTCGAT AACATCTACC GTTATACCTT AGCAGGTACG GAAGTGTCAG 700
CACTTCTCGG TCGTATGCCA TCTGCGGTAG GTTATCAGCC AACCTTAGCA 750
GAAGAAATGG GTGTATTACA AGAGCGTATC ACTTCAACCA AAAGTGGTTC 800
50 TATCACCTC 809

```

2) INFORMATION FOR SEQ ID NO: 310

```

55 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 824 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
60 (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Haemophilus parainfluenzae*
(B) STRAIN: ATCC 7901

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 310

10	CGAATTTC	CAAGATGC	TACCAAAAGT	TTATGATGCA	TTAAAAGTTG	50
	AATCGGGT	TAAACCTTGAA	GTTCAACAAC	AATTAGGTGG	TGGTGTGGTA	100
	CGTTGTAT	CGCACTGGGAGC	TTCTGACGGT	TTAAAACGCA	GTTTAAGCGT	150
	TGAAAATAC	CAATAAACCAA	TTTCAGTACC	GGTTGGTGTA	AAAACCTCTCG	200
	GTCGTATT	TATGAACGTATTG	GGCGAACC	GAAGTTGATG	AGGTCCCTATC	250
15	GGTGC	GGAAG	AAGAATGGGC	AATTCACCGT	TCTACTCCAA	300
	ACAGTCCA	ACAGTACCGAAT	TATTAGAAAC	CGGTATCAAA	GTTATCGACT	350
	TAATTTGT	CCATTTCGCGAAG	GGTGGTAAAG	TTGGTTTATT	CGGTGGTGCG	400
	GGTGTAGG	TATAGACCGTAA	TATGATGGAA	TTAATCCGTA	ATATTGCGAT	450
	TGAGCACT	CAAGGTTACTCCG	TATTTGCCCG	TGTAGGTGAG	CGTACCCCGTG	500
20	AAGGTAAC	GAACTTCTACCAT	GAAATGACAG	AATCTAACGT	ATTAGACAAA	550
	GTATCCCT	AGCACTTTACGACA	AATGAATGAG	CCGCCGGGTA	ACCGTTTACG	600
	TGTTGCTT	TAAACCGGTTTAA	CCATGGCAGA	AAAATTCCGT	GACGAAGGTC	650
	GTGATGTAT	TATCTTCTCGTG	GATAACATCT	ATCGTTATAC	CCTTGCAGGG	700
	ACTGAAGT	ATATCGGCACTTTT	AGGCCGTATG	CCATCAGCGG	TAGGTTATCA	750
25	GCCGACAC	TTGCAGAAAGAA	TGGGTGTGTT	ACAAGAACGT	ATTACATCAA	800
	CCAAAACAG	GTTCTATTACT	TCTG			824

30 2) INFORMATION FOR SEQ ID NO: 311

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 811 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Hafnia alvei*
(B) STRAIN: ATCC 13337

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 311

45	GCCGTGCCTA	AAGTGTATAA	CGCACTTGAG	GTGAAAGGCG	GTGCCACTAA	50
	ACTGGTACTG	GAAGTTCAGC	AGCAGCTAGG	CGGCGGCGTT	GTACGCTGTA	100
	TCGCTATGGG	TACTTCTGAC	GGTCTGCGTC	GCGGACTGGA	CGTTGTTGAC	150
	CTGGAGCACC	CGATTGAAGT	CCCAGTAGGT	AAAGCGACCT	TAGGCCGCAT	200
50	TATGAACGTA	CTGGGTGAGC	CAATTGATAT	GAAGGGTGAT	ATCGGCGAAG	250
	AAGATCGCTG	GGCTATTTCAC	CGTGAAGCTC	CAAGCTACGA	AGAACTGTCT	300
	AACTCGCAAG	AACTGCTGGA	AACTGGTATC	AAGGTAATGG	ACCTGATTTG	350
	TCCGTTTCGCT	AAGGGCGGTA	AAGTTGGTCT	GTTCCGGTGGT	GCGGGTGTTG	400
	GTAACACAGT	AAACATGATG	GAGCTGATCC	GTAACATCGC	GATCGAGCAC	450
55	TCAGGTTACT	CTGTATTTGC	CGGCGTGGGT	GAACGTACTC	GTGAGGGTAA	500
	CGACTTCTAC	CACGAAATGA	CCGACTCCAA	CGTATTGGAC	AAAGTATCAC	550
	TGGTTTATGG	CCAGATGAAC	GAGCCACCAG	GAAACCGTCT	GCGCGTTGCG	600
	CTGACCGGTC	TGACTATGGC	TGAGAAGTTC	CGTGACGAAG	GTCGTGACGT	650
	ACTGCTGTTC	ATCGATAACA	TCTACCGTTA	TACCTTGGCC	GGTACCGAAG	700
60	TATCTGCACT	GTTGGGTCGT	ATGCCTTCTG	CGGTAGGTTA	TCAGCCAACG	750

CTGGCGGAAG AGATGGGTGT TCTGCAAGAA CGTATCACCT CGACCAAAAC 800
GGGTTCAATC A 811

5

2) INFORMATION FOR SEQ ID NO: 312

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 831 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Kingella kingae*
(B) STRAIN: ATCC 23330

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 312

GCGATGCTAT TCCACGCGTT TACGATGCGT TGAAACTGGT TGATGTGGAC 50
TTGACATTAG AAGTGCAACA ACAACTGGGC GATGGCGTAG TGCCTACCAT 100
TGCGATGGGT AGTACCGATG GTTTGAAACG CGGCTTAGCC GTGAACAACA 150
25 CAGGCGCACC TATTACAGTG CCTGTTGGTA AAGCAACATT GGGTCGTATT 200
ATGGACGTAT TGGGTAATCC TGTTGATGAA GCAGGTCCAA TTGGTTCTGA 250
CCAAACGCGT GCTATTCACC AACCAGCTCC TAAATTTGAT GAACTGTCTA 300
GCGCAACCGA ATTGCTGGAA ACAGGCATCA AAGTGATTGA CTTGCTTTGC 350
CCATTTGCAA AAGGTGGTAA AGTAGGTTTG TTTGGTGGTG CAGGTGTGGG 400
30 CAAAACTGTG AACATGATGG AGTTGATTAA CAACATTGCC AAAGCGCACA 450
GTGGTTTGTC TGTATTTGCA GGCGTGGGTG AACGTACTCG CGAAGGTAAT 500
GACTTCTATC ACGAGATGAA AGATTCTAAC GTGTTGGATA AAGTTGCCAT 550
GGTGTATGGT CAAATGAATG AACCTCCTGG CAACCGTTTG CGCGTTGCAT 600
TGACTGGTTT GTCTATGGCA GAACACTTCC GTGATGAAAA AGACGAAAAT 650
35 GGCAAGGTC GCGATGTATT GTTCTTTGTG GACAACATCT ATCGCTACAC 700
ATTGGCAGGT ACAGAAGTAT CGGCATTGCT GGGTCGTATG CCCTCTGCGG 750
TAGGTTATCA ACCAACATTG GCAGAAGAAA TGGGTCGTTT GCAAGAGCGT 800
ATTACTTCAA CGCAAACAGG TTCGATTACT T 831

40

2) INFORMATION FOR SEQ ID NO: 313

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 812 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae* subsp. *ozaenae*
(B) STRAIN: ATCC 11296

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 313

ATGCCGTACC ACGCGTGTAC GAAGCCCTTG AGGTACAGAA TGGTAATGAA 50
GTTCTGGTGC TGGAAGTTCA GCAGCAGCTG GGCGGCGGTA TCGTACGTAC 100
60 CATCGCCATG GGTTCCTCTG ATGGTCTGCG CCGCGGTCTG GATGTAAAAG 150

	ACCTCGAGCA	CCCGATCGAA	GTCCCGGTAG	GTAAAGCAAC	GCTGGGTCGT	200
	ATCATGAACG	TACTGGGTAC	ACCGGTTGAC	ATGAAAGGCG	ACATCGGCGA	250
	AGAAGAGCGT	TGGGCTATCC	ACCGCGCGGC	ACCGTCCTAT	GAAGAGCTGT	300
	CCAGCTCTCA	GGAAGTCTG	GAAACCGGCA	TCAAAGTTAT	CGACCTGATG	350
5	TGTCCGTTTC	CCAAGGGCGG	TAAAGTTGGT	CTGTTCCGGC	GTGCGGGTGT	400
	AGGTAAAAC	GTAAACATGA	TGGAGCTGAT	CCGTAACATC	GCGATCGAGC	450
	ACTCCGGTTA	CTCTGTGTTT	GCGGGCGTAG	GTGAGCGTAC	TCGTGAGGGT	500
	AACGACTTCT	ACCACGAAAT	GACCGACTCC	AACGTTATCG	ATAAAGTATC	550
	CCTGGTGTAC	GGCCAGATGA	ACGAGCCGCC	GGGAAACCGT	CTGCGCGTTG	600
10	CGCTGACCGG	CCTGACCATG	GCTGAGAAAT	TCCGTGACGA	AGGTCGTGAC	650
	GTACTGCTGT	TCGTCGATAA	CATCTATCGT	TACACCCTGG	CCGGTACTGA	700
	AGTATCCGCG	CTGCTGGGTC	GTATGCCTTC	AGCGGTAGGT	TATCAGCCGA	750
	CCCTGGCGGA	AGAGATGGGC	GTTCTGCAGG	AACGTATCAC	CTCCACCAAA	800
15	ACCGGTTCTA	TC				812

2) INFORMATION FOR SEQ ID NO: 314

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 812 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella ornithinolytica*
 (B) STRAIN: ATCC 31898

~~--- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 314~~

	ATGCCGTACC	GCGCGTGTAC	GATGCTCTTG	AGGTACAGAA	TGGTAATGAG	50
35	AGCCTGGTGC	TGGAAGTTCA	GCAGCAGCTC	GGCGGTGGTA	TCGTACGTGC	100
	TATCGCCATG	GGTTCTTCCG	ACGGTCTGCG	TCGTGGTCTG	GAAGTTAAAG	150
	ACCTTGAGCA	CCCGATCGAA	GTCCCGGTTG	GTAAAGCAAC	GCTGGGTCGT	200
	ATCATGAACG	TGCTGGGTCA	GCCAATCGAT	ATGAAAGGCG	ACATCGGCGA	250
40	AGAAGAGCGT	TGGGCTATTC	ACCGTGACGC	TCCGTCTTAT	GAAGAGCTGT	300
	CCAGCTCTCA	GGAAGTCTG	GAAACCGGCA	TCAAAGTTAT	CGACCTGATG	350
	TGTCCGTTTC	CTAAGGGCGG	TAAAGTTGGT	CTGTTCCGGT	GTGCGGGTGT	400
	AGGTAAAACC	GTAAACATGA	TGGAGCTGAT	CCGTAACATC	GCGATCGAGC	450
	ACTCCGGTTA	CTCCGTGTTT	GCGGGCGTAG	GTGAACGTAC	TCGTGAGGGT	500
	AACGACTTCT	ACCACGAAAT	GACCGACTCC	AACGTTCTGG	ATAAAGTATC	550
45	CCTGGTTTTAT	GGCCAGATGA	ACGAGCCGCC	GGGAAACCGT	CTGCGCGTTG	600
	CTCTGACCGG	CCTGACCATG	GCTGAGAAAT	TCCGTGACGA	AGGTCGTGAC	650
	GTTCTGCTGT	TCGTCGATAA	CATCTATCGT	TATACCCTGG	CCGGTACTGA	700
	AGTATCCGCA	CTGCTGGGTC	GTATGCCTTC	AGCGGTAGGT	TATCAGCCGA	750
50	CCCTGGCGGA	AGAGATGGGT	GTTCTGCAGG	AACGTATCAC	CTCCACCAAA	800
	ACCGGTTCTA	TC				812

2) INFORMATION FOR SEQ ID NO: 315

55 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 813 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 60 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Klebsiella oxytoca*
 (B) STRAIN: ATCC 33496

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 315

```

10 GTACCGCGCG TGTACGAGGC TCTTGAGGTA CAAAATGGTA GTGAGAATCT      50
   GGTGCTGGAA GTTCAGCAGC AGCTCGGCGG CCGTATTGTT CGTACCATCG      100
   CCATGGGTTT TTCCGACGGT CTGCGTCGCG GTCTGGAAGT CAAAGACCTC      150
   GAGCATCCGA TCGAAGTCCC GGTAGGTAAA GCAACGCTGG GTCGTATCAT      200
   GAACGTACTG GGCCAACCGG TAGACATGAA AGGCGACATC GGCGAAGAAG      250
15 AGCGTTGGGC GATTACCCGC GCAGCGCCTT CCTACGAAGA GTTGTCAAAC      300
   TCTCAGGAAC TGCTGGAAAC CGGCATCAAA GTTATCGACC TGATGTGTCC      350
   GTTTGCGAAG GGCGGTAAAG TTGGTCTGTT CCGTGGTGCG GGTGTAGGTA      400
   AAACCGTAAA CATGATGGAG CTGATCCGTA ACATCGCGAT CGAGCACTCC      450
   GGTTACTCCG TGTTCGCGG CGTAGGTGAA CGTACTCGTG AGGGTAACGA      500
20 CTTCTACCAC GAAATGACCG ACTCCAACGT TATCGATAAA GTATCCCTGG      550
   TGTATGGCCA GATGAACGAG CCGCCGGGAA ACCGTCTGCG CGTTGCGCTG      600
   ACCGGCCTGA CCATGGCTGA GAAGTTCCTG GACGAAGGTC GTGACGTTCT      650
   GCTGTTTCGTC GATAACATCT ATCGTTACAC CCTGGCCGGT ACTGAAGTAT      700
   CCGCACTGCT GGGTCGTATG CCTTCAGCGG TAGGTTACCA GCCGACTCTG      750
25 GCGGAAGAGA TGGGCGTTCT GCAGGAACGT ATCACCTCCA CCAAACGGG      800
   TTCTATCACT TCC                                     813

```

30 2) INFORMATION FOR SEQ ID NO: 316

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 822 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 40 (A) ORGANISM: *Klebsiella planticola*
 (B) STRAIN: ATCC 33531

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 316

```

45 GATGCCGTAC CGCGCGTGTA CGATGCTCTT GAGGTACAGA ATGGTAATGA      50
   GAGCCTGGTG CTGGAAGTTC AGCAGCAGCT CGGCGGTGGT ATCGTACGTG      100
   CTATCGCCAT GGGTTCTTCT GACGGTCTGC GTCGTGGTCT GGAAGTTAAA      150
   GACCTTGAGC ACCCGATCGA AGTCCCAGTT GGTAAAGCAA CGCTGGGTCTG      200
50 TATCATGAAC GTGCTGGGTC AGCCGATCGA TATGAAAGGC GACATCGGCG      250
   AAGAAGAGCG TTGGGCTATT CACCGCGCAG CTCCGTCTTA TGAAGAGCTG      300
   TCCAGTTCTC AGGAACTGCT GGAAACCGGC ATCAAAGTTA TCGACCTGAT      350
   GTGTCCGTTT GCTAAGGGCG GTAAAGTAGG TCTGTTCCGT GGTGCGGGCG      400
   TAGGTAAAAC CGTAAACATG ATGGAGCTGA TCCGTAACAT CGCGATCGAG      450
55 CACTCCGGTT ACTCCGTGTT TGCGGGCGTC GGTAACGTA CTCGTGAGGG      500
   TAACGACTTC TACCACGAAA TGACCGACTC CAACGTTCTG GATAAAGTAT      550
   CCCTGGTTTA TGGCCAGATG AACGAGCCGC CGGGAAACCG TCTGCGCGTT      600
   GCTCTGACCG GCCTGACCAT GGCTGAGAAA TTCCGTGACG AAGGTCGTGA      650
   CGTTCTGCTG TTCGTCGATA ACATCTATCG TTATACCCTG GCCGGTACTG      700
60 AAGTATCCGC ACTGCTGGGT CGTATGCCTT CAGCGGTAGG TTATCAGCCG      750

```

ACCCTGGCGG AAGAGATGGG TGTTCTGCAG GAACGTATCA CCTCCACCAA 800
 AACCGGTTCT ATCACTTCCG TA 822

5

2) INFORMATION FOR SEQ ID NO: 317

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 785 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae* subsp. *pneumoniae*
 (B) STRAIN: ATCC 13883

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 317

AGAATGGTAA TGAAGTTCTG GTGCTGGAAG TTCAGCAGCA GCTGGGCGGC 50
 GGTATCGTAC GTACCATCGC CATGGGTTCT TCTGATGGTC TGCGCCGCGG 100
 TCTGGATGTA AAAGACCTCG AGCACCCGAT CGAAGTCCCG GTAGGTAAAG 150
 25 CAACGCTGGG TCGTATCATG AACGTACTGG GTCAACCGGT TGACATGAAA 200
 GCGGACATCG GCGAAGAAGA GCGTTGGGCT ATCCACCGCG CGGCACCGTC 250
 CTATGAAGAG CTGTCCAGCT CTCAGGAACT GCTGGAAACC GGCATCAAAG 300
 TTATCGACCT GATGTGTCCG TTCGCCAAGG GCGGTAAAGT TGGTCTGTTC 350
 GGCGGTGCGG GTGTAGGTAA AACTGTAAAC ATGATGGAGC TGATCCGTAA 400
 30 CATCGCGATC GAGCACTCCG GTTACTCTGT GTTTGCGGGC GTAGGTGAGC 450
 GTACTCGTGA GGGTAATGAC TTCTACCACG AAATGACCGA CTCCAACGTT 500
 ATCGATAAAG TATCCCTGGT GTACGGCCAG ATGAACGAGC CGCCGGGAAA 550
 CCGTCTGCGC GTTGCGCTGA CCGGCCTGAC CATGGCTGAG AAATTCCGTG 600
 ACGAAGGTCG TGACGTACTG CTGTTCTGTCG ATAACATCTA TCGTTACACC 650
 35 CTGGCCGGTA CTGAAGTATC CGCACTGCTG GGTTCGTATGC CTTTCAGCGGT 700
 AGGTTATCAG CCGACCCTGG CGGAAGAGAT GGGCGTTCTG CAGGAACGTA 750
 TCACCTCCAC CAAAACCGGT TCTATCACCT CCGTA 785

40

2) INFORMATION FOR SEQ ID NO: 318

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 759 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Kluyvera ascorbata*
 (B) STRAIN: ATCC 33433

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 318

CTGGTGCTGG AAGTTCAGCA GCAGCTCGGC GGCGGTATCG TACGTWCCAT 50
 CGCTATGGGT TCTTCCGACG GTCTGCGTCG CCGTCTGGAT GTTAAAGATC 100
 TCGAGCACCC AATCGAAGTT CCGGTMGGTA AAGCAACMCT GGGTCGTATC 150
 60 ATGAACGTAC TGGGTCAKCC AGTMGACATG AAAGGCGACA TCGGTGAAGA 200

AGAGCGTTGG GCTATCCACC GCGCTGCACC TTCCTACGAA GAGCTGTCTA 250
 GCTCTCAGGA ATTGCTGGAA ACCGGTATCA AAGTTATCGA CCTGATGTGT 300
 CCGTTCGCTA AGGGCGGTAA AGTCGGTCTG TTCGGTGGTG CSGGTGTTGG 350
 TAAAACCGTA AACATGATGG AGCTGATCCG TAACATCGCG ATCGAGCACT 400
 5 CCGGTACTCT CGTGTTTGCG GCGGTAGGTG AACGTACTCG TGAGGGTAAC 450
 GACTTCTACC ACGAAATGAC CGACTCCAAC GTTATCGATA AAGTATCCCT 500
 GGTATATGGC CAGATGAACG AGCCACCGGG AAACCGTCTG CGCGTTGCTC 550
 TGACCGGTCT GACCATGGCT GAGAAATTCC GTGACGAAGG TCGTGACGTA 600
 CTGCTGTTTCG TCGATAACAT CTATCGTTAC ACCCTGGCCG GTACTGAAGT 650
 10 ATCTGCWCTG CTGGGTCGTA TGCCTTCAGC GGTAGGTTAC CAGCCGACCC 700
 TGGCGGAAGA GATGGGCGTT CTGCAGGAAC GTATCACCTC CACCAAGACC 750
 GGTTCTATC 759

15

2) INFORMATION FOR SEQ ID NO: 319

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 831 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Kluyvera cryocrescens*
 (B) STRAIN: ATCC 33435

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 319

TTCCCTCAGG ATGCCGTACC GCGTGTGTAC GAAGCCCTTG AGGTCAGAA 50
 TGGTAATGAA GTGCTGGTGC TGGAAGTTCA GCAGCAGCTC GGCGGCGGTA 100
 TCGTACGTAC CATCGCTATG GGTCTCTCCG ACGGTCTGCG TCGTGGTCTG 150
 35 GATGTAAAAG ACCTCGAGCA CCCGATCGAA GTCCCAGTAG GTAAAGCAAC 200
 ACTGGGTCGT ATCATGAACG TACTGGGCCA ACCGGTAGAC ATGAAAGGCG 250
 ACATCGGTGA AGAAGAACGT TGGGCTATCC ACCGTGCAGC ACCTTCCTAC 300
 GAAGAGCTGT CAAGCTCTCA GGAAGTCTG GAAACCGGCA TCAAAGTTAT 350
 CGACCTGATG TGTCCGTTTG CGAAGGGCGG TAAAGTTGGT CTGTTCGGTG 400
 40 GTGCGGGTGT AGGTAAAACC GTAAACATGA TGGAGCTTAT TCGTAACATC 450
 GCGATTGAGC ACTCCGGTTA TTCTGTGTTT GCGGGCGTAG GTGAACGTAC 500
 TCGTGAGGGT AACGACTTCT ACCACGAAAT GACCGACTCC AACGTTATCG 550
 ATAAAGTTTC CCTGGTTTAC GGCCAGATGA ACAGGCCACC AGGAAACCGT 600
 CTGCGCGTTG CGCTGACTGG TCTGACTATG GCTGAGAAGT TCCGTGACGA 650
 45 AGGTGCGGAC GTACTGCTGT TCGTCGATAA CATCTATCGT TACACCCTGG 700
 CCGGTACAGA AGTATCTGCA CTGCTGGGTC GTATGCCTTC AGCGGTAGGT 750
 TACCAGCCGA CTCTGGCGGA AGAGATGGGC GTTCTGCAGG AACGTATCAC 800
 CTCCACCAAA ACCGGTTCTA TCACCTCCGT A 831

50

2) INFORMATION FOR SEQ ID NO: 320

(i) SEQUENCE CHARACTERISTICS:

55 (A) LENGTH: 810 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

60 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Kluyvera georgiana*

(B) STRAIN: ATCC 51603

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 320

5
10
15
20
25

GCCGTACCGC	GCGTGTACGA	AGCCCTTGAG	GTACAGAATG	GTAATGAAGT	50
GCTGGTGCTG	GAAGTTCAGC	AGCAGCTCGG	TGGCGGTATC	GTGCGTACCA	100
TCGCCATGGG	TTCTTCCGAC	GGTCTGCGTC	GCGGTCTGGA	AGTTAAAGAT	150
CTCGAGCACC	CGATCGAAGT	TCCGGTAGGT	AAAGCAACAC	TGGGTCTGTAT	200
CATGAACGTA	CTGGGTCACC	CGGTAGACAT	GAAAGGCGAC	ATCGGTGAAG	250
AAGAGCGTTG	GGCTATCCAC	CGCGCTGCGC	CTTCCTACGA	AGAGCTGTCC	300
AGCTCTCAGG	AACTGCTGGA	AACCGGTATC	AAAGTTATCG	ACCTGATGTG	350
TCCGTTTCGG	AAGGGCGGTA	AAGTCGGTCT	GTTTCGGCGGT	GCGGGTGTG	400
GTAACACCGT	AAACATGATG	GAGCTGATCC	GTAACATCGC	GATCGAGCAC	450
TCCGGTTACT	CTGTGTTTGC	GGGCGTAGGT	GAACGTACTC	GTGAGGGTAA	500
CGACTTCTAC	CACGAAATGA	CCGACTCCAA	CGTTATCGAT	AAAGTATCCC	550
TGGTGTATGG	CCAGATGAAC	GAGCCGCCGG	GAAACCGTCT	GCGCGTTGCG	600
CTGACCGGCC	TGACCATGGC	TGAGAAATTC	CGTGACGAAG	GTCGTGACGT	650
ACTGCTGTTT	GTCGATAACA	TCTATCGTTA	CACCCTGGCC	GGTACTGAAG	700
TATCTGCACT	GCTGGGTCGT	ATGCCTTCAG	CGGTAGGTTA	CCAGCCGACT	750
CTGGCGGAAG	AGATGGGCGT	TCTGCAGGAA	CGTATCACCT	CCACCAAGAC	800
CGGTTCTATC					810

2) INFORMATION FOR SEQ ID NO: 321

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 834 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Lactobacillus acidophilus*

(B) STRAIN: ATCC 4356

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 321

45
50
55
60

TCGATAAGAA	TTTACCTGAT	ATTAACAACG	CCTTACGTGT	AATCAAGTCC	50
GAAGATGAAA	GCATCGTTCT	TGAAGTTACA	CTTGAACCTG	GTGATGGTGT	100
TTTAAGAACA	ATCGCCATGG	AATCTACCGA	TGGTCTTCGT	CGTGGTATGA	150
AAGTCGAAGA	TACTGGCGCT	CCAATTTTCT	TTCCAGTTGG	AGAAGACACT	200
TTAGGTCGTG	TGTTTAAACG	TTTAGGACAG	CCTATTGATG	GTGGTCCAGC	250
CTTTCCAAAG	GATCACCCAC	GTGAGGGTAT	CCACAAGGAA	GCACCTAAAT	300
ATGAAGATTT	AACTACTAGT	CGTGAAATTC	TTGAAACTGG	TATCAAGGTT	350
ATCGACCTTC	TTGAACCATA	TGTTTCGTGG	GGTAAAGTTG	GTTTGTGTTG	400
TGGTGCCGGT	GTTGGTAAAA	CTACTATTAT	TCAAGAATTA	ATTCACAACA	450
TCGCTCAAGA	ACACGGTGGT	ATTTCGGTAT	TTACTGGTGT	TGGTGAAAGA	500
ACTCGTGAAG	GTAATGACCT	TTACTTTTGA	ATGAAAGCTT	CAGGCGTTTT	550
AAGTAAGACT	GCCATGGTAT	TTGGTCAGAT	GAACGAGCCG	CCTGGTGCCA	600
GAATGCGTGT	TGCATTAACC	GGTTTGACAC	TTGCTGAATA	CTTTAGAGAT	650
GTTGAAGGTC	AAGACGTATT	GCTCTTTATT	GACAATATCT	TTAGATTTAC	700
TCAGGCTGGT	TCAGAGGTAT	CTGCTTTGCT	TGGTCGTATG	CCAAGTGCCG	750
TAGGTTATCA	GCCAACCTTG	GCAACAGAA	TGGGTCAATT	GCAGGAAAGA	800
ATTACTTCTA	CTAAGAAGGG	TTCAATTACT	TCAA		834

2) INFORMATION FOR SEQ ID NO: 322

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 824 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Legionella pneumophila* subsp. *pneumophila*
 (B) STRAIN: ATCC 33152

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 322

```

20  TTCCTCGTGA TAGCGTGCCT AAAGTCAATG ATGCGTTAAA GCTTGTTGAT      50
    AGTGATCTGG TTTTGAAGT GCAGCAGCAA CTTGGAGACG GAGTTGTGCG      100
    TACTATTGCC ATGGGAACAA CCGATGGTTT AAAGCGAGGA TTAAAAGCAG      150
    AAAATACAGG CCATCCTATT CAAGTGCCAG TAGGTAAGAA AACTTTGGGA      200
    CGCATTATGG ATGTTCTTGG GCGTCCTGTA GATGATGCTG GGCCTATCGA      250
25  TGCTGAAGAG ACTTGGGCTA TTCATCGTAA AGCACCAAGT TATGAAGAGC      300
    AAGCTGGCAG CCAGGAATTA TTGGAAACTG GTATTAAAGT AATTGATTG      350
    CTTTGCCCTT TTGCCAAGGG AGGTAAAGTT GGTCTATTCT GTGGTGCCGG      400
    TGTAGGCAAA ACCGTTAACA TGATGGAATT AATACGAAAC ATTGCAATTG      450
    AGCATAGCGG TTATTCAGTG TTTGCAGGGG TTGGTGAACG TACCCGTGAA      500
30  GGAAACGACT TCTATCATGA GATGAAAGAC TCTAATGTAT TGGATAAAGT      550
    ATCGCTTGTT TATGGTCAGA TGAATGAGCC GCCAGGAAAC CGTTTGCGTG      600
    TTGCTCTAAC CGGTTTGACT ATGGCTGAAA AATTCGCGGA TGAAGGGCGA      650
    GACGTTCTTT TGTTTATCGA TAATATTTAT CGTTATACCT TGGCTGGGGT      700
    TGAAGTATCT GCGCTGTTAG GCCGTATGCC TTCTGCAGTA GGATATCAGC      750
35  CGACATTAGC AGAGGAAATG GGTATGCTGC AAGAGCGCAT TACCTCCACA      800
    AAAACAGGTT CTATTACTTC CATA                                     824
  
```

2) INFORMATION FOR SEQ ID NO: 323

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 818 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leminorella grimontii*
 (B) STRAIN: ATCC 33999

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 323

```

55  GACGCCGTAC CGAAAGTGTA CGATGCGCTT GAAGTTCAAA TTGATGCCAA      50
    GCTGGTTCTG GAAGTTCAAC AGCAGCTCGG CGGCGGCGTT GTTCGCTGCA      100
    TCCGATGGG TACTTCAGAC GGCTTAAGCC GCGGTCTGGA CGTGCTCGAT      150
    CTGGAACACC CGATTGAAGT ACCGGTGGGC AAAGCGACGC TGGGCCGCAT      200
60  CATGAACGTG CTTGGTCACC CTATCGACAT GAAGGGCGAC ATCGGCGAAG      250
  
```

	AAGAGCGTTG	GGCTATTTCAC	CGCGCAGCGC	CGAGCTACGA	AGACCTGTCTG	300
	GGCGCAACCG	AGCTGCTGGA	GACCGGCATC	AAGGTTATCG	ACCTGATTTG	350
	TCCGTTCCGC	AAGGGCGGTA	AAGTCGGCCT	GTTCGGCGGC	GCCGGCGTAG	400
	GTAACACCGT	AAACATGATG	GAGCTCATTC	GCAACATTGC	GACCGAGCAC	450
5	TCCGGTTACT	CCGTGTTTGC	AGGCGTAGGT	GAACGTACCC	GTGAGGGTAA	500
	CGACTTCTAG	CACGAAATGA	CTGAATCCAA	CGTATTGGAC	AAGGTGTCTG	550
	TGGTATACGG	TCAGATGAAC	GAGCCGCCCTG	GAAACCGTCT	GCGCGTAGCG	600
	TTAACGGGCT	TGACCATGGC	GGAGAAGTTC	CGTGATGAAG	GCCGTGACGT	650
	TCTGCTGTTT	ATCGACAACA	TTTACCGCTA	TACCCTGGCC	GGTACGGAAG	700
10	TATCCGCACT	GCTGGGCCGT	ATGCCTTCAG	CCGTAGGCTA	CCAGCCGACT	750
	CTGGCTGAGG	AAATGGGCGT	GCTTCAAGAG	CGTATTACCT	CTACCAAGAC	800
	GGGGTCTATC	ACCTCCGT				818

15

2) INFORMATION FOR SEQ ID NO: 324

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Listeria monocytogenes*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 324

30	GTGGAAACTT	ACCTGAAATC	TACAATGCCC	TAGTTATTGA	ATATAAATCT	50
	GATGCAGAAG	AAGCACCAAC	TAGCCAACTT	ACTTTAGAAG	TAGCCATCCA	100
	ATTAGGTGAT	GATGTTGTAC	GTACAATCGC	AATGGCATCA	ACAGATGGTG	150
	TTCAAAGAGG	TATGGAAGTT	ATTGATACTG	GGAGCCCAAT	TACAGTTCCT	200
35	TAGGTACAG	TAACCTCTGG	TCGTGTATTT	AATGTATTAG	GAAACACCAT	250
	CGATTTGGAC	GAACCACTTC	CAAGCGATAT	TAAACGTAAT	AAAATTCACC	300
	GCGAAGCTCC	AACTTTCGAT	CAATTAGCAA	CGACAACAGA	AATTCCTGAA	350
	ACAGGAATTA	AAGTAGTTGA	CTTGCTAGCT	CCTTACTTAA	AAGGTGGTAA	400
	AATCGGATTG	TTCCGGTGGT	CCGGTGTGG	TAAAACCGTT	CTAATTCAAG	450
40	AGCTTATCCA	TAATATCGCA	CAAGAACATG	GTGGTATTTC	TGTGTTTCGCT	500
	GGCGTTGGAG	AACGTACTCG	TGAAGGTAAC	GACCTTTACT	TCGAAATGAA	550
	AGATTTCAGG	GTTATTGAAA	AAACAGCGAT	GGTATTCGGT	CAAATGAACG	600
	AGCCACCAGG	TGCGCGTATG	CGTGTTGCCT	TAACCTGGTCT	AACAATTGCT	650
	GAATATTTCC	GTGATGAAGA	ACATCAAGAT	GTACTTTTAT	TCATTGATAA	700
45	CATTTTCCGT	TTCACACAAG	CTGGTTCAGA	GGTTTCGGCT	TTACTAGGTC	750
	GTATGCCATC	TGCGGTAGGT	TACCAACCAA	CCCTAGCTAC	TGAAATGGGT	800
	CAACTACAAG	AACGTATTAC	ATCTACTAAC	GTTGG		835

50

2) INFORMATION FOR SEQ ID NO: 325

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Micrococcus lylae*
 (B) STRAIN: ATCC 27566

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 325

```

10  CCCGCGTGGC GAGTTGCCGG CACTGTTCAA CGCGCTGACT GTCGAGGTCA      50
    CCCTCGAAGC AGTCGCTAAA ACCATTACCC TTGAGGTTGC TCAGCACCTC      100
    GGCGACAAC TGGTTCGTGC CGTGTCCATG GCACCGACCG ACGGTCTCGT      150
    CCGTGGCGCT GCTGTGATCG ACAGCGGTAA GCCGATCTCA GTTCCCGTTG      200
    GTGACGTAGT CAAGGGACAC GTCTTCAACG CTCTGGGTGA TTGCCTCGAT      250
    GAGCCAGGTC TTGGCCGTGA CGGTGAGCAG TGGGGCATCC ACCGCGATCC      300
    GCCACCTTTT GACCAGCTTG AGGGTAAGAC CGAGATTCTG GAAACCGGTA      350
    TTAAGGTCAT CGACCTGCTG ACCCCGTATG TTAAGGGCGG CAAGATCGGC      400
    15  CTGTTCCGGTG GTGCTGGTGT GGGTAAGACC GTTCTTATCC AGGAAATGAT      450
    CACCCGTATC GCTCGCGAGT TCTCCGGTAC CTCGGTGTTC GCAGGCGTGG      500
    GTGAGCGTAC CCGTGAGGGC ACCGACCTCT TCCTGGAAAT GGAAGAGATG      550
    GGCGTTCTCC AGGACACCGC TCTTGTGTTC GGCCAGATGG ACGAGCCTCC      600
    AGGAGTTCGT ATGCGCGTGG CGCTGTCCGG CCTGACCATG GCGGAGTACT      650
    20  TCCGCGATGT GCAGCACCAG GACGTGCTTC TGTTTCATCGA CAACATCTTC      700
    CGTTTCACCC AGGCAGGTTT CGAGGTTTCC ACCCTCCTAG GCCGCATGCC      750
    TTCTGCCGTG GGTACCAGC CAACGCTGGC AGACGAGATG GGTGTTCTGC      800
    AGGAGCGTAT TACCTCCACA AAGGGTAA      828
  
```

25

2) INFORMATION FOR SEQ ID NO: 326

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 822 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Moellerella wisconsensis*
 (B) STRAIN: ATCC 35017

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 326

```

45  GATGCCGTAC CAAAAGTGTA CGATGCTCTT GAGGTTCTTA ACGGTAAAGA      50
    AAAATTGGTG CTGGAAGTTC AGCAACAATT AGGCGGTGGT GTTGTTCGTT      100
    GTATCGCAAT GGGTACATCA GATGGTTTAA GCCGCGGTTT AGAAGTTAAA      150
    AATACAGATC ATCCGATCGA AGTTCCTGTC GGTGTTAAAA CGCTTGGCCG      200
    TATCATGAAC GTGCTGGGTG ACCCAATCGA CATGAAAGGT GATATCGGCG      250
    AAGAAGAACG CTGGTCAATT CACCGCGCAG CACCAAGCTA TGAAGATCTG      300
    GCTAACTCAA CAGAACTTCT AGAAACAGGT ATCAAAGTTA TGGACCTGAT      350
    50  TTGCCCATTG GCTAAAGGGG GTAAAGTGGG TCTGTTCCGT GGTGCGGGTG      400
    TCGGTAAAAC AGTTAACATG ATGGAGCTTA TTCGTAATAT CGCGATTGAG      450
    CACTCAGGTT ATTCTGTATT CGCGGGTGTT GGTGAACGTA CTCGTGAAGG      500
    TAACGATTTC TACCATGAAA TGACAGACTC AAACGTTCTG GATAAAGTTT      550
    CATTGGTTTA TGGCCAGATG AATGAGCCAC CAGGAAACCG TCTGCGTGTT      600
    55  GCTCTGACTG GTCTGACTAT GGCAGAGAAA TTCCGTGACG AAGGTCGTGA      650
    CGTACTGTTA TTCGTAGATA ATATTTATCG TTATACCTTA GCAGGGACAG      700
    AAGTATCTGC ATTGCTGGGT CGTATGCCTT CAGCGGTGGG TTATCAGCCA      750
    ACGCTGGCGG AAGAGATGGG TGTTCTGCAA GAACGTATCA CCTCGACTAA      800
    GACCGGCTCT ATCACTTCCG TA      822
  
```

60

2) INFORMATION FOR SEQ ID NO: 327

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 854 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- 10 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Branhamella catarrhalis*
 15 (B) STRAIN: ATCC 43628

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 327

	CCGTGGCGAT	GTCCCCCAA	TCTTTGATGC	ACTTCATGTT	GATGGTACTG	50
20	AAACCACCCT	TGAAGTCCAA	CAACAGTTAG	GTGATGGTGT	GGTGCGTACC	100
	ATTGCCATGG	GTTCTACCGA	AGGCTTAAAG	CGTGGCTTGC	CTGTCTCTAA	150
	TTCAGGTGCA	CCCATTTCGG	TACCAGTCGG	TCAAGCAACA	CTGGGTCGCA	200
	TTATGGATGT	CCTAGGTCGC	CCAATCGATG	AAGCAGGTCC	GGTAAATGCT	250
	GAACAAAAAT	GGTCCATTCA	TCGTGAAGCA	CCAAGTTATG	ATGAACAGTC	300
25	AAATAGTACA	GAACCTTTTAG	AAACAGGCAT	CAAAGTGATT	GATTTGCTTT	350
	GTCCATTTGC	CAAAGGTGGT	AAAGTCGGTC	TGTTTCGGTGG	TGCTGGTGTT	400
	GGTAAGACCG	TTAACATGAT	GGAGCTTATC	AATAATATCG	CCCTAAAACA	450
	CTCAGGTCTG	TCGGTTTTTTG	CTGGTGTGGG	TGAGCGTACT	CGTGAGGGTA	500
	ATGACTTCTA	CCATGAAATG	CAAGAAGCAG	GCGTTGTTAA	TACCGAAGAT	550
30	TTTACTCAGT	CAAAAGTTGC	CATGGTTTAT	GGTCAGATGA	ATGAGCCACC	600
	AGGAAACCGT	CTGCGTGTTG	CCTTAACCTGG	TTTGACCATG	GCAGAGTATT	650
	TCCGTGATGA	AAAAGACGAA	GCAACGGGCA	AAGGCCGTGA	TGTTCTGCTG	700
	TTCGTTGATA	ATATTTATCG	TTACACATTG	GCAGGTACTG	AGGTATCAGC	750
	ACTTTTAGGT	CGTATGCCAT	CTGCGGTAGG	TTATCAGCCG	ACTTTGGCCG	800
35	AAGAGATGGG	CTTGCTACAA	GAGCGTATCA	CCTCCACCCA	ATCAGGCTCA	850
	ATTA					854

40 2) INFORMATION FOR SEQ ID NO: 328

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 831 bases
 (B) TYPE: Nucleic acid
 45 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- 50 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Moraxella osloensis*
 (B) STRAIN: ATCC 19976

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 328

55	CCGTCAAAGC	GTACCAAGAA	TTTATGATGC	CTTAAAAGTT	GAAGGCACAG	50
	AAACTACATT	AGAAGTACAA	CAACAATTGG	GTGATGGTAT	CGTACGTACT	100
	ATTGCCATGG	GTTCTACTGA	AGGTCTAAAA	CGTGGTCTAC	CAGTTAGCAA	150
	CACTGGCGCA	CCAATCTCTG	TACCTGTGGG	TAAAGGTACA	CTAGGTCGTA	200
60	TCATGGACGT	TTTAGGACAC	CCAATCGATG	AGGCAGGTCC	GGTAGAGCAT	250

```

AGTAACACTT GGGCGATTCA CCGTGAAGCG CCAAGCTATG ATGAACAATC 300
AAACTCTACT GAACTTTTAG AAACCGGTAT TAAAGTAATT GACTTACTAT 350
GCCCATTTGC TAAAGGTGGT AAAGTCGGTC TGTTCGGTGG CGCGGGTGTT 400
GGTAAAACCG TTAACATGAT GGAAC TTATC AATAACATCG CAAAAGCACA 450
5 CTCAGGTTTA TCGGTATTTG CTGGTGTAGG TGAGCGTACT CGTGAAGGTA 500
ATGACTTCTA CCACGAGATG AAAGACTCAA ACGTACTTGA TAAAGTTGCG 550
ATGGTGTATG GTCAGATGAA TGAGCCACCA GGAAACCGTT TACGTGTTGC 600
CCTGACAGGT TTAACCATGG CAGAATACTT CCGTGACGAA AAAGATGAAA 650
ACGGTAAAGG TCGTGACGTA TTATTGTTTCG TTGACAATAT TTATCGTTAC 700
10 ACGCTAGCGG GTACCGAAGT ATCAGCATTA TTAGGTCGTA TGCCATCTGC 750
AGTAGGGTAT CAGCCAACGC TTGCAGAAGA GATGGGTGTA CTACAAGAAC 800
GTATTACTTC AACCCAATCA GGCTCTATTA C 831

```

```

15 2) INFORMATION FOR SEQ ID NO: 329

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 835 bases
        (B) TYPE: Nucleic acid
        (C) STRANDEDNESS: Double
        (D) TOPOLOGY: Linear

    (ii) MOLECULE TYPE: Genomic DNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Morganella morganii subsp. morganii
        (B) STRAIN: ATCC 25830

```

```

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 329

CGAATTTCTT CAGGATGCAG TACCGAAAGT GTACGATGCG CTTGAGGTAA 50
CAAATGGTAA AGAAAACTG GTGCTGGAAG TTCAGCAGCA GTTAGGCGGC 100
GGGGTTGTCC GTTGATTCGC TATGGGTACA TCTGATGGTC TGAGCCGTAA 150
35 TCTGGAAGTA ACCGATTTAG GCCACCCGAT CGAAGTCCCT GTCGGCGTGA 200
AAACCTTAGG ACGTATCATG AACGTTCTGG GTGATCCGAT CGATATGAAA 250
GGTGACATCG GCGCAGAAGA AAAATGGTCT ATTCACCGTG CTGCACCAAC 300
ATACGAAGAA CTGTCTAACT CCCAGGAACT GCTGGAAACA GGTATCAAAG 350
TAATGGACCT GATCTGCCCC TTCGCGAAGG GTGGTAAAGT CGGTCTGTTC 400
40 GGTGGTGCGG GTGTGGGTAA AACCGTAAAC ATGATGGAAC TGATCCGTAA 450
CATCGCGATC GAGCACTCCG GTTACTCTGT ATTCGCAGGG GTCGGTGAGC 500
GTACCCGTGA AGGTAACGAC TTCTATCATG AAATGACAGA CTCCAACGTT 550
CTGGACAAAG TATCACTCGT GTACGGCCAG ATGAACGAGC CACCGGGAAA 600
CCGTCTGCGC GTTGCTCTGA CCGTCTGAC CATGGCGGAA AAATTCCGTG 650
45 ATGAAGGCCG CGATGTACTG CTGTTCTGTT ATAACATCTA CCGTTATACC 700
CTGGCCGGTA CTGAAGTATC CGCGCTGTTA GGCCGTATGC CTTCAGCGGT 750
AGGTTACCAG CCGACACTGG CGGAAGAAAT GGGTGTGCTT CAGGAACGTA 800
TCACATCGAC CAAAACAGGC TCTATCACGT CTGTA 835

```

```

50 2) INFORMATION FOR SEQ ID NO: 330

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 824 bases
        (B) TYPE: Nucleic acid
        (C) STRANDEDNESS: Double
        (D) TOPOLOGY: Linear

```

```

60 (ii) MOLECULE TYPE: Genomic DNA

```

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pantoea agglomerans*
 (B) STRAIN: ATCC 27155

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 330

```

5      GACGCGGTAC CGCAAGTGTA CAGCGCCCTC GAGGTTATGA ATGGTGATGC      50
      GCGTCTGGTG CTGGAAGTTC AGCAGCAGCT CGGCGGCGGC GTAGTACGTA      100
10     CCATCGCAAT GGGTACGTCT GACGGCCTGA AGCGTGGTCT GAGCGTCAAC      150
      GACCTGCAGA AACCGATTCA GGTACCCGTC GGTAAGCGA CCCTGGGCCG      200
      TATCATGAAC GTTCTCGGCG AGCCAATCGA TATGAAAGGC GAGCTGAAAG      250
      AAGAAGATGG CAGCGCAGTA GAGATCGCCT CTATTACCG CGCAGCCCCT      300
      TCTTATGAAG ATCAGTCTAA CTCGCAGGAA CTGCTGGAAA CCGGCATCAA      350
15     GGTATATCGAC CTGATGTGTC CGTTTGCTAA AGGCGGTAAA GTCGGTCTGT      400
      TCGGTGGTGC GGGTGTAGGT AAAACCGTCA ACATGATGGA ACTGATCCGT      450
      AACATCGCGG CTGAACACTC AGGTACTCTA GTGTTTGCCG GTGTGGGTGA      500
      CCGTACTCGT GAGGGTAACG ACTTCTACCA CGAAATGACT GACTCTAACG      550
      TTATCGATAA AGTTGCACTG GTCTATGGCC AGATGAACGA GCCGCCGGGT      600
20     AACCGTCTGC GCGTAGCACT GACCGGTCTG ACCATGGCGG AAAAATTCGG      650
      TGATGAAGGT CGCGACGTTT TGCTGTTTCAT CGATAACATC TACCGTTATA      700
      CCCTGGCCGG TACAGAAGTT TCTGCACTGC TGGGTGCTAT GCCATCTGCG      750
      GTAGGTTACC AGCCAACGCT GGCAGAAGAG ATGGGTGTGT TGCAGGAGCG      800
      TATTACCTCC ACCAAGACCG GTTC      824
25

```

2) INFORMATION FOR SEQ ID NO: 331

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 808 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pantoea dispersa*
 (B) STRAIN: ATCC 14589

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 331

```

45     TATACAGCGC TCTCGAGGTA AAAAATGGTG ATGCTCGTCT GTGCTGGAA      50
      GTACAGCAGC AGCTGGGCGG TGCGTGGTG CGTACCATCG CCATGGGTTTC      100
      TTCTGACGGC CTGAAGCGCG GTCTGGAAGT CACCGACCTG AAAAAACCTA      150
      TCCAGGTTCC GGTGGTAAA GCAACACTCG GCCGTATCAT GAACGTGCTG      200
      GGTGAGCCAA TCGACATGAA AGGCGACCTG AAAGAAGAAG ACGGCAGCGC      250
      TGTAGAGGTT TCCTCTATTC ATCGCGCAGC GCCTTCTTAT GAAGATCAGT      300
50     CAAACTCGCA GGAAGTGTG GAAACCGGCA TCAAGGTTAT CGACCTGATG      350
      TGTCGGTTTC CGAAGGGCGG TAAAGTCGGT CTGTTTCGGTG GTGCGGGTGT      400
      AGGTAAAACC GTAAACATGA TGGAGCTGAT CCGTAACATC GCGGCTGAGC      450
      ACTCAGGTTA TTCCGTCTTT GCCGGCGTGG GTGAGCGTAC TCGTGAGGGT      500
      AACGACTTCT ACCACGAAAT GACGGACTCC AACGTTATCG ATAAAGTAGC      550
      GCTGGTGTAT GGCCAGATGA ACGAGCCGCC GGGTAACCGT CTGCGCGTAG      600
      CACTGACCGG TCTGACCATG GCGGAAAAAT TCCGTGATGA AGGCCGTGAC      650
      GTTCTGCTGT TCATCGACAA CATCTACCGT TACACCCTGG CCGGTACAGA      700
      GGTTTCTGCA CTGCTGGGTC GTATGCCATC GCGGTAGGT TATCAGCCAA      750
      CGCTGGCTGA AGAGATGGGT GTGCTGCAGG AGCGTATTAC CTCCACCAAG      800
60     ACCGGTTC      808

```

2) INFORMATION FOR SEQ ID NO: 332

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 805 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pasteurella multocida*
 (B) STRAIN: NCTC 10322

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 332

20	GATGCAGTAC	CAAAAGTATA	TGATGCCTTA	AATGTTGAAA	CAGGTTTAGT	50
	ACTTGAAGTT	CAACAACAAT	TAGGTGGTGG	TGTAGTTCGC	TGTATCGCAA	100
	TGGGATCATC	TGATGGATTA	AAACGCGGTT	TAAGCGTAAC	AAATACGAAT	150
	AACCCAATTT	CTGTTCCAGT	GGGAACGAAA	ACATTGGGTC	GTATCATGAA	200
	CGTATTGGGT	GAACCAATCG	ATGAGCAAGG	TGAAATCGGT	GCAGAAGAGA	250
25	ATTGGTCTAT	TCACCGTGCG	CCACCAAGTT	ATGAAGAACA	ATCTAACAGT	300
	ACTGAAC TTT	TAGAAACGGG	AATTAAAGTT	ATCGACTTAG	TTTGTCCGTT	350
	TGCGAAAGGG	GGTAAAGTAG	GTTTATTCCG	TGGTGCGGGT	GTCGGTAAAA	400
	CCGTCAATAT	GATGGAATTA	ATCCGTAACA	TCGCAATTGA	GCACTCAGGT	450
	TACTCTGTCT	TTGCGGGGGT	AGGTGAGCGT	ACGCGTGAAG	GTAACGACTT	500
30	CTATCATGAG	ATGAAAGACT	CTAACGTATT	AGATAAAGTG	TCTCTTGTTT	550
	ATGGTCAAAT	GAACGAGCCA	CCAGGTAACC	GTTTACGTGT	GGCATTAACA	600
	GGCTTAACTA	TGGCGGAAAA	ATTCCGTGAT	GAAGGTCGTG	ATGTCTTATT	650
	CTTCGTTGAT	AATATTTATC	GTTATACTCT	TGCTGGTACA	GAAGTTTCTG	700
	CATTATTAGG	TCGTATGCCA	TCTGCGGTAG	GTTATCAACC	AACCCTTGCA	750
35	GAAGAAATGG	GTGTTCTGCA	AGAGCGTATT	ACCTCAACCA	AAACAGGTTC	800
	TATTA					805

2) INFORMATION FOR SEQ ID NO: 333

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pragia fontium*
 (B) STRAIN: ATCC 49100

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 333

55	TTTCCTCAAG	ACGCCGTACC	AAAAGTG TAC	GACGCGCTTG	AAGTTCAGAA	50
	CGATGCCAAG	CTGGTGCTGG	AAGTTCAACA	ACAGCTCGGT	GGTGGTGTCG	100
	TTCGTTGTAT	CGCAATGGGT	ACTTCCGATG	GCTTAAGCCG	CGGTTTAAAA	150
	GTGCTTGATT	TAGAACATCC	TATCGAAGTA	CCGGTTGGTA	CTGCGACGCT	200
60	GGGCCGTATT	ATGAACGTGC	TCGGTCAGCC	AATCGATATG	AAAGGCGATA	250

TTGGTGAAGA AGAGCGTTGG GCTATTCACC GTGAAGCACC AAGTTATGAA 300
 GATTTATCTG GCGCCAATGA ACTGCTGGAA ACGGGTATCA AGGTTATCGA 350
 CCTGATTTGT CCGTTTGCTA AAGGTGGTAA AGTTGGTCTG TTTGGTGGTG 400
 CGGGTGTAGG TAAAACCGTA AACATGATGG AGCTGATTCG TAACATTGCG 450
 5 ACTGAGCACT CAGGTTACTC CGTATTCGCC GGTGTAGGGG AACGTACCCG 500
 TGAAGGTAAT GACTTCTACC ACGAAATGAC CGAATCAAAC GTACTGGATA 550
 AAGTATCTCT GGTTTATGGC CAGATGAACG AGCCACCAGG AAACCGTCTG 600
 CGCGTGGCGT TAACGGGTTT GACCATGGCT GAAAAATTCC GTGATGAAGG 650
 TCGTGACGTT CTGTTATTTA TCGATAACAT TTATCGCTAT ACCTTAGCCG 700
 10 GTACCGAAGT ATCAGCACTG TTGGGGCGTA TGCCATCAGC GGTAGGTTAT 750
 CAGCCAACGT TAGCAGAAGA GATGGGTGTG TTGCAGGAAC GTATTACTTC 800
 AACCAAAACC GGTTCATCA CTTCTGTA 828

15

2) INFORMATION FOR SEQ ID NO: 334

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 807 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Proteus mirabilis*
 (B) STRAIN: ATCC 25933

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 334

GTCCCTAAAG TATACGACGC TCTTGAGGTT ATGAATGGTA AAGAAAAACT 50
 GGTGCTGGAA GTTCAGCAAC AGTTAGGCGG TGGTATCGTT CGTTGTATCG 100
 CAATGGGTAC ATCAGACGGT TTAAGCCGTG GCTTAAAGGT TGAAGATTTA 150
 35 GGCCACCCAA TTGAAGTACC AGTAGGTAAA GCGACTTTAG GACGTATCAT 200
 GAACGTTCTG GGTACACCTA TTGATATGAA AGGTGAGATT GAAACCGAAG 250
 AGCGTTGGTC AATCCACCGT GAAGCACCAA CTTACGAAGA GTTATCAAAC 300
 TCTCAAGAAC TGCTTGAAAC CGGTATCAAA GTTATGGACT TAATCTGTCC 350
 ATTTGCTAAA GGTGGTAAAG TCGGTCTGTT CGGTGGTGCG GGTGTTGGTA 400
 40 AAACAGTTAA CATGATGGAA TTGATCCGTA ATATCGCGAT CGAGCACTCA 450
 GGTTACTCTG TATTTGCTGG TGTTGGTGAG CGTACTCGTG AGGGTAACGA 500
 CTTCTATCAT GAAATGACAG ATTCTAACGT TCTTGACAAA GTATCGTTAG 550
 TTTACGGTCA GATGAATGAG CCACCAGGAA ACCGTCTGCG TGTGCACTG 600
 ACTGGTCTGA CTATGGCTGA GAAATTCCGT GATGAAGGCC GTGACGTACT 650
 45 GTTATTCGTC GATAACATCT ATCGTTACAC CTTAGCCGGT ACAGAAGTAT 700
 CAGCACTGTT AGGTCGTATG CCATCAGCGG TAGGTTACCA ACCAACATTG 750
 GCTGAAGAGA TGGGTGTTCT GCAAGAGCGT ATCACTTCAA CCAAACAGG 800
 TTCTATC 807

50

2) INFORMATION FOR SEQ ID NO: 335

(i) SEQUENCE CHARACTERISTICS:

55 (A) LENGTH: 811 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

60 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Proteus vulgaris*

(B) STRAIN: ATCC 13315

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 335

5
10
15
20
25

```

CCCTAAAGTA TACGACGCTC TTGAGGTTAT GAATGGTAAA GAGAAACTGG      50
TGCTAGAAAGT TCAGCAACAG TTAGGCGGTG GTATCGTTTCG TTGTATCGCA      100
ATGGGTACAT  CAGACGGTTT AAGCCGTGGC TTAAAAGTTG AAAACTTAGG      150
CCACCCAATT  GAAGTACCAG TAGGTAAAGC AACACTGGGA CGTATCATGA      200
ACGTTCTGGG  TACACCTATC GATATGAAAG GTGATATTGC AACTGAAGAA      250
CGTTGGTCTA  TTCACGCGCA AGCGCCAACC TATGAAGAGT TATCAAGCTC      300
TCAAGAACTA  CTAGAAAACCG GTATCAAAGT AATGGACTTA ATCTGTCCGT      350
TTGCTAAAGG  TGGTAAAGTA GGTCTCTTCG GTGGTGCGGG TGTGTTGTTAA      400
ACAGTTAACA  TGATGGAATT GATCCGTAAC ATCGCGATTG AGCACTCAGG      450
TTATTCTGTA  TTTGCAGGTG TTGGTGAGCG TACTCGTGAG GGTAACGACT      500
TCTATCATGA  AATGACAGAT TCTAACGTTT TTGACAAAGT ATCGTTAGTT      550
TATGGTCAGA  TGAATGAGCC ACCAGGAAA CGTCTACGTG TAGCACTGAC      600
GGGTTTAACC  ATGGCGGAAA AATTCCGTGA TGAAGGCCGT GACGTACTGT      650
TATTCGTCGA  TAACATCTAT CGTTACACCT TAGCCGGTAC CGAAGTATCA      700
GCACTGTTAG  GCCGTATGCC ATCAGCAGTA GGTACCAAC CAACATTGGC      750
TGAAGAGATG  GGTGTTCTGC AAGAACGTAT CACTTCAACC AAAACAGGTT      800
CAATCACCTC  T

```

2) INFORMATION FOR SEQ ID NO: 336

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 806 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Providencia alcalifaciens*

(B) STRAIN: ATCC 9886

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 336

45
50
55
60

```

TCAAGATAAC GTACCAAAAG TGTACGATGC TCTTGAGGTT ATTAACGGTA      50
AAGAAAAACT GGTGTTGGAA GTTCAACAAC AGTTAGGTGG TGGTGTGTGC      100
CGTTGTATCG CAATGGGTAC ATCAGATGGT CTGAGCCGTG GTTTAGAAGT      150
TGTAAGCTTA GAGCACCCAA TCGAAGTACC AGTCGGTAAA GCAACTCTGG      200
GACGTATCAT GAACGTTCTG GGTGAACCAA TCGACATGAA AGGTGATATC      250
GGCGAAGAAG AGCGCTGGTC TATTCACCGT GCTGCACCAA GCTACGAAGA      300
ATTAGCTAAC TCAACTGAAC TGCTGGAAAC CGGTATCAAA GTAATGGACT      350
TAATCTGTCC ATTCGCGAAA GGTGGTAAAG TAGGTCTGTT CGGTGGTGCG      400
GGTGTGTTGGTA AAACCGTAAA CATGATGGAA CTGATCCGTA ACATCGCGAT      450
TGAGCACTCA GGTTACTCAG TGTTGCTGGT TGTGTTGGTGGT CGTACCCGTG      500
AAGGTAACGA CTTCTATCAT GAAATGACAG ACTCAAACGT TCTGGATAAA      550
GTATCACTGG TTTATGGCCA GATGAACGAG CCACCAGGAA ACCGTCTGCG      600
TGTTGCGCTG ACTGGTCTGA CTATGGCTGA AAAATTCCGT GACGAAGGTC      650
GTGACGTACT GCTGTTTCGT GACAACATTT ATCGTTATAC ACTGGCAGGT      700
ACTGAAGTAT CAGCACTGTT AGGTCGTATG CCATCAGCGG TAGGTTACCA      750
ACCAACGCTG GCGGAAGAGA TGGGTGTTCT TCAAGAACGT ATTACCTCAA      800
CTCAA

```

2) INFORMATION FOR SEQ ID NO: 337

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 830 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Providencia rettgeri*
 (B) STRAIN: ATCC 9250

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 337

20	TTCCCTCAAG ATGACGTACC AAAAGTGTAC GACGCTCTTG AGGTTGTTAA	50
	CGGTAAAGAA ACACTGGTGC TGGAAAGTTCA GCAACAGTTA GGCGGTGGTG	100
	TTGTCCGTTG TATCGCAATG GGTACATCAG ATGGCCTGAG CCGTGGTTTA	150
	GAAGTTGTAA ACTTAGAGCA CCCAATTGAA GTACCAGTAG GTAAAGCAAC	200
	TTTAGGACGT ATCATGAACG TTCTGGGTCA GCCTATTGAT ATGAAAGGTG	250
25	ATATCGGCGA AGAAGAGCGC TGGTCAATTC ACCGTGCTGC ACCTAGCTAC	300
	GAAGAGTTAG CTAACCTAAC AGAGCTGCTG GAAACCGGTA TCAAAGTAAT	350
	GGACTTAATC TGTCCATTCG CGAAAGGTGG TAAAGTTGGT CTGTCGGTG	400
	GTGCGGGTGT TGGTAAAACA GTAAACATGA TGGAACTGAT CCGTAACATC	450
	GCGATTGAGC ACTCAGGTTA CTCAGTATTC GCTGGTGTTG GTGAGCGTAC	500
30	TCGTGAAGGG AACGACTTCT ATCATGAAAT GACTGACTCA AACGTTCTGG	550
	ATAAAGTATC ACTGGTTTAT GGCCAGATGA ATGAGCCACC AGGAAACCGT	600
	CTGCGCGTTG CGTTGACTGG TCTGACTATG GCTGAAAAAT TCCGTGACGA	650
	AGGTCGTGAC GTACTACTGT TCGTTGACAA CATCTATCGT TATACTACTGG	700
	CAGGTACTGA AGTATCAGCA CTGTTAGGTC GTATGCCTTC AGCGGTAGGT	750
35	TATCAGCCAA CGCTGGCGGA AGAGATGGGT GTTCTGCAAG AACGTATTAC	800
	CTCAACTCAA ACGGGTTCTA TCACTTCCGT	830

2) INFORMATION FOR SEQ ID NO: 338

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 812 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Providencia rustigianii*
 (B) STRAIN: ATCC 33673

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 338

55	AGCGTACCAA AAGTGACGA TGCTCTTGAG GTTATTAACG GTAAAGAAAA	50
	ACTGGTGTG GAAGTTCAGC AGCAGTTAGG CGGTGGTGTT GTCCGTTGTA	100
	TCGCAATGGG TACATCAGAT GGTCTGAGCC GTGGTTTAGA AGTTGTAAAC	150
	TTAGAACACC CAATTGAAGT ACCAGTAGGT AAAGCAACTC TGGGACGTAT	200
60	CATGAACGTT CTGGGTGACC CTATTGATAT GAAAGGTGAT ATCGGCGAAG	250

	AAGAGCGCTG	GTCTATTCAC	CGTTCAGCGC	CAAGCTATGA	AGAATTAGCT	300
	AACTCAACAG	AACTGCTAGA	AACCGGTATC	AAAGTAATGG	ACTTAATCTG	350
	TCCATTCGCG	AAAGGTGGTA	AAGTTGGTCT	GTTCGGTGGT	GCGGGTGTTG	400
	GTAACACAGT	AAACATGATG	GAAGTATCC	GTAACATCGC	GATTGAGCAC	450
5	TCAGGTTACT	CAGTATTCGC	TGGTGTGGT	GAGCGTACCC	GTGAAGGTAA	500
	CGACTTCTAT	CATGAAATGA	CTGATTCTAA	CGTTCTGGAT	AAAGTATCAC	550
	TGGTTTATGG	CCAGATGAAC	GAGCCACCAG	GAAACCGTCT	GCGTGTTGCG	600
	CTGACTGGTC	TGACTATGGC	TGAAAAATTC	CGTGACGAAG	GTCGTGACGT	650
	ACTGCTGTTC	GTTGACAACA	TTTATCGTTA	TACACTGGCA	GGTACTGAAG	700
10	TATCAGCACT	GTTAGGTCGT	ATGCCTTCAG	CGGTAGGTTA	TCAGCCAACA	750
	TTGGCAGAAG	AGATGGGTGT	TCTACAAGAA	CGTATCACTT	CTACCAAAAC	800
	CGGTTCTATC	AC				812

15

2) INFORMATION FOR SEQ ID NO: 339

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 819 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Providencia stuartii*
 (B) STRAIN: ATCC 33672

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 339

	TCAAGATGCA	GTACCAAAAG	TGTACGATGC	GCTTGAGGTT	GTTAACGGTA	50
	AAGAAAAACT	GGTGCTGGAA	GTCAGCAAC	AGTTAGGCGG	TGGTGTTGTC	100
	CGTTGTATCG	CAATGGGTAC	ATCAGATGGC	CTAAGCCGTG	GTTTAGAAGT	150
35	TAAAAATTTA	GAACACCCAA	TTGAAGTACC	AGTAGGTAAA	GCAACACTCG	200
	GACGTATCAT	GAACGTTCTG	GGTGACCCTA	TTGATATGAA	AGGTGATATC	250
	GGCGAAGAAG	AGCGTTGGTC	TATTCACCGC	GCTGCACCAA	GCTACGAAGA	300
	GCTATCGAGC	TCAACTGAAC	TGCTAGAGAC	AGGTATCAAA	GTCATGGACT	350
	TGATCTGTCC	ATTCGCGAAA	GGTGGTAAAG	TTGGTCTGTT	CGGTGGTGCG	400
40	GGTGTTGGTA	AAACGGTAAA	CATGATGGAA	CTTATCCGTA	ACATCGCGAT	450
	TGAGCACTCA	GGTTACTCAG	TATTCGCAGG	TGTTGGTGAG	CGTACCCGTG	500
	AAGGTAACGA	CTTCTATCAT	GAAATGACAG	ATTCAAACGT	TCTTGACAAA	550
	GTATCACTGG	TTTATGGTCA	GATGAATGAG	CCACCAGGAA	ACCGTCTACG	600
	CGTAGCATTG	ACTGGTTTGA	CTATGGCTGA	GAAATTCCGT	GACGAAGGCC	650
45	GTGATGTTCT	GTTGTTCGTG	GATAACATCT	ATCGTTATAC	ACTGGCAGGT	700
	ACAGAAGTAT	CGGCTCTGTT	AGGTCGTATG	CCATCAGCAG	TAGGTTATCA	750
	GCCAACATTG	GCAGAAGAGA	TGGGTGTTCT	TCAAGAACGT	ATCACTTCTA	800
	CTAAGACAGG	TTCTATCAC				819

50

2) INFORMATION FOR SEQ ID NO: 340

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 907 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

406

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Psychrobacter phenylpyruvicus*
 (B) STRAIN: ATCC 23333

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 340

```

5      AACCGCACTG ACGTGCCTCA AATTTATGAC GCGTTAGTTG TAGATGGTAC      50
      CGAAACCACC CTAGAAGTTC AGCAGCAGCT GGGCGATGGT GTGGTACGTA      100
10     CTATTGCAAT GGGATCTACT GAAGGTCTTA AGCGTGGTTT ACCAGTAACA      150
      AACACTGGTG CCCCAATTAC AGTTCCAGTA GGTGATGCGA CTTTAGGTCG      200
      TATTATGGAC GTTTTAGGTC GTCCAATTGA CGAACAAGGT CCAGTTAATT      250
      CTGAAGACCA TTGGTCAATC CACCGTCAAG CGCCATCATA TGATGAGCAA      300
      GCTAACAGTA CTGACCTATT AGAGACAGGT ATTAAAGTAA TTGACTTACT      350
15     TTGTCCGTTT GCTAAAGGGG GTAAAGTTGG TCTGTTCCGGT GGTGCCGGTG      400
      TTGGTAAAAC CGTAAACATG ATGGAATTGA TTAATAACAT CGCTCTTAAG      450
      CACTCAGGTT TATCAGTATT CGCTGGTGTG GGTGAGCGTA CTCGTGAAGG      500
      TAACGACTTC TACCACGAGA TGCAAGAAGC GGGTGTTGTT GACGTTGAAA      550
      ACTTCACCAA CTCAAAAGTT GCGATGGTTT ATGGTCAGAT GAATGAGCCA      600
20     CCAGGTAACC GTTTACGTGT TGCCTTAACC GGTCTGACTA TGGCTGAGTA      650
      CTTCCGTGAT CAAAAGATG AAAACGGTAA AGGTAAAGAC GTTCTATTAT      700
      TCGTTGATAA CATCTACCGC TACACGCTAG CCGGTACTGA AGTATCAGCA      750
      CTTCTAGGTC GTATGCCATC AGCAGTAGGT TATCAGCCAA CACTAGCGGA      800
      AGAGATGGGT GTACTACAAG AGCGTATTAC TTCAACTCAG ACTGGTTCTA      850
25     TTACTTC                                         907
  
```

2) INFORMATION FOR SEQ ID NO: 341

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 832 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Rahnella aquatilis*
 (B) STRAIN: DSM 4594

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 341

```

45     GTTCCCTCAG GATGCAGTAC CGAACGTGTA CAATGCTCTT GAGGTAGAAA      50
      ACGGTACCTC CAAACTGGTG CTGGAAGTTC AGCAACAGTT AGGCGGCGGC      100
      GTTGTTCGTT GTATCGCAAT GGGTACCTCA GACGGCCTGC GTCGCGGTCT      150
      GAAAGTGAAC AACCTGGAAC ACCCAATTGA AGTACCGGTA GGTAAAGCGA      200
      CTCTGGGTCG TATCATGAAC GTATTGGGTG AACCAATCGA CATGAAAGGT      250
50     GAAATCGGCG AAGAAGAACG TCGTGCTATT CACCGTGCTG CGCCTTCTTA      300
      TGAAGAGCTG GCAAACTCCC AGGAATTGCT GGAAACCGGT ATCAAAGTTA      350
      TGGACCTGAT GTGTCCGTTT GCTAAGGGCG GTAAAGTTGG TCTGTTCCGGT      400
      GGTGCGGGTG TAGGTAAAAC TGTGAACATG ATGGAGCTGA TCCGTAACAT      450
      TGCGATCGAG CACTCCGGTT ATTCTGTGTT TGCAGGCGTG GGTGAACGTA      500
55     CTCGTGAGGG TAACGACTTC TACCACGAAA TGACTGATTC CAACGTTATC      550
      GACAAAGTTT CCCTGGTGTA TGGCCAGATG AATGAGCCAC CAGGTAACCG      600
      TCTGCGCGTT GCACTGACCG GCCTGACCAT GCGCGAAAAA TTCCGTGATG      650
      AAGGTCGTGA CGTACTGCTG TTCCTTGACA ACATTACCG TTACACCCTG      700
      GCCGCTACCG AAGTGTCGCG ACTTCTGGGC CGTATGCCAT CGGCGGTAGG      750
60     TTATCAGCCA ACGCTGGCGG AAGAGATGGG CGCTCTGCAA GAACGTATCA      800
  
```

CCTCGACCAA AAGTGGTTCT ATCACCTCCG TA

832

5 2) INFORMATION FOR SEQ ID NO: 342

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 824 bases
 (B) TYPE: Nucleic acid
 10 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *arizonae*
 (B) STRAIN: ATCC 13314

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 342

20 TTCCCTCAGG ATGCCGTACC ACGCGTGTAC GATGCTCTTG AGGTGCAGAA 50
 TGGTAATGAG AAGCTGGTGC TGGAAAGTTCA GCAGCAGCTT GGCGGCGGTA 100
 TCGTGCGTAC CATCGCGATG GGGTCTTCTG ACGGTCTGCG TCGCGGTCTT 150
 GATGTAAAG ATCTCGAACA CCCGATCGAA GTCCCGGTAG GTAAAGCCAC 200
 25 GCTGGGTCGT ATCATGAACG TCCTGGGCGA ACCGGTCGAT ATGAAAGGCG 250
 AGATCGGCGA AGAAGAGCGT TGGGCTATTC ACCGCGCGGC GCCGTCCTAC 300
 GAAGAGTTGT CAAACTCTCA GGAAGTGTG GAAACCGGTA TAAAAGTTAT 350
 CGACCTGATG TGTCCGTTTCG CGAAGGGCGG TAAAGTCGGT CTGTTCGGTG 400
 GCGCGGGTGT AGGTAAAACC GTAAACATGA TGGAGCTTAT CCGTAACATC 450
 30 GCGATCGAGC ACTCCGGTTA CTCTGTGTTT GCGGGCGTAG GTGAACGTAC 500
 TCGTGAGGGT AACGACTTCT ACCACGAAAT GACCGACTCT AACGTTATCG 550
 ATAAAGTATC CCTGGTGTAT GGCCAGATGA ACGAGCCACC GGGAAACCGT 600
 CTGCGCGTTG CATTGACCGG CCTGACCATG GCGGAAAAAT TCCGTGATGA 650
 AGGTCGTGAC GTTCTGCTGT TCGTCGACAA CATCTACCGT TATACCCTCG 700
 35 CCGGTACGGA AGTATCCGCA CTGCTGGGTC GTATGCCTTC CGCGGTAGGT 750
 TAYCASCCGA CTCTGGCGGA AGAGATGGGC GTTCTGCAGG AACGTATCAC 800
 CTCCACCAAA ACCGGTTCTA TCAC 824

40 2) INFORMATION FOR SEQ ID NO: 343

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 820 bases
 45 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
 serotype *Choleraesuis*
 (B) STRAIN: ATCC 7001

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 343

GATGCCGTAC CACGCGTGTA CGATGCCCTT GAGGTGCAGA ATGGTAATGA 50
 GAAGCTGGTG CTGGAAGTTC AGCAGCAGCT TGGCGGCGGT ATCGTGCGTA 100
 60 CCATCGCGAT GGGGTCTTCT GACGGTCTGC GTCGCGGTCT GGATGTAAAA 150

```

5  GATCTCGAAC ACCCGATCGA AGTCCCGGTA GGTAAAGCCA CGCTGGGTCG 200
   TATCATGAAC GTCCTGGGCG AACCGGTCGA CATGAAAGGC GAGATCGGCG 250
   AAGAAGAGCG TTGGGCGATT CACCGCGCAG CACCTTCCTA CGAAGAGTTG 300
   TCAAACCTCTC AGGAACTGCT GGAAACCGGT ATCAAAGTTA TCGACCTGAT 350
   GTGTCCGTTC GCGAAGGGCG GTAAAGTCGG TCTGTTCGGT GGTGCGGGTG 400
   TAGGTAAAAC CGTAAACATG ATGGAGCTTA TTCGTAACAT CGCGATCGAG 450
   CACTCCGGTT ACTCAGTGTT TGCGGGCGTA GGGGAACGTA CTCGTGAGGG 500
   TAACGACTTC TACCACGAAA TGACCGACTC CAACGTTATC GATAAAGTAT 550
   CCCTGGTGTA TGGCCAGATG AACGAGCCGC CGGGAACCG TCTGCGCGTT 600
10 GCACTGACCG GCCTGACCAT GCGGAGAAA TTCCGTGACG AAGGTCGTGA 650
   TGTACTGCTG TTCGTCGATA ACATCTATCG TTACACCCTG GCCGGTACGG 700
   AAGTATCCGC ACTGCTGGGC CGTATGCCTT CCGCAGTAGG TTACCAGCCG 750
   ACTCTGGCGG AAGAGATGGG CGTCTGTCAG GAACGTATCA CCTCCACCAA 800
   AACCGGTTCT ATCACCTCCG 820
15

```

2) INFORMATION FOR SEQ ID NO: 344

```

20 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 831 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear
25 (ii) MOLECULE TYPE: Genomic DNA
    (vi) ORIGINAL SOURCE:
    (A) ORGANISM: Salmonella choleraesuis subsp. diarizonae
30 (B) STRAIN: ATCC 43973
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 344

```

```

35 TTCCCTCAGG ATGCCGTACC ACGCGTGTAC GATGCTCTTG AGGTGCAGAA 50
   TGGTAATGAG AAGCTGGTGC TGGAAGTTCA GCAGCAGCTT GGCGGCGGTA 100
   TCGTGCGTAC CATCGCGATG GGGTCTTCTG ACGGTCCTGCG TCGCGGTCTT 150
   GATGTAAAAG ATCTCGAACA CCCGATCGAA GTCCCGGTAG GTAAAGCAAC 200
   GCTGGGTCGT ATCATGAACG TCCTGGGTGA ACCGTCGAT ATGAAAGGCG 250
   AGATCGGCGA AGAAGAGCGT TGGGCGATTG ACCGCGCGGC GCCGTCCTAC 300
40 GAAGAGTTGT CAAACTCTCA GGAAGTCTG GAAACCGGTA TCAAAGTTAT 350
   CGACCTGATG TGTCCGTTCG CGAAGGGCGG TAAAGTCGGT CTGTTCTGGTG 400
   GCGCGGGTGT AGGTAAAACC GTAAACATGA TGGAGCTTAT CCGTAACATC 450
   GCGATCGAGC ACTCCGGTTA CTCTGTGTTT GCGGGCGTAG GTGAACGTAC 500
   TCGTGAGGGT AACGACTTCT ACCACGAAAT GACCGACTCT AACGTTATCG 550
45 ATAAAGTATC CCTGGTGTAT GGCCAGATGA ACGAGCCACC GGGAAACCGT 600
   CTGCGCGTTG CATTGACCGG CCTGACCATG GCGGAAAAAT TCCGTGATGA 650
   AGGTCGTGAC GTTCTGCTGT TCGTCGACAA CATCTACCGT TATACCCTCG 700
   CCGGTACGGA AGTATCCGCA CTGCTGGGTC GTATGCCTTC CGCGGTAGGT 750
   TATCAGCCGA CTCTGGCTGA AGAAATGGGC GTTCTGCAGG AACGTATCAC 800
50 CTCCACCAA ACCGGTTCTA TCACCTCCGT A 831

```

2) INFORMATION FOR SEQ ID NO: 345

```

55 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 831 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
60 (D) TOPOLOGY: Linear

```

(ii)MOLECULE TYPE: Genomic DNA

(vi)ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Salmonella choleraesuis* subsp. *houtenae*
 (B) STRAIN: ATCC 43974

(xi)SEQUENCE DESCRIPTION: SEQ ID NO: 345

```

10 TTCCCTCAGG ATGCCGTACC ACGCGTGTAC GATGCTCTTG AGGTGCAGAA      50
   TGGTAATGAG AAGCTGGTGC TGGAAGTTCA GCAGCAGCTT GGCGGCGGTA      100
   TCGTACGTAC CATCGCGATG GGGTCTTCTG ACGGTCTGCG TCGCGGTCTG      150
   GATGTAAAAG ATCTCGAACA CCCGATCGAA GTCCCAGGTAG GTAAAGCTAC      200
   GCTGGGTCGT ATCATGAACG TCCTGGGCGA ACCGGTCGAT ATGAAAGGCG      250
15 AGATCGGCGA AGAAGAGCGT TGGGCGATTC ACCGCGCTGC GCCGTCCTAC      300
   GAAGAGTTGT CAAACTCTCA GGAAGTGTG GAAACCGGTA TCAAAGTTAT      350
   CGACCTGATG TGTCCGTTTC CGAAGGGCGG TAAAGTCGGT CTGTTCCGGT      400
   GCGCGGGTGT AGGTAAAACC GTAAACATGA TGGAGCTTAT CCGTAACATC      450
   GCGATCGAGC ACTCCGGTTA CTCCGTGTTT GCGGGCGTAG GTGAACGTAC      500
20 TCGTGAGGGT AACGACTTCT ACCACGAAAT GACCGACTCC AACGTTATCG      550
   ATAAAGTATC CCTGGTGTAT GGTACAGATGA ACGAGCCGCC GGGAAACCGT      600
   CTGCGCGTTG CATTGACCGG CCTGACCATG GCGGAAAAAT TCCGTGACGA      650
   AGGTCGTGAC GTTCTGCTGT TCGTCGATAA CATCTATCGT TACACCCTGG      700
   CCGGTACGGA AGTATCCGCA CTGCTGGGTC GTATGCCTTC CGCGGTAGGT      750
25 TATCAGCCGA CGCTGGCGGA AGAGATGGGC GTTCTGCAGG AACGTATCAC      800
   CTCCACCAAG ACCGGTTCTA TCACCTCCGT A                          831
  
```

30 2) INFORMATION FOR SEQ ID NO: 346

(i)SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii)MOLECULE TYPE: Genomic DNA

40 (vi)ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *indica*
 (B) STRAIN: ATCC 43974

(xi)SEQUENCE DESCRIPTION: SEQ ID NO: 346

```

45 TTCCCTCAGG ATGCCGTACC ACGCGTGTAC GATGCCCTTG AGGTGCAGAA      50
   TGGTAATGAG AAGCTCGTGC TGGAAGTTCA GCAGCAGCTT GGCGGCGGTA      100
   TCGTGCGTAC CATCGCGATG GGGTCTTCTG ACGGTCTGCG TCGCGGTCTG      150
   GATGTAAAAG ATCTCGAACA CCCGATCGAA GTCCCAGGTAG GTAAAGCCAC      200
50 GCTGGGTCGT ATCATGAACG TCCTGGGCGA ACCGGTCGAT ATGAAAGGCG      250
   AGATCGGCGA AGAAGAGCGT TGGGCGATTC ACCGCGCGGC GCCGTCCTAT      300
   GAAGAGTTGT CAAACTCTCA GGAAGTGTG GAAACCGGTA TCAAAGTTAT      350
   CGACCTGATG TGTCCGTTTC CGAAGGGCGG TAAAGTCGGT CTGTTCCGGT      400
   GTGCGGGCGT AGGTAAAACC GTAAACATGA TGGAGCTTAT CCGTAACATC      450
55 GCGATCGAGC ACTCCGGTTA CTCTGTGTTT GCGGGCGTAG GTGAACGTAC      500
   TCGTGAGGGT AACGACTTCT ACCACGAAAT GACCGACTCC AACGTTATCG      550
   ACAAAGTATC CCTGGTGTAT GGCCAGATGA ACGAGCCGCC GGGAAACCGT      600
   CTGCGCGTTG CACTGACCGG CCTGACCATG GCGGAGAAGT TCCGTGACGA      650
   AGGTCGTGAC GTACTGCTGT TCGTCGATAA CATCTATCGT TATACCCTGG      700
60 CCGGTACGGA AGTTTCCGCA CTGCTGGGTC GTATGCCTTC CGCGGTAGGT      750
  
```

TATCAGCCAA CTCTGGCGGA AGAGATGGGC GTTCTGCAGG AACGTATCAC 800
CTCCACCAAA ACCGGTCTTA TCACCTCCG 829

5

2) INFORMATION FOR SEQ ID NO: 347

(i) SEQUENCE CHARACTERISTICS:

10

- (A) LENGTH: 817 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
serotype Paratyphi A
- (B) STRAIN: ATCC 9150

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 347

25

30

35

40

GCCGTACCAC	GCGTGTACGA	TGCCCTTGAG	GTGCAGAATG	GTAATGAGAA	50
GCTGGTGCCTG	GAAGTTCAGC	AGCAGCTTGG	CGGCGGTATC	GTGCGTACCA	100
TCGCGATGGG	GTCTTCTGAC	GGTCTGCGTC	GCGGTCTGGA	TGTAAAAGAT	150
CTCGAACACC	CGATCGAAGT	CCCGGTAGGT	AAAGCTACGC	TGGGTCTGAT	200
CATGAACGTC	CTGGGCGAAC	CGGTCGACAT	GAAAGGCGAG	ATCGGCGAAG	250
AAGAGCGTTG	GGCGATTAC	CGCGCAGCGC	CTTCCTACGA	AGAGTTGTCA	300
AACTCTCAGG	AACTGCTGGA	AACCGGTATC	AAAGTTATCG	ACCTGATGTG	350
TCCGTTTCGG	AAGGGCGGTA	AAGTCGGTCT	GTTTCGGTGGT	GCGGGTGTAG	400
GTAACACCGT	AAACATGATG	GAGCTTATCC	GTAACATCGC	GATCGAGCAC	450
TCCGGTTACT	CTGTGTTTGC	GGGCGTAGGT	GAACGTACTC	GTGAGGGTAA	500
CGACTTCTAC	CATGAAATGA	CCGACTCCAA	CGTTATCGAT	AAAGTATCCC	550
TGGTGATATG	CCAGATGAAC	GAGCCGCCGG	GAAACCGTCT	GCGCGTTGCA	600
CTGACCGGCC	TGACCATGGC	GGAGAAATTC	CGTGACGAAG	GTCGTGACGT	650
ACTGCTGTTT	GTCGATAACA	TCTATCGTTA	CACCCTGGCC	GGTACGGAAG	700
TATCCGCACT	GCTGGGTCGT	ATGCCTTCCG	CGGTAGGTTA	CCAGCCGACT	750
CTGGCGGAAG	AGATGGGCGT	TCTGCAGGAA	CGTATCACCT	CCACCAAGAC	800
CGGTTCTATC	ACCTCCG				817

2) INFORMATION FOR SEQ ID NO: 348

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 806 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

55

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
serotype Paratyphi B
- (B) STRAIN: ATCC 8759

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 348

60 GCCGTACCAC GCGTGTACGA TGCCCTTGAG GTGCAGAATG GTAATGAGAA 50

```

5  GCTGGTGCCTG GAAGTTCAGC AGCAGCTTGG CGGCGGTATT GTGCGTACCA 100
   TCGCGATGGG GTCTTCTGAC GGTCTGCGTC GCGGTCTGGA TGTAAGAGAT 150
   CTCGAACACC CGATCGAAGT CCCGGTAGGT AAAGCCACGC TGGGTCGTAT 200
   CATGAACGTC CTGGGCGAAC CGGTTCGACAT GAAAGGCGAG ATCGGCGAAG 250
   AAGAGCGTTG GGCATTCAC CGCGCAGCGC CTTCCTACGA AGAGTTGTCA 300
   AACTCTCAGG AACTGCTGGA AACCAGGTATC AAAGTTATCG ACCTGATGTG 350
   TCCGTTTCGG AAGGGCGGTA AAGTCGGTCT GTTCGGTGGT GCGGGTGTGG 400
   GTAAACCGT AAACATGATG GAGCTTATCC GTAACATCGC GATCGAGCAC 450
   TCCGTTTACT CTGTGTTTGC GGGCGTAGGT GAACGTACTC GTGAGGGTAA 500
10 CGACTTCTAC CACGAAATGA CCGACTCCAA CGTTATCGAT AAAGTATCCC 550
   TGGTGTATGG CCAGATGAAC GAGCCGCCGG GAAACCGTCT GCGCGTTGCA 600
   TTGACCGGTC TGACCATGGC GGAGAAATTC CGTGACGAAG GTCGTGACGT 650
   ACTGCTGTTT GTCGATAACA TCTATCGTTA CACCCTGGCC GGTACGGAAG 700
   TATCCGCACT GCTGGGCCGT ATGCCTTCCG CAGTAGGTTA CCAGCCGACT 750
15 CTGGCGGAAG AGATGGGCGT TCTGCAGGAA CGTATCACCT CCACCAAAC 800
   CGGTTC 806

```

20 2) INFORMATION FOR SEQ ID NO: 349

(i) SEQUENCE CHARACTERISTICS:

```

25  (A) LENGTH: 831 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

```

  (A) ORGANISM: Salmonella choleraesuis subsp. salamae
  (B) STRAIN: ATCC 43972

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 349

```

35  TTCCCTCAGG ATGCCGTACC ACGCGTGTAC GATGCCCTTG AGGTGCAGAA 50
   TGGTAATGAG AAGCTGGTGC TGGAAAGTTCA GCAGCAGCTT GGCGGCGGTA 100
   TCGTGCGTAC CATCGCGATG GGGTCTTCTG ACGGTCTGCG TCGKGGTCTG 150
   GATGTAAAG ATCTCGAACA CCCGATCGAA GTCCCGGTAG GTAAAGCAAC 200
40  GCTGGGCCGT ATCATGAACG TACTGGGCGA ACCGGTCGAC ATGAAAGGCG 250
   AGATTGGTGA AGAAGAGCGT TGGGCTATTC ACCGTGCTGC GCCGTCCTAC 300
   GAAGAGTTGT CAAACTCTCA GGAAGTCTG GAAACCGGTA TCAAAGTTAT 350
   CGACCTGATG TGTCCGTTTC CGAAGGGCGG TAAAGTCGGT CTGTTCCGGT 400
   GCGCGGGTGT AGGTAAAACC GTAAACATGA TGGAGCTCAT CCGTAACATC 450
45  GCGATCGAGC ACTCCGGTTA CTCCGTGTTT GCGGGCGTAG GTGAACGTAC 500
   TCGTGAGGGT AACGACTTCT ACCACGAAAT GACCGACTCC AACGTTATCG 550
   ATAAAGTATC CCTGGTGTAT GGCCAGATGA ACGAGCCGCC GGGAAACCGT 600
   CTGCGCGTTG CACTGACCGG CCTGACCATG GCGGAAAAAT TCCGTGACGA 650
   AGGTGCTGAC GTACTGCTGT TCGTCGATAA CATCTATCGT TATACCCTGG 700
50  CCGGTACGGA AGTATCCGCA CTGCTGGGTC GTATGCCTTC CGCGGTAGGT 750
   TATCAGCCGA CGCTGGCGGA AGAGATGGGC GTTCTGCAGG AACGTATCAC 800
   CTCCACTAAA ACCGGTTCTA TCACCTCCGT A 831

```

55 2) INFORMATION FOR SEQ ID NO: 350

(i) SEQUENCE CHARACTERISTICS:

```

60  (A) LENGTH: 823 bases
    (B) TYPE: Nucleic acid

```

(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
serotype Typhi
(B) STRAIN: ATCC 10749

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 350

	TTCCCTCAGG	ATGCCGTACC	ACGCGTGTAC	GATGCCCTTG	AGGTGCAGAA	50
	TGGTAATGAG	AAGCTGGTGC	TGGAAGTTCA	GCAGCAGCTT	GGCGGCGGTA	100
15	TCGTGCGTAC	CATCGCGATG	GGGTCTTCTG	ACGGTCTGCG	TCGCGGTCTG	150
	GATGTAAAAG	ATCTCGAACA	CCCGATCGAA	GTCCCCGGTAG	GTAAAAGCTAC	200
	GCTGGGTTCG	ATCATGAACG	TCCTGGGCGA	ACCGGTCGAC	ATGAAAGGCG	250
	AGATCGGCGA	AGAAGAGCGT	TGGGCGATTC	ACCGCGCAGC	GCCTTCCTAC	300
	GAAGAGTTAT	CAAACCTCTA	GGAACCTGCTG	GAAACCGGTA	TCAAAGTTAT	350
20	CGACCTGATG	TGTCCGTTTCG	CGAAGGGCGG	TAAAGTCGGT	CTGTTTCGGTG	400
	GTGCGGGTGT	AGGTAAAACC	GTAACATGA	TGGAGCTTAT	CCGTAACATC	450
	GCGATCGAGC	ACTCCGGTTA	CTCTGTGTTT	GCGGGCGTAG	GTGAACGTAC	500
	TCGTGAGGGT	AACGACTTCT	ACCATGAAAT	GACCGACTCC	AACGTTATCG	550
	ATAAAGTATC	CCTGGTGTAT	GGCCAGATGA	ACGAGCCGCC	GGGAAACCGT	600
25	CTGCGCGTTG	CACTGACCGG	CCTGACCATG	GCGGAGAAAT	TCCGTGACGA	650
	AGGTCGTGAC	GTACTGCTGT	TCGTTCGATAA	CATCTATCGT	TACACCCTGG	700
	CCGGTACGGA	AGTATCCGCA	CTGCTGGGTC	GTATGCCTTC	CGCGGTAGGT	750
	TACCAGCCGA	CTCTGGCGGA	AGAGATGGGC	GTTCTGCAGG	AACGTATCAC	800
	CTCCACCAAG	ACCGGTTCTA	TCA			823

2) INFORMATION FOR SEQ ID NO: 351

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 831 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
serotype Typhimurium
(B) STRAIN: ATCC 14028

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 351

50	TTCCCTCAGG	ATGCCGTACC	ACGCGTGTAC	GATGCCCTTG	AGGTGCAGAA	50
	TGGTAATGAG	AAGCTGGTGC	TGGAAGTTCA	GCAGCAGCTT	GGCGGCGGTA	100
	TTGTGCGTAC	CATCGCGATG	GGGTCTTCTG	ACGGTCTGCG	TCGCGGTCTG	150
	GATGTAAAAG	ATCTCGAACA	CCCGATCGAA	GTCCCCGGTAG	GTAAAAGCTAC	200
	GCTGGGTTCG	ATCATGAACG	TCCTGGGCGA	ACCGGTCGAC	ATGAAAGGCG	250
55	AGATCGGCGA	AGAAGAGCGT	TGGGCGATTC	ACCGCGCAGC	GCCTTCCTAC	300
	GAAGAGTTGT	CAAACCTCTA	GGAACCTGCTG	GAAACCGGTA	TCAAAGTTAT	350
	CGACCTGATG	TGTCCGTTTCG	CGAAGGGCGG	TAAAGTCGGT	CTGTTTCGGTG	400
	GTGCGGGTGT	AGGTAAAACC	GTAACATGA	TGGAGCTTAT	CCGTAACATC	450
	GCGATCGAGC	ACTCCGGTTA	CTCAGTGTTT	GCGGGCGTAG	GGGAACGTAC	500
60	TCGTGAGGGT	AACGACTTCT	ACCACGAAAT	GACCGACTCC	AACGTTATCG	550

ATAAAGTATC CCTGGTGTAT GGCCAGATGA ACGAGCCGCC GGGAAACCGT 600
 CTGCGCGTTG CATTGACCGG TCTGACCATG GCGGAGAAAT TCCGTGACGA 650
 AGGTCGTGAC GTACTGCTGT TCGTCGATAA CATCTATCGT TACACCCTGG 700
 CCGGTACGGA AGTATCCGCA CTGCTGGGCC GTATGCCTTC CGCAGTAGGT 750
 5 TACCAGCCGA CTCTGGCGGA AGAGATGGGC GTTCTGCAGG AACGTATCAC 800
 CTCCACCAA ACCGGTTCTA TCACCTCCGT A 831

10 2) INFORMATION FOR SEQ ID NO: 352

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 810 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
 serotype Virchow
 (B) STRAIN: ATCC 51955

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 352

GCCGTACCAC GCGTGTACGA TGCCCTTGAG GTGCAGAATG GTAATGAGAA 50
 GCTGGTGTCTG GAAGTTCAGC AGCAGCTTGG CGGCGGTATC GTGCGTACCA 100
 TCGCGATGGG GTCTTCTGAC GGTCTGCGTC GCGGTCTGGA TGTAAGAT 150
 30 CTGGAACACC CGATCGAAGT CCGGTAGGT AAAGCCACGC TGGGTCTGAT 200
 CATGAACGTC CTGGGCGAAC CCGTCGACAT GAAAGGCGAG ATCGGCGAAG 250
 AAGAGCGTTG GGCGATTAC CGCGCAGCAC CTTCTACGA AGAGTTGTCA 300
 AACTCTCAGG AACTGCTGGA AACCAGTATC AAAGTTATCG ACCTGATGTG 350
 TCCGTTTCGCG AAGGGCGGTA AAGTCGGTCT GTTCGGTGGT GCGGGTGTAG 400
 35 GTAAACCGT AAACATGATG GAGCTTATTC GTAACATCGC GATCGAGCAC 450
 TCCGGTTACT CTGTGTTTGC GGGCGTAGGG GAACGTACTC GTGAGGGTAA 500
 CGACTTCTAC CACGAAATGA CCGACTCCAA CGTTATCGAT AAAGTCTCCC 550
 TGGTGTATGG CCAGATGAAC GAGCCGCCGG GAAACCGTCT GCGCGTTGCA 600
 TTGACCGGTC TGACCATGGC GGAGAAATTC CGTGACGAAG GTCGTGACGT 650
 40 ACTGCTGTTT GTCGATAACA TCTATCGTTA CACCCTGGCC GGTACGGAAG 700
 TATCCGCACT GCTGGGCCGT ATGCCTTCCG CAGTAGGTTA CCAGCCGACT 750
 CTGGCGGAAG AGATGGGCGT TCTGCAGGAA CGTATCACCT CCACCAAAC 800
 CGGTTCTATC 810

45

2) INFORMATION FOR SEQ ID NO: 353

(i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 820 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Serratia ficaria*
 (B) STRAIN: ATCC 33105

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 353

```

5  GATGCCGTAC CAAAAGTGTA CGATGCCCTT GAGGTAGAAA ACGGTACCGA 50
   GAAACTGGTG CTGGAAGTTC AGCAGCAGCT GGGCGGTGGC GTCGTTCGCT 100
   GTATCGCAAT GGGGACCTCT GACGGTCTGC GTCGCGGTCT GAAAGTGAAC 150
   AACCTGGAAC ACCCGATTGA AGTGCCGGTG GGTAAAGCTA CCCTGGGCCG 200
   TATCATGAAC GTATTGGGCG AACCAATCGA CATGAAAGGC GAGATCGGCG 250
   AAGAAGAGCG TTGGGCGATT CACCGTCCTG CGCCAAGCTA CGAAGAGCTG 300
   TCCAAC TCCC AGGACCTGCT GGAAACCGGT ATCAAGGTAA TGGACCTGAT 350
10 TTGTCCGTTT GCCAAGGGCG GTAAAGTCGG TCTGTTCGGT GGTGCGGGCG 400
   TGGGCAAAAC CGTAAACATG ATGGAGCTGA TCCGTAACAT CGCGATCGAG 450
   CACTCCGGTT ATTCCGTGTT TCGGGGCGTG GCGGAGCGTA CTCGTGAGGG 500
   TAACGACTTC TACCACGAAA TGAACGACTC CAACGTTCTG GACAAAGTAT 550
   CCCTGGTTTA CGGCCAGATG AACGAGCCGC CGGGTAACCG TCTGCGCGTT 600
15 GCATTGACCG GCCTGACCAT GGCGGAGAAA TTCCGTGACG AAGGCCGCGA 650
   CGTTCTGCTG TTCGTTGACA ACATTTACCG TTACACCCTG GCCGGTACCG 700
   AAGTGTCCGC ACTTCTGGGC CGTATGCCAT CCGCGGTAGG TTATCAGCCA 750
   ACGCTGGCGG AAGAGATGGG CGTTCTGCAA GAACGTATCA CCTCGACCAA 800
   GACCGGTTCC ATCACCTCCG 820
20

```

2) INFORMATION FOR SEQ ID NO: 354

```

25 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 816 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

```

30 (ii) MOLECULE TYPE: Genomic DNA

```

(vi) ORIGINAL SOURCE:

```

35 (A) ORGANISM: Serratia fonticola
    (B) STRAIN: ATCC 29844

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 354

```

40 GATGCCGTAC CGAAAGTGTA CAACGCTCTT GAGGTTGCAA ACGGCACCGA 50
   GAAATTGGTG CTGGAAGTTC AGCAACAGCT GGGTGGCGGC GTGGTTCGCT 100
   GTATCGCAAT GGGGACCTCA GACGGTCTGC GTCGTGGTCT GGCCGTAACC 150
   GACCTGCAGC ACCCAATTGA AGTACCGGTA GGTAAAGCTA CCCTGGGCCG 200
   TATCATGAAC GTATTGGGTG AACCAATCGA CATGAAGGGC GACATCGGCG 250
   AAGAAGAACG TTGGGCTATT CACCGCCCTG CGCCAAGCTA CGAAGAGCTG 300
45 TCCAGCTCCC AGGATCTGCT GGAAACCGGT ATCAAGGTAA TGGACCTGAT 350
   CTGCCCCTTC GCCAAGGGTG GTAAAGTTGG TCTGTTCGGT GGTGCTGGTG 400
   TAGGTAAAAC CGTAAACATG ATGGAGCTGA TCCGTAACAT CGCGATCGAG 450
   CACTCCGGTT ATTCTGTGTT TCGGGGCGTG GGTGAACGTA CTCGTGAGGG 500
   TAACGACTTC TACCACGAAA TGACCGATTG CAACGTACTG GACAAAGTTT 550
50 CCCTGGTTTA CGGCCAGATG AACGAGCCAC CAGGTAACCG TCTGCGCGTT 600
   GCGCTGACCG GCCTGACCAT GGCTGAGAAG TTCCGTGACG AAGGTCGTGA 650
   CGTACTGCTG TTCGTCGATA ACATCTACCG TTATACCCTG GCCGGTACCG 700
   AAGTGTCCGC ACTTCTGGGC CGTATGCCAT CCGCGGTAGG TTATCAGCCA 750
   ACGCTGGCGG AAGAGATGGG TGTCTGCAA GAACGTATCA CCTCTACCAA 800
55 GACTGGTTCA ATCACC 816

```

2) INFORMATION FOR SEQ ID NO: 355

60

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Serratia grimesii*
 (B) STRAIN: ATCC 14460

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 355

```

15  GATGCCGTAC CAAAAGTGTA CAACGCTCTT GAGGTAGAAA ACGGTGCCAA      50
    TAAGCTGGTG CTGGAAGTTC AGCAACAGTT GGGCGGTGGC GTGGTTCGCT      100
    GTATCGCAAT GGGGACCTCT GATGGTCTGC GTCGCGGTCT GAAAGTCACA      150
    GACCTGGACC ACCCAATTGA AGTACCGGTA GGTAAAGCTA CTCTGGGCCG      200
    TATCATGAAC GTATTGGGTG AACCAATCGA CATGAAGGGC GATATCGGCG      250
20  AAGAAGAACG TTGGGCGATT CACCGTCCGG CGCCAAGCTA CGAAGATTG      300
    GCCAAGTCCC AGGATCTGCT GGAACCCGGT ATCAAGGTAA TGGACCTGAT      350
    CTGCCCCGTT GCCAAGGTG GTAAAGTCGG TCTGTTCGGT GGTGCGGGTG      400
    TTGGTAAAC CGTAAACATG ATGGAGCTGA TCCGTAACAT CGCGATCGAG      450
    CACTCCGGTT ATTCTGTGTT TCGGGGCGTG GGTGAGCGTA CTCGTGAGGG      500
25  TAACGACTTC TACCACGAAA TGAACGACTC CAACGTA CTG GACAAAGTAT      550
    CCCTGGTTTA CGGCCAGATG AACGAGCCAC CGGGTAACCG TCTGCGCGTT      600
    GCTCTGACCG GTCTGACCAT GGCTGAGAAA TTCCGTGACG AAGGCCGTGA      650
    CGTTCTGCTG TTCGTTGATA ACATCTACCG TTATACCCTG GCCGGTACCG      700
    AAGTGTCGCG ACTTCTGGGC CGTATGCCAT CGGCGGTAGG TTATCAGCCA      750
30  ACGCTGGCGG AAGAGATGGG TGTTCTGCAA GAACGTATCA CCTCTACCAA      800
    GACTGGTTCA ATCACCTCCG TA                                     822
  
```

35 2) INFORMATION FOR SEQ ID NO: 356

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 819 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Serratia liquefaciens*
 (B) STRAIN: ATCC 27592

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 356

```

50  ATGCCGTACC AAAAGTGTA AATGCTCTTG AGGTAGAAAA CCGTACCGAG      50
    AAGCTGGTGC TGGAAGTTCA GCAGCAGTTG GCGCGGTGGCG TAGTTCGCTG      100
    TATCGCGATG GGGACCTCAG ATGGTCTGCG CCGCGGTCTG AAAGTGAACG      150
    ATCTGGAACA CCCAATTGAA GTACCGGTAG GTAAAGCTAC CCTGGGCCGT      200
55  ATCATGAACG TATTGGGTGA ACCAATCGAC ATGAAAGGCG ACATCGGCGA      250
    AGAAGAACGT TGGGCGATTC ACCGTCCAGC GCCAAGCTAC GAAGATTTGT      300
    CAAACTCCCA GGATCTGCTG GAAACCGGTA TCAAGGTTAT GGACCTGATT      350
    TGTCCGTTTC CTAAGGGCGG TAAAGTTGGT CTGTTTCGGT GTGCTGGTGT      400
    TGGTAAAACC GTAAACATGA TGGAGCTGAT CCGTAACATC GCGATCGAGC      450
60  ACTCCGGTTA TTCCGTGTTT GCAGGCGTGG GTGAGCGTAC TCGTGAGGGT      500
  
```

	AACGACTTCT	ACCACGAAAT	GAACGACTCC	AACGTACTGG	ACAAAGTATC	550
	CCTGGTTTAC	GGCCAGATGA	ACGAGCCACC	GGGTAACCGT	CTGCGCGTTG	600
	CTCTGACCGG	TCTGACCATG	GCGGAGAAAT	TCCGTGACGA	AGGCCGCGAC	650
	GTTCTGCTGT	TCGTTGATAA	CATTTACCGT	TATACCCTGG	CCGGTACCGA	700
5	AGTGTCCGCA	CTTCTGGGCC	GTATGCCATC	TGCGGTAGGT	TATCAGCCAA	750
	CGCTGGCGGA	AGAGATGGGC	GTTCTGCAAG	AACGTATCAC	CTCTACCAAG	800
	ACCGGTTCTA	TCACTTCCG				819

10

2) INFORMATION FOR SEQ ID NO: 357

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 805 bases
15	(B)	TYPE: Nucleic acid
	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20

(vi) ORIGINAL SOURCE:

	(A)	ORGANISM: <i>Serratia marcescens</i>
	(B)	STRAIN: ATCC 13880

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 357

	TCAGGATGCC	GTACCGAAAG	TGTACGACGC	CCTTGAGGTA	GAAAACGGCA	50
	CCGAAAAACT	GGTGTTGGAA	GTTCAGCAAC	AGCTGGGCGG	TGGCGTGGTT	100
	CGCTGTATCG	CAATGGGGAC	CTCCGACGGT	CTGCGTCGCG	GTCTGAAAGT	150
30	GAACAACCTG	GACCACCCGA	TTGAAGTGCC	GGTGGGTAAA	GCTACCCTGG	200
	GTCGTATCAT	GAACGTATTG	GGTCAACCGA	TCGACATGAA	AGGCGACATC	250
	GGCGAAGAAG	AGCGTTGGGC	GATTCACCGC	GCGGCGCCAA	GCTACGAAGA	300
	GCTGTCAAGC	TCTCAGGAAC	TGCTGGAAAC	CGGTATCAAG	GTAATGGACC	350
	TGATTTGTCC	GTTTCGCCAAG	GGCGGTAAAG	TCGGTCTGTT	CGGCGGTGCG	400
35	GGCGTAGGTA	AAACCGTAAA	CATGATGGAG	CTGATCCGTA	ACATCGCGAT	450
	CGAGCACTCC	GGTTATTCCG	TGTTTGCGGG	CGTGGGCGAG	CGTACTCGTG	500
	AGGGTAACGA	CTTCTACCAC	GAAATGACCG	ACTCCAACGT	TCTGGACAAA	550
	GTATCCCTGG	TTTACGGCCA	GATGAACGAG	CCACCAGGTA	ACCGTCTGCG	600
	CGTTGCGCTG	ACCGGTCTGA	CCATGGCGGA	GAAATTCCGT	GACGAAGGCC	650
40	GTGACGTTCT	GCTGTTCTGT	GACAACATCT	ACCGTTACAC	CCTGGCCGGT	700
	ACCGAAGTGT	CCGCACTTCT	GGGCCGTATG	CCATCCGCGG	TAGGTTATCA	750
	GCCAACGCTG	GCGGAAGAGA	TGGGCGTTCT	GCAAGAACGT	ATCACCTCGA	800
	CCAAG					805

45

2) INFORMATION FOR SEQ ID NO: 358

(i) SEQUENCE CHARACTERISTICS:

50	(A)	LENGTH: 822 bases
	(B)	TYPE: Nucleic acid
	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

	(A)	ORGANISM: <i>Serratia odorifera</i>
60	(B)	STRAIN: ATCC 33077

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 358

```

5  GATGCCGTAC CAAAAGTGTA CGATGCCCTT GAGGTAGAAA ACGGTACCGA 50
   AACTCTGGTG CTGGAAGTTC AGCAGCAGCT GGGCGGTGGC GTGGTTCGTT 100
   GTATCGCTAT GGGCACCTCC GACGGTTTGC GTCGCGGCCT GAAAGTGAAC 150
   GATCTGCAAC ACCCAATCGA AGTCCCGGTT GGCAAGGCAA CGCTGGGTCG 200
   TATCATGAAC GTATTGGGTC AACCAATCGA CATGAAAGGC GACATCGGCG 250
   AAGAAGAGCG TTGGGCGATT CACCGCGCGG CGCCAAGCTA CGAAGAACTG 300
   TCCAATCCC AGGATCTGCT GGAAACCGGT ATCAAGGTTA TGGACCTGAT 350
10 CTGCCCCGTTT GCCAAGGGTG GTAAAGTCGG TCTGTTCGGT GGTGCGGGTG 400
   TTGGTAAAC CGTAAACATG ATGGAGCTGA TCCGTAAACAT CGCGATCGAG 450
   CACTCCGGTT ATTCAAGTGT TCGGGGCGTG GGTGAGCGTA CTCGTGAGGG 500
   TAACGACTTC TACCACGAAA TGACCGACTC CAACGTAAGT GACAAGGTTT 550
   CCCTGGTTTA CGGCCAGATG AACGAGCCAC CGGGTAACCG TCTGCGCGTT 600
15 GCGCTGACCG GTCTGACCAT GGCCGAGAAA TTCCGTGACG AAGGTCGTGA 650
   CGTTCTGCTG TTCGTTGACA ACATTTACCG TTACACCCTG GCCGGTACCG 700
   AAGTGTCTGC ACTTCTGGGC CGTATGCCAT CGGCGGTAGG TTATCAGCCA 750
   ACGCTGGCGG AAGAGATGGG CGTTCTGCAA GAACGTATCA CCTCGACCAA 800
   GACCGGTTCT ATCACCTCCG TA 822
20

```

2) INFORMATION FOR SEQ ID NO: 359

```

25 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 805 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

```

30 (ii) MOLECULE TYPE: Genomic DNA

```

(vi) ORIGINAL SOURCE:

```

35 (A) ORGANISM: Serratia plymuthica
    (B) STRAIN: ATCC 183

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 359

```

40 GTGTACAACG CTCTTGAGGT AGAAAACGGT GCCAATAAGC TGGTGCTGGA 50
   AGTTCAGCAA CAGCTGGGCG GTGGCGTGGT TCGCTGTATC GCGATGGGGA 100
   CCTCTGATGG TCTGCGTCGC GGTCTGAAAG TGATCGACCT GGATCACCCG 150
   ATTGAAGTAC CGGTAGGTAA AGCTACCCTG GGCCGTATCA TGAACGTATT 200
   GGGTGAACCA ATCGACATGA AAGGCGACAT CGGCGAAGAA GAACGTTGGG 250
   CAATTCACCG TCCAGCGCCA AGCTACGAAG ATTTGGCCAA CTCCCAGGAT 300
45 CTGCTGGAAA CCGGTATCAA GGTATGGAC CTGATCTGTC CGTTCGCTAA 350
   GGGCGGTAAA GTGGGTCTGT TCGGCGGTGC GGGCGTGGGT AAAACCGTAA 400
   ACATGATGGA GCTGATCCGT AACATCGCGA TCGAACACTC CGGTATATTC 450
   GTGTTTGCGG GCGTGGGTGA GCGTACTCGT GAGGGTAACG ACTTCTACCA 500
   CGAAATGAAC GACTCCAACG TACTGGACAA AGTATCCCTG GTTTACGGCC 550
50 AGATGAACGA GCCACCGGGT AACCGTCTGC GCGTTGCTCT GACCGGTCTG 600
   ACCATGGCGG AGAAATTCCG TGACGAAGGC CGCGACGTTT TGCTGTTCGT 650
   TGATAACATC TACCGTTATA CCCTGGCCGG TACCGAAGTG TCCGCACTTC 700
   TGGGCCGTAT GCCATCTGCG GTAGGTTATC AGCCAACGCT GGCGGAAGAG 750
   ATGGGCGTTC TGCAAGAACG TATCACCTCT ACCAAGACCG GTTCTATCAC 800
55 CTCCG 805

```

2) INFORMATION FOR SEQ ID NO: 360

60

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Serratia rubidaea*
 (B) STRAIN: ATCC 27593

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 360

```

15  TTCCCTCAGG ATGCCGTACC AAAAGTGTAC GATGCCCTTG AGGTAGAGAA      50
    CCGTAACGAA AAACCTGGTGC TGGAAGTTCA GCAGCAGCTG GGCGGCGGCG      100
    TTGTACGCTG TATCGCCATG GGTACTTCCG ACGGTCTGCG TCGCGGTCTG      150
    AAAGTTAACG ACCTCGAGCA CCCAATCGAA GTGCCAGTTG GTAAAGCAAC      200
    GCTGGGTCTG ATCATGAACG TATTGGGTCA GCCAATCGAC ATGAAAGGCG      250
20  ACATCGGCGA AGAAGAGCGT TGGGCGATTC ACCGCGCGGC GCCAAGCTAC      300
    GAAGAGCTGT CCAGCTCCCA AGAGCTGCTG GAAACCGGTA TCAAGGTAAT      350
    GGACCTGATC TGCCCGTTCT CCAAGGGTGG TAAAGTTGGT CTGTTCCGGT      400
    GTGCGGGCGT AGGTAAAACC GTAAACATGA TGGAGCTGAT CCGTAACATC      450
    GCGATCGAGC ACTCCGGTTA CTCTGTGTTT GCGGGCGTGG GTGAGCGTAC      500
25  TCGTGAGGGT AACGACTTCT ACCACGAAAT GACCGACTCC AACGTACTGG      550
    ACAAAGTATC CCTGGTTTAC GGCCAGATGA ACGAGCCGCC GGGTAACCGT      600
    CTGCGCGTTG CACTGACCGG CCTGACCATG GCGGAAAAAT TCCGTGATGA      650
    AGGCCGCGAC GTTCTGCTGT TCGTGGATAA CATCTACCGT TACACCCTGG      700
    CCGGTACCGA AGTGTCCGCA CTGCTCGGCC GTATGCCATC TGCGGTAGGT      750
30  TATCAGCCAA CGCTGGCGGA AGAGATGGGC GTTCTGCAAG AACGTATCAC      800
    CTCGACCAAG ACCGGTTCAA TCACCTCCGT A                        831
  
```

35 2) INFORMATION FOR SEQ ID NO: 361

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 406 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas putida*
 (B) STRAIN: LCDC D7172

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 361

```

50  CCGTAAACAT GATGGAAC TG ATCCGTAACA TCGCCATCGA GCACAGCGGT      50
    TATTCCGTGT TCGCCGGTGT GGGTGAGCGT ACTCGTGAGG GTAACGACTT      100
    CTACCACGAG ATGAAGGACT CCAACGTTCT CGACAAGGTA GCGCTGGTCT      150
    ACGGTCAGAT GAACGAGCCA CCAGGAAACC GTCTGCGCGT AGCGCTGACC      200
55  GGCCTGACCA TGGCCGAGAA GTTCCGTGAC GAAGGTAACG ACGTTCTGCT      250
    GTTCGTGAC AACATCTATC GTTACACCTT GGCCGGTACC GAAGTATCCG      300
    CACTGCTGGG CCGTATGCCT TCGGCGGTAG GTTACCAGCC GACCCTGGCT      350
    GAAGAGATGG GCGTTCTGCA AGAACGTATC ACTTCGACCA AGGAAGGTTT      400
    GATCAC                                           406
  
```

2) INFORMATION FOR SEQ ID NO: 362

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 831 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- 10 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Shigella boydii*
 15 (B) STRAIN: ATCC 9207
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 362

	TTCCCTCAGG	ATGCCGTACC	GCGCGTGTAC	GATGCTCTTG	AGGTGCAAAA	50
20	TGGTAATGAG	CGTCTGGTGC	TGGAAGTTCA	GCAGCAGCTC	GGCGGCGGTA	100
	TCGTGCGTAC	CATCGCAATG	GGTTCCTCCG	ACGGTCTGCG	TCGCGGTCCTG	150
	GATGTAAAAG	ACCTCGAACA	CCCgatCGAA	GTCCCGGTAG	GTAAAGCGAC	200
	TCTGGGCCGT	ATCATGAACG	TACTGGGTGA	ACCGGTCGAC	ATGAAAGGCG	250
	AGATCGGTGA	AGAAGAGCGT	TGGGCGATTC	ACCGCGCAGC	ACCTTCCTAC	300
25	GAAGAGCTGT	CAAACCTCTCA	GGAAC TGCTG	GAAACCGGTA	TCAAAGTTAT	350
	CGACCTGATG	TGTCCGTTCG	CTAAGGGCGG	TAAAGTTGGT	CTGTTCCGGTG	400
	GTGCGGGTGT	AGGTAAAACC	GTAAACATGA	TGGAGCTCAT	TCGTAAACATC	450
	GCGATCGAGC	ACTCCGGTTA	CTCTGTGTTT	GCGGGCGTAG	GTGAACGTAC	500
	TCGTGAGGGT	AACGACTTCT	ACCACGAAAT	GACCGACTCC	AACGTTATCG	550
30	ACAAAGTATC	CCTGGTGTAT	GGCCAGATGA	ACGAGCCGCC	GGGAAACCGT	600
	CTGCGCGTTG	CTCTGACCGG	TCTGACCATG	GCTGAGAAAT	TCCGTGACGA	650
	AGGTCGTGAC	GTTCTGCTGT	TCGTTGACAA	CATCTATCGT	TACACCCTGG	700
	CCGGTACGGA	AGTATCCGCA	CTGCTGGGCC	GTATGCCTTC	AGCGGTAGGT	750
	TATCAGCCGA	CCCTGGCGGA	AGAGATGGGC	GTTCTGCAGG	AACGTATCAC	800
35	CTCCACCAAA	ACTGGTTCTA	TCACCTCCGT	A		831

2) INFORMATION FOR SEQ ID NO: 363

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 802 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 45 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 50 (A) ORGANISM: *Shigella dysenteriae*
 (B) STRAIN: ATCC 11835
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 363

55	GCCGTACCGC	GCGTGTACGA	TGCTCTTGCG	GTGCAAAATG	GTAATGAGCG	50
	TCTGGTGCTG	GAAGTTCAGC	AGCAGCTCGG	CGGCGGTATC	GTGCGTACCA	100
	TCGCAATGGG	TTCTCCGAC	GGTCTGCGTC	GCGGTCTGGA	TGTAAAAGAC	150
	CTCGAACACC	CGATCGAAGT	CCCGGTAGGT	AAAGCGACTC	TGGGCCGTAT	200
	CATGAACGTA	CTGGGTGAAC	CGGTCGACAT	GAAAGCGGAG	ATCGGTGAAG	250
60	AAGAGCGTTG	GGCTATTAC	CGCGCAGCAC	CTTCCTACGA	AGAGCTGTCA	300

```

      AACTCTCAGG AACTGCTGGA AACCGGTATC AAAGTTATCG ACCTGATGTG      350
      TCCGTTTCGCT AAGGGCGGTA AAGTTGGTCT GTTCGGTGGT GCGGGTGTAG      400
      GTAAAACCGT AAACATGATG GAGCTCATTC GTAACATCGC GATCGAGCAC      450
      TCCGGTTACT CTGTGTTTGC GGGCGTAGGT GAACGTA CTC GTGAGGGTAA      500
5     CGACTTCTAC CACGAAATGA CCGACTCCAA CGTTATCGAC AAAGTATCCC      550
      TGGTGTATGG CCAGATGAAC GAGCCGCCGG GAAACCGTCT GCGCGTTGCT      600
      CTGACCGGTC TGACCATGGC TGAGAAATTC CGTGACGAAG GTCGTGACGT      650
      TCTGCTGTTT GTTGACAACA TCTATCGTTA CACCCTGGCC GGTACGGAAG      700
      TATCCGCACT GCTGGGCCGT ATGCCTTCAG CCGTAGGTTA TCAGCCGACC      750
10    CTGGCGGAAG AGATGGGCGT TCTGCAGGAA CGTATCACCT CCACCAAAC      800
      CG                                         802

```

15 2) INFORMATION FOR SEQ ID NO: 364

(i) SEQUENCE CHARACTERISTICS:

```

      (A) LENGTH: 819 bases
      (B) TYPE: Nucleic acid
20    (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

```

      (A) ORGANISM: Shigella flexneri
      (B) STRAIN: ATCC 12022

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 364

```

30    ATGCCGTACC GCGCGTGTAC GATGCTCTTG AGGTGCAAAA TGGTAATGAG      50
      CGTCTGGTGC TGGAAAGTTCA GCAGCAGCTC GCGGGCGGTA TCGTGCGTAC      100
      CATCGCAATG GGTTCCCTCCG ACGGTCTGCG TCGCGGTCTG GATGTAAAAG      150
      ACCTCGAACA CCCGATCGAA GTCCCGGTAG GTAAAGCGAC TCTGGGCCGT      200
35    ATCATGAACG TACTGGGTGA ACCGGTCGAC ATGAAAGGCG AGATCGGTGA      250
      AGAAGAGCGT TGGGCGATTG ACCGCGCAGC ACCTTCCTAC GAAGAGCTGT      300
      CAAACTCTCA GGAAGTGTG GAAACCGGTA TCAAAGTTAT CGACCTGATG      350
      TGTCCGTTCG CTAAGGGCGG TAAAGTTGGT CTGTTTCGGTG GTGCGGGTGT      400
      AGGTAAAACC GTAAACATGA TGGAGCTCAT TCGTAACATC GCGATCGAGC      450
40    ACTCCGGTTA CTCTGTGTTT GCGGGCGTAG GTGAACGTAC TCGTGAGGGT      500
      AACGACTTCT ACCACGAAAT GACCGACTCC AACGTTATCG ACAAAGTATC      550
      CCTGGTGTAT GGCCAGATGA ACGAGCCGCC GGGAAACCGT CTGCGCGTTG      600
      CTCTGACCGG TCTGACCATG GCTGAGAAAT TCCGTGACGA AGGTCGTGAC      650
      GTTCTGCTGT TCGTTGACAA CATCTATCTG TACACCCTGG CCGGTACGGA      700
45    AGTATCCGCA CTGCTGGGCC GTATGCCTTC AGCGGTAGGT TATCAGCCGA      750
      CCCTGGCGGA AGAGATGGGC GTTCTGCAGG AACGTATCAC CTCCACCAA      800
      ACTGGTTCTA TCACCTCCG                                         819

```

50 2) INFORMATION FOR SEQ ID NO: 365

(i) SEQUENCE CHARACTERISTICS:

```

      (A) LENGTH: 802 bases
55    (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Shigella sonnei*
 (B) STRAIN: ATCC 29930

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 365

```

GTACCGCGCG TGTACGATGC TCTTGAGGTG CAAAATGGTA ATGAGCGTCT 50
GGTGCTGGAA GTTCAGCAGC AGCTCGGCGG CGGTATCGTG CGTACCATCG 100
CAATGGGTTC CTCCGACGGT CTGCGTCGCG GTCTGGATGT AAAAGACCTC 150
10 GAACACCCGA TCGAAGTCCC GGTAGGTAAA GCGACTCTGG GCCGTATCAT 200
GAACGTACTG GGTGAACCGG TCGACATGAA AGGCGAGATC GGTGAAGAAG 250
AGCGTTGGGC GATTACCCGC GCAGCACCTT CCTACGAAGA GCTGTCAAAC 300
TCTCAGGAAC TGCTGGAAAC CGGTATCAAA GTTATCGACC TGATGTGTCC 350
GTTTCGCTAAG GGCGGTAAAG TTGGTCTGTT CGGTGGTGCG GGTGTAGGTA 400
15 AAACCGTAAA CATGATGGAG CTCATTCGTA ACATCGCGAT CGAGCACTCC 450
GGTTACTCTG TGTTTGCGGG CGTAGGTGAA CGTACTCGTG AGGGTAACGA 500
CTTCTACCAC GAAATGACCG ACTCCAACGT TATCGACAAA GTATCCCTGG 550
TGTATGGCCA GATGAACGAG CCGCCGGGAA ACCGTCTGCG CGTTGCTCTG 600
ACCGGTCTGA CCATGGCTGA GAAATTCCGT GACGAAGGTC GTGACGTTCT 650
20 GCTGTTTCGTT GACAACATCT ATCGTTACAC CCTGGCCGGT ACGGAAGTAT 700
CCGCACTGCT GGGCCGTATG CTTTCAGCGG TAGGTTATCA GCCGACCCTG 750
GCGGAAGAGA TGGGCGTTCT GCAGGAACGT ATCACCTCCA CCAAACTGG 800
TT 802

```

25

2) INFORMATION FOR SEQ ID NO: 366

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 785 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 366

```

TAACGCCTTG GTTATTGATG TGCCTAAAGA AGAAGGTACA ATACAACTAA 50
CATTAGAAAGT TGCGCTGCAA TTAGGTGACG ACGTTGTTTCG TACAATTGCG 100
ATGGATTCAA CTGATGGTGT CCAAAGAGGC ATGGATGTAA AAGATACAGG 150
45 CAAAGAAATT AGTGTAACCTG TTGGTGATGA AACATTAGGT CGTGTATTTA 200
ATGTACTAGG TGAAACAATT GACCTTAAAG AAGAAATTAG TGATTCTGTT 250
CGCCGCGATC CTATCCATCG TCAAGCACCA GCATTCGATG AACTTTCAAC 300
AGAAGTTCAA ATTTTAGAAA CAGGTATTAA AGTAGTAGAT TTACTAGCAC 350
CTTATATTAA AGGTGGTAAA ATCGGATTGT TCGGTGGTGC CGGTGTAGGT 400
50 AAAACAGTAT TAATCCAAGA ATTAATTAAC AACATCGCTC AAGAGCACGG 450
TGGTATTTCT GTATTCGCCG GTGTAGGTGA ACGTACTCGT GAAGGTAACG 500
ATTTATACTT CGAAATGAGT GATAGTGGTG TAATTAAGAA AACAGCCATG 550
GTATTCGGGC AAATGAATGA GCCACCTGGT GCACGTATGC GTGTTGCATT 600
ATCTGGTTTA ACAATGGCTG AATATTTCCG TGACGAACAA GGTCAAGACG 650
55 TATTATTATT CATCGATAAC ATTTTCAGAT TTACACAAGC TGGTTCTGAG 700
GTATCTGCAT TATTAGGTCG TATGCCTTCT GCAGTAGGTT ACCAACCAAC 750
ACTTGCTACT GAAATGGGAC AATTACAAGA ACGTA 785

```

60

2) INFORMATION FOR SEQ ID NO: 367

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 843 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus auricularis*
 (B) STRAIN: ATCC 33753

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 367

GAACATAACG	AAGTGCCTAA	TATTAATAAC	GCCTTAGTAC	TCGATGTTGA	50
AAGAGAAGAC	GGAACAGTGT	CTTTAACTTT	AGAAGTAGCT	TTACAATTAG	100
GCGATGACGT	TGTTTCGTACC	ATTGCAATGG	ATTCAACTGA	TGGTGTTAAA	150
CGTGGTAACG	AAGTCAAAGA	TACTGGTAAT	AGCATTAGCG	TACCAGTCGG	200
AGACGAAACT	TTAGGACGTG	TCTTCAACGT	TCTAGGTGAA	ACAATTGATT	250
TAGAAGATAA	ACTTGATGAT	TCTGCGCGAC	GTGACCCTAT	ACATAGAGAA	300
GCGCCAGCGT	TTGATCAATT	ATCAACTCAA	GTTGAAATTT	TAGAAACAGG	350
AATTAAAGTT	GTTGACTTAT	TAGCACCTTA	TATTAAAGGT	GGTAAAGTTG	400
GACTCTTCGG	TGGTGCCGGT	GTTGGTAAAA	CCGTTTTAAT	CCAAGAATTA	450
ATCAACAACA	TCGCTCAAGA	ACACGGTGGT	ATTTTCAGTCT	TTGCCGGTGT	500
AGGTGAACGT	ACACGTGAAG	GTAACGACTT	GTACTATGAA	ATGAGCGACA	550
GTGGTGTAAT	CAAGAAAACA	GCCATGGTCT	TCGGACAAAT	GAACGAACCA	600
CCTGGCGCAC	GTATGCGTGT	TGCTTTATCT	GGTTTAAACAA	TGGCTGAATA	650
TTTCCGTGAT	GAACAAGGAC	AAGACGTATT	GTTATTCATC	GACAATATTT	700
TCCGTTTCAC	ACAAGCCGGT	TCAGAAGTTT	CTGCCTTACT	AGGTCGTTTA	750
CCATCAGCCG	TTGGTTATCA	ACCTACATTA	GCAACAGAAA	TGGGACAATT	800
ACAAGAACGT	ATTACTTCAA	CAACAAAAGG	ATCAGTTACT	TCA	843

2) INFORMATION FOR SEQ ID NO: 368

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 849 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus capitis* subsp. *capitis*
 (B) STRAIN: ATCC 27840

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 368

GCTTTGAACA	TAATGAAGTT	CCTGATATTA	ACAATGCCTT	ACACATCGAA	50
GTTCCCTAAG	AAGATAGCAC	ACTTCATTTA	ACTTTAGAAG	TTGCACTTCA	100
ATTAGGTGAC	GATGTAGTAC	GTACAATCGC	AATGGACTCA	ACTGACGGCG	150
TTCAAAGAGG	TATGGAAGTT	AAAGATACAG	GTAAAGATAT	TAGCGTACCT	200
GTTGGTGATG	CAACTTTAGG	AAGAGTATTT	AACGTATTAG	GAGAAACAAT	250
CGATTTAGAT	GAAAAGATTG	ATGATTCAGT	ACGTCGTGAT	CCTATTCATA	300
GACAGGCACC	TGGCTTCGAT	GAATTATCTA	CTAAAGTAGA	AATCTTAGAA	350
ACAGGTATCA	AAGTAGTAGA	CTTATTAGCA	CCTTACATTA	AAGGTGGTAA	400

AATTGGATTA TTCGGTGGTG CCGGTGTTGG TAAGACAGTT TTAATCCAAG 450
 AACTTATCAA TAATATCGCT CAAGAGCATG GTGGTATTTT AGTATTCGCC 500
 GGTGTTGGTG AACGTACACG TGAAGGTAAC GACCTTTACT ATGAAATGAG 550
 CGATAGTGGT GTAATTAAGA AAACAGCGAT GGTATTCGGT CAGATGAACG 600
 5 AGCCACCTGG TGCTCGTATG CGTGTTGCAT TATCAGGTTT AACAAATGGCA 650
 GAATATTTCC GTGATGAAGA AGGCCAAGAC GTATTATTAT TCATTGATAA 700
 TATCTTCAGA TTCACACAAG CTGGTTCTGA AGTTTCAGCA TTAATTGGAC 750
 GTATGCCTTC AGCCGTTGGT TATCAACCAA CACTTGCTAC TGAAATGGGT 800
 CAATTACAAG AACGTATTAG TTCAACTAAT AAAGGTTCTG TTAATTCAA 849

2) INFORMATION FOR SEQ ID NO: 369

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 830 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 20 (ii) MOLECULE TYPE: Genomic DNA
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Staphylococcus cohnii*
 25 (B) STRAIN: DSM 20260

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 369

GAAGTTCCAG AAATTAATAA TGCCTTAGTT CTCGATATAG AAAGAGAAGA 50
 30 AGGTACTGTT GAATTAACGT TAGAAGTTGC ATTACAACCT GGTGATGACG 100
 TAGTACGAAC AATCGCAATG GATTCAACTG ATGGTGTTAA ACGTGGTACA 150
 GAAGTTAGAG ATAGCGGAAA TAGTATCAGC GTACCAGTTG GTAATGAAAC 200
 ATTAGGTAGA GTATTTAATG TATTAGGTGA TACGATAGAT TTAGATGAAG 250
 ACATAGATGA CTCAGTGCGT CGTGACCCAA TTCATAGAGA AGCACCTGCA 300
 35 TTTGATCAGT TATCTACTAA AGTTGAAATT TTAGAAACAG GTATCAAAGT 350
 CATTGATTTA TTAGCACCAT ATATCAAAGG TGGTAAAGTT GGATTATTCTG 400
 GTGGTGCCGG TGTTGGTAAA ACTGTATTAA TTCAAGAATT AATCAATAAT 450
 ATCGCTCAAG AGCATGGTGG TATATCCGTA TTTGCTGGTG TAGGTGAGCG 500
 TACGCGTGAA GGTAATGACC TATACCTTGA AATGAGTGAT AGTGGTGTTA 550
 40 TTAAAAAGAC AGCTATGGTA TTTGGACAAA TGAACGAACC ACCTGGTGCG 600
 CGTATGCGAG TAGCACTTTC TGGTTTAAAC ATGGCTGAAT ATTTCCGGGA 650
 TGAACAAGGA CAAGATGTTT TATTATTCAT AGATAACATC TTTAGATTTA 700
 CTCAAGCTGG TTCAGAAGTT TCTGCGTTAT TAGGTCGTAT GCCTTCAGCT 750
 GTTGGTTACC AACCAACGTT AGCAACTGAA ATGGGACAAT TACAAGAACG 800
 45 TATTACTTCT ACAACTAAAG GTTCAGTAAC 830

2) INFORMATION FOR SEQ ID NO: 370

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 787 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 55 (D) TOPOLOGY: Linear
 (ii) MOLECULE TYPE: Genomic DNA
 (vi) ORIGINAL SOURCE:
 60 (A) ORGANISM: *Staphylococcus epidermidis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 370

```

5  AATAATGCAT TACACATCGA AGTTCCTAAA GAAGATGGAG CGCTTCAATT 50
AACATTAGAA GTTGCACTTC AACTAGGTGA CGATGTAGTT CGTACAATTG 100
CAATGGACTC AACTGACGGC GTTCAAAGAG GAATGGAAGT TAAAGATACA 150
GGTAGAGACA TAAGTGTACC TGTCGGTGAC GTAACCTAG GAAGAGTGTT 200
TAACGTACTA GGAGAAACTA TTGACTTAGA TGAAAAAATT GATGATTCAG 250
TACGACGTGA CCCTATCCAT AGACAAGCTC CAGGATTCGA CGAATTATCA 300
10 ACAAAGTAG AAATCTTAGA AACTGGTATT AAAGTAGTAG ACTTATTAGC 350
ACCTTACATA AAAGGTGGTA AAATTGGATT ATTTGGTGGT GCCGGTGTAG 400
GTAAACCGT ACTAATCCAA GAACCTATTA ATAACATCGC TCAAGAACAC 450
GGTGGTATCT CAGTATTCGC TGGTGTGGT GAACGTACAC GTGAAGGTAA 500
TGATCTTTAC TATGAAATGA GTGACAGTGG TGTATCAAG AAAACTGCAA 550
15 TGGTCTTTGG TCAAATGAAT GAGCCACCTG GTGCACGTAT GCGTGTAGCA 600
TTATCCGGAT TAACAATGGC CGAATATTTT CGAGATGAAG AAGGCCAAGA 650
TGTGTTATTA TTCATTGATA ACATTTTCAG ATTCACTCAA GCTGGTTCAG 700
AAGTTTCTGC GTTATTAGGT CGTATGCCAT CAGCTGTTGG TTATCAACCT 750
ACACTTGCTA CAGAAATGGG TCAATTACAA GAACGTA 787
20

```

2) INFORMATION FOR SEQ ID NO: 371

```

25 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 830 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear
30 (ii) MOLECULE TYPE: Genomic DNA
    (vi) ORIGINAL SOURCE:
    (A) ORGANISM: Staphylococcus haemolyticus
35 (B) STRAIN: ATCC 29970

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 371

```

40 GAAGTACCTG AAATTAATAA CGCCTTAATC ATCGAAGTTC CCAAAGAAGA 50
TGGTACTTTT GAATTAACGC TTGAAGTTGC ATTACAAC TA GGTGATGACG 100
TTGTTTCGTAC AATTGCTATG GATTCAACAG ATGGTGTTCA ACGTGGTATG 150
GAAGTTCAGA AACTGGAAA AGACATTTCA GTACCAGTTG GCGAAGTAAC 200
TTTAGGACGT GTATTTAACG TATTAGGTGA CACAATTGAT TTAGAAGATA 250
AATTAGATGG TTCAGTAAGA CGTGATCCAA TTCATAGACA ATCACCTAAC 300
45 TTTGACGAAT TATCTACTGA AGTAGAAATT CTTGAAACTG GAATCAAAGT 350
TGTAGACTTA TTAGCACCAT ACATCAAAGG TGGTAAAATC GGTCTATTTG 400
GTGGTGCCGG TGTGGTAAA ACCGTTTTAA TCCAAGAATT GATTAATAAT 450
ATCGCACAAG AACATGGTGG TATCTCAGTA TTTGCTGGTG TAGGTGAACG 500
TACACGTGAA GGTAACGACC TATATTATGA AATGAGAGAT AGTGGTGT TA 550
50 TTAAGAAAAC AGCAATGGTA TTTGGTCAA TGAACGAGCC ACCTGGTGCA 600
CGTATGCGTG TGGCACTTTC TGCAATTGACA ATGGCTGAGT ATTTCCGTGA 650
TGAACAAGGA CAAGACGTTT TGTATTTCAT CGATAACATT TTCAGATTTA 700
CTCAAGCAGG TTCAGAAGTA TCAGCATTAT TGGGACGTAT GCCTTCAGCT 750
GTAGGTTATC AACCTACTTT AGCTACAGAA ATGGGTCAAT TACAAGAACG 800
55 TATTACATCA ACGAATAAAG GTTCAGTAAC 830

```

2) INFORMATION FOR SEQ ID NO: 372

60

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 846 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus hominis* subsp. *hominis*
 (B) STRAIN: ATCC 27844

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 372

```

15  TCGAACATAA TGAAGTCCCT GAAATTAATA ATGCCCTAAT TATTGAAGTA      50
    CCCAAAAATG ATGGCACATT TAAATTAACA TTAGAAGTTG CATTGCAACT      100
    AGGTGATGAT GTTGTTTCGTA CTATTGCAAT GGATTCAACT GATGGTGTTT      150
    AACGTGGTAT GCAAGTTGTG AATACTGGTA AAGATATTAG TGTTCCCTGTA      200
    GGTGAAGAAA CACTTGGACG TGTGTTTAAAC GTTTTAGGAG AAACAATAGA      250
    TTTAAACGAA AAAATAGATA GTTCTGTTAG ACGTGATCCA ATTCATCGTC      300
    GTCAACCTAA TTTTGATGAA TTATCTACTG AAGTAGAAAT TCTTGAAACA      350
    GGTATTAAAG TTGTAGACTT ATTAGCACCT TATATTAAAG GTGGTAAGAT      400
    TGGTTTATTC GGTGGTGCCG GCGTAGGTAA AACTGTATTA ATTCAAGAAT      450
    TAATCAATAA TATCGCTCAA GAACATGGTG GTATTTCTGT ATTCGCTGGT      500
    GTAGGTGAAC GTACTCGTGA AGGTAACGAT TTATACTATG AAATGAGCGA      550
    TAGTGGCGTT ATCAATAAAA CAGCCATGGT ATTTGGGCAA ATGAATGAGC      600
    CGCCAGGTGC GCGTATGCGT GTTGCTTTAT CAGCATTGAC AATGGCTGAA      650
    TATTTCCGTG ATGAACAAGG TCAAGATGTA CTTTTATTCA TTGACAATAT      700
    TTTCCGCTTT ACTCAAGCTG GTTCTGAAGT TTCAGCATTA TTAGGACGTA      750
    TGCCTTCAGC TGTAGGTTAT CAACCTACAT TAGCAACTGA AATGGGTCAA      800
    TTACAAGAAC GTATTACATC TACTAATAAA GGTTCAGTCA CTTCAA          846
  
```

2) INFORMATION FOR SEQ ID NO: 373

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 846 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus hominis*
 (B) STRAIN: CSG 175

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 373

```

50  TCGAACATAA TGAAGTCCCT GAAATTAATA ATGCCCTAAT TATTGAAGTA      50
    CCCAAAAATG ATGGCACATT CAAATTAACA TTAGAAGTTG CATTGCAACT      100
    AGGTGATGAT GTTGTTTCGTA CTATTGCAAT GGATTCAACT GATGGTGTTT      150
    AACGTGGTAT GCAAGTTGTG AATACTGGTA AAGATATTAG TGTTCCCTGTA      200
    GGTGAAGAAA CACTTGGACG TGTGTTTAAAC GTTTTAGGAG AAACAATAGA      250
    TTTAAACGAA AAAATAGATA GTTCTGTTAG ACGTGATCCA ATTCATCGTC      300
    GTCAACCTAA TTTTGATGAA TTATCTACTG AAGTAGAAAT TCTTGAAACA      350
    GGTATTAAAG TTGTAGACTT ATTAGCACCT TATATTAAAG GTGGTAAGAT      400
    TGGTTTATTC GGTGGTGCCG GCGTAGGTAA AACTGTATTA ATTCAAGAAT      450
    TAATCAATAA TATCGCTCAA GAACATGGTG GTATTTCTGT ATTCGCTGGT      500
  
```

	GTAGGTGAAC	GTACTCGTGA	AGGTAACGAT	TTATACTATG	AAATGAGCGA	550
	TAGTGGCGTT	ATCAATAAAA	CAGCCATGGT	ATTTGGGCAA	ATGAATGAGC	600
	CGCCAGGTGC	GCGTATGCGT	GTTGCTTTAT	CAGCATTGAC	AATGGCTGAA	650
	TATTTCCGTG	ATGAACAAGG	TCAAGATGTA	CTTTTATTCA	TTGACAATAT	700
5	TTTCCGCTTT	ACTCAAGCTG	GTTCTGAAGT	TTCAGCATTA	TTAGGACGTA	750
	TGCCTTCAGC	TGTAGGTTAT	CAACCTACAT	TAGCAACTGA	AATGGGTCAA	800
	TTACAAGAAC	GTATTACATC	TACTAATAAA	GGTTCAGTCA	CTTCAA	846

10

2) INFORMATION FOR SEQ ID NO: 374

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 835 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus lugdunensis*
(B) STRAIN: ATCC 43809

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 374

	ATAATGAAGT	GCCTGAAATA	AATAATGCGC	TCATTGTTGA	AATTCCTAAA	50
	AGTGATACAA	CAATCAGTTT	AACACTTGAA	GTTGCTTTGC	AATTAGGTGA	100
	CGATGTTGTA	CGTACTATTG	CAATGGATTC	AACTGATGGC	GTTCAACGTG	150
30	GTATGGAAGT	TCAAAACACA	GGTAAAGACA	TCAGTGTACC	TGTTGGAGAT	200
	GAAACATTAG	GAAGAGTATT	TAACGTTTTA	GGAGAATCTA	TTGATTTAGA	250
	AGAAAAGCTA	GATGACTCTG	TGCGTAGAGA	TCCAATTCAT	AGACTAGCAC	300
	CTAAATTTGA	TGAATTATCT	ACAGAAGTAG	AAATTCTTGA	AACTGGTATT	350
	AAAGTTGTTG	ATTTATTAGC	ACCATATATT	AAAGGTGGTA	AAGTTGGATT	400
35	GTTTGGTGGT	GCCGGAGTAG	GTAAAACGGT	ATTAATTCAA	GAATTAATCA	450
	ACAATATTGC	TCAAGAACAT	GGTGGTATTT	CTGTGTTTGC	CGGAGTAGGT	500
	GAACGTACAC	GTGAAGGTAA	TGACTTATAT	TATGAAATGA	GCGATAGTGG	550
	CGTAATTAAG	AAAACAGCGA	TGGTATTTGG	CCAAATGAAT	GAACCACCTG	600
	GTGCACGTAT	GAGAGTTGCG	TTATCTGCCT	TAACAATGGC	TGAATATTTT	650
40	CTGTACGAGC	AAGGACAAGA	CGTATTGCTG	TTTATCGATA	ATATATTCCG	700
	TTTTACACAA	GCAGGTTTCA	AAGTATCTGC	ATTACTTGGA	CGTATGCCAT	750
	CTGCCGTTGG	TTATCAACCA	ACATTGGCTA	CAGAAATGGG	ACAATTGCAA	800
	GAAAGAATTA	CATCTACAAA	TAAAGGTTCT	GTAAC		835

45

2) INFORMATION FOR SEQ ID NO: 375

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 842 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus saprophyticus*
(B) STRAIN: ATCC 15305

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 375

```

5  GAGCACAATG AAGTTCCAGA AATTAACAAT GCCTTAGTCG TAGACGTTGA 50
   AAGAGATGAA GGTACAGTAT CTCTTACATT AGAAGTGGCA TTACAACCTG 100
   CGCATGATGT CGTACGTACA ATTGCAATGG ATTCTACTGA TGGTGTTAAA 150
   CGTGGTACAG AAGTTCGAGA TAGCGGAGAT AGCATCAGTG TTCCAGTTGG 200
   TGATGCTACG TTAGGACGTG TGTTTAATGT TCTTGGTGAT ACAATTGACT 250
   TAGACGAGAA GCTTGATACT TCTGTCAAAC GTGATCCAAT TCATAGAGAA 300
   GCACCTGCAT TCGATCAATT ATCAACAAAA GTTGAAATCT TAGAAACAGG 350
10  TATTAAAGTA ATTGATTTAC TTGCACCATA TATTAAAGGT GGTAATTCG 400
   GTTTATTCGG TGGCGCTGGT GTAGGTAAAA CAGTATTAAT TCAAGAATTA 450
   ATTAATAATA TAGCTCAAGA ACATGGTGGT ATTTCAGTAT TTGCCGGCGT 500
   AGGTGAACGT ACGCGTGAAG GTAATGACTT ATACTACGAA ATGAGTGATA 550
   GTGGTGTTAT TAAGAAAACA GCTATGGTCT TCGGACAAAT GAATGAGCCA 600
15  CCTGGTGCGC GTATGCGTGT TGCTTTATCA GGCTTAACAA TGGCTGAACA 650
   CTTCCGTGAT GTACAAGGAC AAGATGTTTT ACTATTTATT GATAACATAT 700
   TCAGATTTAC GCAAGCTGGT TCAGAAGTAT CAGCACTATT AGGTCGTATG 750
   CCATCAGCCG TTGGTTATCA ACCTACCCTT GCTACTGAAA TGGGTCAATT 800
   ACAAGAACGT ATTACATCAA CAACTAAAGG ATCTGTAACG TC 842
20

```

2) INFORMATION FOR SEQ ID NO: 376

```

25  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 842 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear

```

```

30  (ii) MOLECULE TYPE: Genomic DNA

```

(vi) ORIGINAL SOURCE:

```

35  (A) ORGANISM: Staphylococcus simulans
      (B) STRAIN: ATCC 27848

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 376

```

40  TGATGAACTG CCTAAGATTA ATAACGCATT AGTGCTAGAT GTACCTAAGA 50
   AAGATGGCAC GACTGAATCT CTTACATTAG AAGTAGCACT TGAATTAGGC 100
   GACGACGTAG TTAGAACTAT CGCCATGGAC TCTACAGACG GAATTAAACG 150
   TGGTGACGAC GTTAAAGACA CTGGTCGTCC AATCAGTGTA CCTGTCGGTG 200
   AAGATACGTT AGGAAGAGTA TTTAACGTTT TAGGTGATCC AATCGATAAT 250
   GATGGACCGA TTTCTGAATC AGTTCCACGT GAACCAATTC ATAGACAACC 300
45  ACCTAAATTT GATGAATTAT CAACAAAAGT TGAACACTTT GAAACTGGTA 350
   TCAAAGTAGT AGACTTATTA GCACCATATA TCAAAGGTGG TAAAGTTGGT 400
   TTATTCCGTT GTGCCGGAGT AGGTAAAAC GTATTAATCC AAGAATTAAT 450
   TAATAACATC GCTCAAGAAC ACGGCGGTAT TTCAGTATTC GCAGGTGTTG 500
   GTGAACGTAC ACGTGAAGGT AACGACTTGT ACTTCGAAAT GAGCGACAGT 550
50  GGTGTTATCA AGAAAACAGC GATGGTATTC GGACAAATGA ACGAACCACC 600
   TGGTGACGCT ATGCGTGTAG CTTTATCAGG TTTAACAATG GCTGAATACT 650
   TCCGTGATGT TAAAGGACAA GACGTTCTTT TATTCATCGA TAACATTTTC 700
   CGCTTCACAC AAGCAGGTTT TGAGGTATCA GCATTGCTTG GCCGTATGCC 750
   ATCAGCCGTT GGTTACCAAC CAACATTGGC AACAGAAATG GGTCAATTAC 800
55  AAGAACGTAT CACTTCTACA ATGAAAGGTT CTATCACATC TA 842

```

2) INFORMATION FOR SEQ ID NO: 377

60

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 841 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus warneri*
 (B) STRAIN: ATCC 27836

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 377

```

15  CATAACGAAG TCCCTGATAT TAATAATGCC CTTATTATTG AAGTTCCAAA      50
    AGAAGATGGA ACGTTAAACT TAACATTAGA AGTTGCACTA CAATTAGGTG      100
    ATGATGTTGT ACGTACAATT GCAATGGATT CAACTGATGG TGTTCAAAGA      150
    GGCATGGATG TTAAGACAC AGGTAAAGAT ATTAGTGTAC CTGTAGGCGA      200
    TGAAACGCTT GGAAGAGTGT TTAATGTACT AGGTGAAACA ATTGACTTGG      250
20  AAGAGAAAAT TGATGATTCC GTACGTCGTG ATCCAATCCA TAGACAATCA      300
    CCAGGTTTCG ATGAATTATC TACTGAAGTA GAAATCTTAG AAACAGGTAT      350
    TAAAGTAGTA GACTTATTAG CACCTTACAT TAAAGGTGGT AAAGTTGGAC      400
    TATTCGGTGG TGCCGGAGTA GGTAACCCTG TTTTAATCCA AGAATTAATT      450
    AACAATATTG CACAAGAACA TGGTGGTATT TCAGTATTCT CCGGTGTAGG      500
25  TGAACGTACT CGTGAAGGTA ATGATTATA CTATGAAATG AGTGATAGTG      550
    GTGTAATTAA GAAAACAGCG ATGGTATTTG GACAAATGAA TGAACCACCT      600
    GGCACACGTA TCGGTGTAGC TTTATCTGGT TTAACATATG CTGAATACTT      650
    CCGTGATGAA CAAGGACAAG ACGTACTTTT ATTCATCGAT AATATTTTCA      700
    GATTTACACA AGCTGGTTCT GAAGTTTCTG CATTACTTGG TCGTATGCCT      750
30  TCAGCCGTTG GTTACCAACC AACATTAGCA ACTGAAATGG GTCAATTACA      800
    AGAACGAATT ACATCTACAA ATAAAGGTTT TGTAACATCT A              841
  
```

35 2) INFORMATION FOR SEQ ID NO: 378

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 846 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus acidominimus*
 (B) STRAIN: ATCC 51726

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 378

```

50  TTTAACACGA ATGAACCGCT TCCTGAGATA AATAATGCAC TTGTTGTTTA      50
    CAAAGACAGT GAGAAAAAAC ATAAAATCGT TCTTGAAGTA GCTCTTGAAC      100
    TTGGTGAAGG CCTCGTTCGT ACCATTGCTA TGGAAATCAAC TGATGGTTTG      150
    ACACGTGGTC TAGAAGTTCT TGATACAGGC CGTGCAATCA GTGTACCAGT      200
55  TGGTAAAGAA ACGCTTGGAC GTGTCTTCAA CGTTCTTGGT GATGCTATCG      250
    ATCTTGAAGA ACCATTTGGA GAAGATGCAG AACGTCACCC CATTCTAAG      300
    AGTGCCCCAA CTTTGTGATGA ATTATCAACG TCAACAGAAA TCCTTGAAAC      350
    AGGGATTAAA GTTATCGACC TACTTGCCCC TTAATAAAA GGAGGGAAGG      400
    TTGGACTTTT GGTGGTGCC GGAGTTGGTA AGACCGTTCT TATCCAAGAG      450
60  TTGATTCTAT ACATTGCTCA AGAGCATGGT GGTATTTCAG TATTTACCGG      500
  
```



```

AGTTGGTGAA CGTACACGTG AAGGTAATGA CCTCTATTGG GAAATGAAAG 550
AATCAGGCGT TATTGAAAAA ACAGCTATGG TATTTGGTCA GATGAATGAG 600
CCACCTGGTG CACGTATGCG TGTAGCCCTT ACTGGTTTGA CAATCGCTGA 650
ATATTTCCGT GATGTTGAAG GACAGGACGT GCTTCTCTTT ATTGATAACA 700
5 TTTTTCGTTT CACACAAGCA GGTTCTGAAG TTTCAGCTCT TCTTGGACGT 750
ATGCCATCAG CCGTTGGTTA TCAACCAACC TTGGCAACTG AAATGGGTCA 800
ATTGCAAGAA CGTATCACGT CAACTAAAAA AGTTTCTGTT ACATCA 846

```

10

2) INFORMATION FOR SEQ ID NO: 379

(i) SEQUENCE CHARACTERISTICS:

```

15 (A) LENGTH: 846 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

20

(vi) ORIGINAL SOURCE:

```

    (A) ORGANISM: Streptococcus agalactiae
    (B) STRAIN: ATCC 12403

```

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 379

```

TTGCAAGTGG CGACAAACTT CCTGAGATTA ATAATGCATT GATTGTCTAT 50
AAAAATGGCG ATAAGTCACA AAAAGTAGTA CTTGAAGTTA CTCTTGAAC 100
TGGTGACGGC CTCGTTTCGTA CAATCGCTAT GGAATCAACT GATGGGCTTA 150
30 CACGTGGTTT GGAAGTATTA GATACTGGTC GCGCAATTAG TGTGCCGGTT 200
GGTAAGGATA CTTTGGGTCG TGTCTTCAAC GTTCTTGGAG ATGCTATTGA 250
CCTTGAAGAG CCTTTTGCAG AAGATGCAGA ACGTCAACCA ATCCATAAAA 300
AAGCACCATC GTTTGATGAA TTATCAACAT CATCAGAAAT CTTAGAAACA 350
GGTATTAAAG TTATTGACTT ATTAGCACCT TACTTAAAAG GTGGTAAAGT 400
35 TGGACTTTTC GGTGGTGCAG GTGTTGGTAA AACCGTTCTT ATTCAAGAAT 450
TAATCCACAA CATCGCCCAA GAACATGGTG GTATTTTCAGT ATTTACTGGT 500
GTAGGAGAAC GTACTCGTGA AGGGAATGAC CTTTATTGGG AAATGAAAGA 550
ATCTGGCGTT ATTGAAAAAA CGGCTATGGT CTTTGGTCAA ATGAATGAAC 600
CACCAGGAGC ACGTATGCGT GTGGCACTTA CTGGTCTTAC AATAGCTGAG 650
40 TACTTCCGTG ATGTAGAAGG ACAAGATGTG CTTCTCTTCA TTGATAATAT 700
CTTCCGTTTC ACACAAGCTG GGTCAGAAGT GTCAGCGCTT TTAGGTCGTA 750
TGCCTTCAGC CGTTGGTTAT CAACCAACAC TTGCTACAGA AATGGGACAA 800
TTACAAGAGC GTATCACTTC AACTAAAAAA GGTTCGTGTT CCTCAA 846

```

45

2) INFORMATION FOR SEQ ID NO: 380

(i) SEQUENCE CHARACTERISTICS:

```

50 (A) LENGTH: 846 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

55 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

```

    (A) ORGANISM: Streptococcus agalactiae
    (B) STRAIN: ATCC 13813

```

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 380

```

5   TTGCAAGTGG CGACAAACTT CCTGAGATTA ATAATGCATT GATTGTCTAT    50
    AAAAATGGCG ATAAGTCACA AAAAGTAGTA CTTGAAGTTG CTCTTGAACT    100
    TGGTGACGGC CTCGTTTCGTA CAATCGCTAT GGAATCAACT GATGGGCTTA    150
    CACGTGGTTT GGAAGTATTA GATACTGGTC GCGCAATTAG TGTGCCGGTT    200
    GGTAAAGATA CTTTGGGTCG TGTCTTCAAC GTTCTTGGAG ATGCTATTGA    250
    TCTTGAAGAG CCTTTTGCAG AAGATGCAGA ACGTCAACCA ATCCATAAAA    300
    AAGCACCATC GTTTGATGAA TTATCAACAT CATCAGAAAT CTTAGAAACT    350
10  GGTATTAAAG TTATTGACTT ATTAGCACCT TACTTAAAAG GTGGTAAAGT    400
    TGGACTTTTC GGTGGTGCGG GTGTTGGTAA AACCGTTCTT ATTCAAGAAT    450
    TAATCCACAA CATCGCCCAA GAACATGGTG GTATTTCAGT ATTTACTGGT    500
    GTAGGAGAAC GTACTCGTGA AGGGAATGAC CTTTATTGGG AAATGAAAGA    550
    ATCTGGCGTT ATTGAAAAAA CGGCTATGGT CTTTGGTCAA ATGAATGAAC    600
15  CACCAGGAGC ACGTATGCGT GTGGCACTTA CTGGTCTTAC AATAGCTGAG    650
    TACTTCCGTG ATGTAGAAGG ACAAGATGTG CTTCTCTTCA TTGATAATAT    700
    CTTCCGTTTC ACACAAGCTG GGTCAGAAGT GTCAGCGCTT TTAGGTCGTA    750
    TGCCTTCAGC CGTTGGTTAT CAACCAACAC TTGCTACAGA AATGGGACAA    800
    TTACAAGAGC GTATCACTTC AACTAAAAAA GGTCTGTGTA CCTCAA      846
20

```

2) INFORMATION FOR SEQ ID NO: 381

```

25  (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 845 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear
30

```

```

--(ii) MOLECULE TYPE: Genomic DNA

```

(vi) ORIGINAL SOURCE:

```

35  (A) ORGANISM: Streptococcus agalactiae
    (B) STRAIN: ATCC 12973

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 381

```

40  TTGCAAGTGG CGACAAACTT CCTGAGATTA ATAATGCATT GATTGTCTAT    50
    AAAAATGGCG ATAAGTCACA AAAAGTAGTA CTTGAAGTTG CTCTTGAACT    100
    TGGTGACGGC CTCGTTTCGTA CAATCGCTAT GGAATCAACT GATGGGCTTA    150
    CACGTGGTTT GGAAGTATTA GATACTGGTC GTGCAATTAG TGTGCCGGTT    200
    GGTAAAGATA CTTTGGGTCG TGTCTTCAAC GTTCTTGGAG ATGCTATTGA    250
    CCTTGAAGAG CCTTTTGCAG AAGATGCAGA ACGTCAACCA ATCCATAAAA    300
45  AAGCACCATC ATTTGATGAA TTATCAACAT CATCAGAAAT CTTAGAAACA    350
    GGTATTAAAG TTATTGACTT ATTAGCACCT TACTTAAAAG GTGGTAAAGT    400
    TGGACTTTTC GGTGGTGCGG GTGTTGGTAA AACCGTTCTT ATTCAAGAAT    450
    TAATCCACAA CATCGCCCAA GAACATGGTG GTATTTCAGT ATTTACTGGT    500
    GTAGGAGAAC GTACTCGTGA AGGGAATGAC CTTTATTGGG AAATGAAAGA    550
50  ATCTGGCGTT ATTGAAAAAA CGGCTATGGT CTTTGGTCAA ATGAATGAAC    600
    CACCAGGAGC ACGTATGCGT GTGGCACTTA CTGGTCTTAC AATAGCTGAG    650
    TACTTCCGTG ATGTAGAAGG ACAAGATGTG CTTCTCTTCA TTGATAATAT    700
    CTTCCGTTTC ACACAAGCTG GGTCAGAAGT GTCAGCGCTT TTAGGTCGTA    750
    TGCCTTCAGC CGTTGGTTAT CAACCAACAC TTGCTACAGA AATGGGACAA    800
55  TTACAAGAGC GTATCACTTC AACTAAAAAA GGTCTGTGTA CCTCA      845

```

2) INFORMATION FOR SEQ ID NO: 382

60

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 845 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus agalactiae*
 (B) STRAIN: ATCC 27591

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 382

```

15 TTGCAAGTGG CGACAAACTT CCTGAGATTA ATAATGCATT GATTGTCTAT      50
   AAAAATGGCG ATAAGTCACA AAAAGTAGTA CTTGAAGTTG CTCTTGAACT      100
   TGGTGACGGC CTCGTTTCGTA CAATCGCTAT GGAATCAACT GATGGGCTTA      150
   CACGTGGTTT GGAAGTATTA GATACTGGTC GCGCAATTAG TGTGCCGGTT      200
   GGTAAGGATA CTTTGGGTCG TGTCTTCAAC GTTCTTGGAG ATGCTATTGA      250
20 CCTTGAAGAG CTTTTCGAG AAGATGCAGA ACGTCAACCA ATCCATAAAA      300
   AAGCACCATC GTTTGATGAA TTATCAACAT CATCAGAAAT CTTAGAAACT      350
   GGTATTAAAG TTATTGACTT ATTAGCACCT TACTTAAAAG GTGGTAAAGT      400
   TGGACTTTTC GGTGGTGCAG GTGTTGGTAA AACCGTTCTT ATTCAAGAAT      450
   TAATCCACAA CATCGCCCAA GAACATGGTG GTATTTTCAGT ATTTACTGGT      500
25 GTAGGAGAAC GTACTCGTGA AGGGAATGAC CTTTATTGGG AAATGAAAGA      550
   ATCTGGCGTT ATTGAAAAAA CGGCTATGGT CTTTGGTCAA ATGAATGAAC      600
   CACCAGGAGC ACGTATGCGT GTGGCACTTA CTGGTCTTAC AATAGCTGAG      650
   TACTTCCGTG ATGTAGAAGG ACAAGATGTG CTTCTCTTCA TTGATAATAT      700
   CTTCCGTTTC ACACAAGCTG GGTCAGAAGT GTCAGCGCTT TTAGGTCGTA      750
30 TGCCTTCAGC CGTTGGTTAT CAACCAACAC TTGCTACAGA AATGGGACAA      800
   TTACAAGAGC GTATCACTTC AACTAAAAAA GGTTCGTGTA CATCA          845

```

35 2) INFORMATION FOR SEQ ID NO: 383

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 845 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus agalactiae*
 (B) STRAIN: CDC ssl073

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 383

```

50 TTGCAAGTGG CGACAAACTT CCTGAGATTA ATAATGCATT GATTGTCTAT      50
   AAAAATGGCG ATAAGTCACA AAAAGTAGTA CTTGAAGTTG CTCTTGAACT      100
   TGGTGACGGC CTCGTTTCGTA CAATCGCTAT GGAATCAACT GATGGGCTTA      150
   CACGTGGTTT GGAAGTATTA GATACTGGTC GCGCAATTAG TGTGCCGGTT      200
55 GGTAAGGATA CTTTGGGTCG TGTCTTCAAC GTTCTTGGAG ATGCTATTGA      250
   CCTTGAAGAG CTTTTCGAG AAGATGCAGA ACGTCAACCA ATCCATAAAA      300
   AAGCACCATC GTTTGATGAA TTATCAACAT CATCAGAAAT CTTAGAAACT      350
   GGTATTAAAG TTATTGACTT ATTAGCACCT TACTTAAAAG GTGGTAAAGT      400
   TGGACTTTTC GGTGGTGCAG GTGTTGGTAA AACCGTTCTT ATTCAAGAAT      450
60 TAATCCACAA CATCGCCCAA GAACATGGTG GTATTTTCAGT ATTTACTGGT      500

```

	GTAGGAGAAC	GTACTCGTGA	AGGGAATGAC	CTTTATTGGG	AAATGAAAGA	550
	ATCTGGCGTT	ATTGAAAAAA	CGGCTATGGT	CTTTGGTCAA	ATGAATGAAC	600
	CACCAGGAGC	ACGTATGCGT	GTGGCACTTA	CTGGTCTTAC	AATAGCTGAG	650
	TACTTCCGTG	ATGTAGAAGG	ACAAGATGTG	CTTCTCTTCA	TTGATAATAT	700
5	CTTCCGTTTC	ACACAAGCTG	GGTCAGAAGT	GTCAGCGCTT	TTAGGTCGTA	750
	TGCCTTCAGC	CGTTGGTTAT	CAACCAACAC	TTGCTACAGA	AATGGGACAA	800
	TTACAAGAGC	GTATCACTTC	AACTAAAAAA	GGTTCTGTTA	CATCA	845

10

2) INFORMATION FOR SEQ ID NO: 384

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 845 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus dysgalactiae*
(B) STRAIN: ATCC 43078

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 384

	TTGCTAGTGG	GGACAAACTT	CCAGAGATTA	ATAATGCATT	GATTGTTTAT	50
	AAAGATAGTG	ATAAAAAGCA	AAAAATCGTC	CTTGAAGTTG	CTCTGGAACT	100
	TGGTGACGGT	ATGGTGCGAA	CAATCGCTAT	GGAATCAACT	GATGGGCTTA	150
30	CACGTGGGTT	AGAAGTTCTT	GACACTGGTC	GTGCGATTAG	TGTACCAGTA	200
	GGTAAAGAAA	CTTTGGGACG	CGTCTTTAAT	GTACTTGGAG	AAACCATTGA	250
	CTTGGAAGAA	CCATTGTCAG	AAGACGTTGA	CCGTCAGCCA	ATCCATAAAA	300
	AAGCACCATC	GTTTGATGAA	TTATCAACAT	CATCAGAAAT	TCTTGAAACT	350
	GGTATCAAGG	TAATTGACCT	TCTTGCCCCT	TACCTTAAAG	GTGGTAAAGT	400
35	TGGACTTTTC	GGGGGTGCCG	GAGTTGGTAA	GACTGTCCTT	ATCCAAGAAT	450
	TAATCCACAA	TATCGCCCAA	GAACACGGAG	GTATTTTCAGT	ATTTACCGGT	500
	GTTGGTGAGC	GAACACGTGA	AGGAAATGAC	CTTTACTGGG	AAATGAAAGA	550
	ATCAGGCGTT	ATTGAGAAAA	CTGCCATGGT	TTTTGGTCAG	ATGAATGAGC	600
	CGCCTGGGGC	ACGTATGCGT	GTAGCCCTTA	CTGGTTTAAC	CATTGCTGAG	650
40	TATTTCCGTG	ATGTAGAAGG	CCAAGATGTT	TTGCTCTTTA	TTGATAATAT	700
	CTTCCGTTTC	ACTCAGGCAG	GTTCAGAAGT	ATCAGCCCTC	TTAGGCCGTA	750
	TGCCTTCTGC	TGTTGGTTAC	CAACCGACCC	TTGCTACTGA	AATGGGACAA	800
	TTGCAAGAAC	GTATTACGTC	AACTCAAAAA	GGATCTGTTA	CTTCT	845

45

2) INFORMATION FOR SEQ ID NO: 385

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 846 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus equi* subsp. *equi*
(B) STRAIN: ATCC 9528

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 385

```

5  TTGCGAGTGG GGACAAACTA CCAGAGATTA ATAATGCGTT GATAGTTTAT 50
   AAAGATGGCG ATAAAAAGCA AAAAATCGTT CTCGAGGTTG CCCTAGAGCT 100
   TGGAGACGGT ATGGTACGTA CAATTGCTAT GGAATCAACC GATGGGCTTA 150
   CACGTGGATT AGAGGTTCTT GATACTGGTC GTGCCATTAG TGTACCAGTT 200
   GGTAAAGAGA CTCTAGGTCG TGTTTTCAAC GTTCTTGGTG AAACCATCGA 250
   CCTAGAAGCA CCATTTGCAG ATGATGTTAA TCGTGAACCG ATCCATAAAA 300
   AAGCACCAGC CTTTGATGAA TTGTCAACAT CATCAGAAAT TCTTGAAACA 350
10  GGTATCAAGG TTATTGACCT GCTTGCCCCC TACTTAAAGG GTGGTAAGGT 400
   CGGTCTTTTC GGTGGTGCCG GAGTTGGTAA AACCGTTCTT ATCCAAGAAT 450
   TAATCCACAA TATCGCTCAA GAGCATGGTG GGATCTCGGT ATTTACCGGT 500
   GTTGGTGAGC GTACGCGTGA AGGAAATGAC CTTTACTGGG AAATGAAGGA 550
   ATCAGGCGTT ATTGAAAAAA CAGCCATGGT TTTTGGTCAG ATGAATGAAC 600
15  CACCAGGAGC CCGTATGCGT GTTGCCCTGA CCGGCTTGAC AATTGCTGAA 650
   TATTTCCGCG ATGTTGAAGG CCAAGACGTC CTGCTCTTCA TTGACAATAT 700
   TTTCCGCTTT ACTCAAGCAG GCTCAGAGGT ATCAGCCCTT CTAGGTCGTA 750
   TGCCTTCAGC CGTTGGTTAC CAGCCAACAC TTGCCACTGA AATGGGACAA 800
   TTGCAAGAGC GTATCACCTC AACGAAAAAA GGCTCTGTTA CCTCTA 846
20

```

2) INFORMATION FOR SEQ ID NO: 386

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 846 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus anginosus*
 35 (B) STRAIN: ATCC 27335

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 386

```

40  TTGCAGCTGG TGATAAATTA CCTGAGATAA ATAATGCACT TGTAGTCTAT 50
   AAAAATGACG AAAATAAATC AAAAATCGTC CTTGAAGTAG CTCTTGAGCT 100
   TGGTGATGGA GTGGTTGCGA CTATTGCCAT GGAATCCACT GATGGGTTGA 150
   CTCGTGGCAT GGAAGTTCTA GATACTGGTC GACCAATTTC TGTTCCAGTT 200
   GGGAAAGAAA CACTTGGTCG CGTCTTTAAC GTTTTAGGCG ATACCATTGA 250
   TTTGGATACT CCATTCGGCG AAGATGCAGA ACGTCAACCA ATCCATAAAA 300
45  AAGCTCCAAC TTTTGATGAG TTATCTACTT CATCAGAAAT CTTAGAAACA 350
   GGAATAAAGG TTATTGACCT TTTAGCCCCC TACCTCAAAG GTGGGAAAGT 400
   CGGCCTCTTC GGTGGTGCTG GCGTTGGGAA AACTGTCTTG ATTCAAGAGT 450
   TGATTCTATA TATCGCCCAA GAACACGGCG GGATTTCAGT CTTTACTGGT 500
   GTTGGGGAAC GAACTCGTGA AGGGAATGAC CTGTACTGGG AAATGAAAGA 550
50  ATCTGGTGTT ATCGAAAAGA CGGCTATGGT CTTTGGGCAA ATGAATGAAC 600
   CGCCTGGAGC ACGTATGCGT GTAGCTTTGA CTGGGTTAAC GATTGCAGAG 650
   TATTTCCGTG ATGTGGAAGG TCAAGATGTT CTTTGTGTTA TTGATAATAT 700
   TTTCCGTTTC ACTCAAGCTG GTTCTGAAGT GTCAGCCCTT CTTGGTCGTA 750
   TGCCATCAGC TGTTGGTTAC CAACCAACCT TGGCTACTGA AATGGGGCAA 800
55  TTACAAGAAC GTATTACATC AACGAAAAAA GGTTCGTGTTA CCTCAA 846

```

2) INFORMATION FOR SEQ ID NO: 387

60

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 843 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus salivarius*
 (B) STRAIN: ATCC 7073

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 387

```

15 GCAGCTGGTG ATAAACTTCC TGAGATTAAC AATGCATTGG TCGTTTATAC      50
   TGATGAACAA AAGTCTAAAC GTATCGTGCT CGAAGTAGCT CTTGAACTTG      100
   GAGAAGGTGT GGTTCGTACC ATTGCCATGG AATCTACTGA TGGATTGACT      150
   CGTGGACTAG AAGTTCTGGA CACTGGTCGT CCAATCAGCG TTCCTGTTGG      200
   TAAAGATACC CTTGGACGTG TCTTTAACGT TCTTGGTGAT ACCATTGACT      250
20 TGAAGACACC TTTTGCAGAC GATGCAGAGC GTGAACCAAT TCACAAAAAA      300
   GCACCAACTT TCGATGAATT GTCAACATCT ACTGAAATCC TTGAAACAGG      350
   GATTAAAGTT ATCGACTTGC TAGCCCCCTTA CCTTAAGGGT GGTAAGTCG      400
   GACTCTTCGG TGGTGCCGGT GTTGGTAAAA CCGTTCCTTAT TCAAGAGTTG      450
   ATTCACAACA TTGCCCAAGA GCACGGTGGT ATTTCCGTGT TTACAGGTGT      500
25 TGGTGAACGT ACACGTGAAG GTAATGACCT TTAAGGGGAA ATGAAAGAAT      550
   CTGGCGTTAT CGAGAAAACA GCCATGGTCT TCGGTCAAAT GAACGAACCA      600
   CCTGGAGCAC GTATGCGTGT TGCCCTTACT GGTTTGACAA TTGCGGAATA      650
   CTTCCGTGAT GTCGAGGGTC AAGACGTTCT TCTCTTCATC GATAACATCT      700
   TCCGTTTCAC TCAAGCAGGT TCTGAGGTTT CTGCCCTTCT TGGTCGTATG      750
30 CCATCAGCCG TTGGTTACCA ACCTACACTT GCTACTGAAA TGGGTCAATT      800
   GCAAGAACGT ATCACATCAA CTAAAAAAGG TTCTGTTACA TCT          843

```

2) INFORMATION FOR SEQ ID NO: 388

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 841 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus suis*
 (B) STRAIN: ATCC 43765

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 388

```

50 TTGCAGCAGA AGATAAACTT CCTGAGATTA ACAACGCACT CGTTGTATAT      50
   AAAAATGATG ATTCCAAACA AAAAGTCGTG CTTGAAGTGG CTTTGGAACT      100
   TGGTGATGGC GTTGTACGGA CCATTGCCAT GGAATCAACG GATGGATTGA      150
   CACGTGGGAT GGAAGTTCTC GATACAGGTC GTCCCATCTC TGTTCCAGTC      200
55 GGTAAGAAA CGCTGGGTCG TGTCTTCAAT GTGTTGGGAG ATACCATTGA      250
   CCTTGAAGAG TCTTTTCCGG CAGATTTTGA ACGTGAGCCT ATCCATAAGA      300
   AAGCGCCGGC TTTTGACGAA TTATCTACTT CAAGCGAAAT TTTGGAAACA      350
   GGGATTAAGG TTATCGACCT CCTAGCACCT TATCTAAAAG GTGGTAAGGT      400
   TGGTCTCTTC GGTGGTGCTG GTGTTGGTAA AACCGTTCTT ATCCAAGAAT      450
60 TGATTCACAA TATTGCCCAA GAACACGGTG GTATCTCTGT ATTTACCGGA      500

```

GTTGGCGAGC GTACCCGTGA AGGGAACGAT CTTTACTGGG AAATGAAAGA 550
 ATCAGGTGTT ATTGAAAAAA CGGCCATGGT ATTTGGTCAG ATGAATGAGC 600
 CACCAGGAGC CCGTATGCGT GTTGCTCTTA CTGGTTTGAC TATTGCGGAA 650
 TACTTCCGTG ATGTGGAAGG GCAGGATGTT CTTCTGTTCA TCGATAATAT 700
 5 CTTCCGTTTC ACACAGGCTG GTTCAGAAGT GTCTGCCCTC TTGGGTCGTA 750
 TGCCATCAGC CGTTGGTTAT CAGCCAACAC TTGCGACGGA GATGGGACAA 800
 TTGCAGGAGC GTATTACCTC AACCAAGAAG GGTTCGTGTA C 841

10

2) INFORMATION FOR SEQ ID NO: 389

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 844 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus uberis*
 (B) STRAIN: ATCC 19436

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 389

GCAAACGGTG AAAAATTACC AGAGATTAAT AATGCATTGA TAGTTTATAA 50
 AGGTAGCGAT AAAAAACAAA AGATTGTTCT TGAAGTTGCT TTGGAAGTTG 100
 GGGACGGAAT GGTTTCGTACA ATCGCTATGG AATCAACTGA TGGGCTTACA 150
 30 CGTGGAATTAG AAGTTTTAGA TACTGGCCGT GCCATTAGTG TACCAGTCGG 200
 AAAAGAAACT TTGGGTCGTG TTTTCAATGT GCTTGGTGAA ACCATTGATT 250
 TGGATGAACC ATTTGCCGCT GATGCTGCAA GAGAACCCAT CCATAAAAAA 300
 GCCCCAGCAT TTGATGAAC ATCAACGTCT TCAGAAATTC TTGAAACCGG 350
 AATAAAAGTT ATTGACTTAT TAGCCCCTTA TCTCAAAGGT GGTAAGTTG 400
 35 GTTTATTTGG TGGTGCCGGA GTAGGTAAAA CGGTTTTAAT TCAAGAATTA 450
 ATTCATAATA TTGCACAAGA ACATGGTGGT ATTTCAGTAT TTACCGGTGT 500
 TGGTGAAAGA ACTCGTGAAG GTAATGACCT TTATTGGGAA ATGAAAGAAT 550
 CTGGCGTTAT TGAAAAACA GCCATGGTAT TTGGACAAAT GAACGAACCA 600
 CCAGGAGCAC GTATGCGCGT TGCTTTAACA GGTTTAACCA TTGCTGAATA 650
 40 TTTCCGGGAT GTTGAAGGTC AAGATGTTTT GCTCTTTATT GACAACATTT 700
 TCCGTTTCAC GCAAGCTGGT TCAGAAAGTT CAGCCCTATT GGGTCGTATG 750
 CCTTCAGCGG TAGGATACCA ACCAACACTT GCTACCGAAA TGGGACAATT 800
 GCAAGAAAGA ATTACCTCAA CTAACAAGGG ATCTGTTACT TCTA 844

45

2) INFORMATION FOR SEQ ID NO: 390

(i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 896 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tatumella ptyseos*
 (B) STRAIN: ATCC 33301

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 390

```

5  TTCCCTCAGG  ACGCTGTACC  ACAGGTGTAC  AACGCTCTTG  AGGTTGAAAA  50
   TGGTGATACC  CGTCTGGTGC  TGGAAGTTCA  GCAGCAGCTG  GGCGGTGGTG  100
   TCGTTCGTAC  GATTGCAATG  GGAACCTCTG  ACGGCCTGAA  ACGTGGCCTT  150
   AAGGTGACCG  ATCTGCAAAA  ACCGATTCAG  GTACCGGTCG  GTAAAGCGAC  200
   GCTGGGCCGT  ATCATGAACG  TACTGGGTCA  GCCAATCGAT  ATGAAAGGCG  250
   ACCTGAAGAA  CGAAGATGGT  AGCAATGTTG  AGGTGAACTC  TATTCACCGT  300
   GCAGCGCCAA  GCTACGAAGA  ACTGGCTAAC  TCTACTGAGC  TGCTGGAAAC  350
10  GGGTATCAAG  GTTATCGACC  TGATCTGTCC  GTTTGCAAAA  GCGGGTAAAG  400
   TGGGTCTGTT  CGGTGGTGCG  GGTGTAGGTA  AGACCGTCAA  CATGATGGAA  450
   CTGATCCGTA  ACATCGCTAT  CGAGCACTCT  GGTTACTCTG  TATTTGCAGG  500
   GGTGGGTGAG  CGTACCCGTG  AAGGTAACGA  CTTCTACCAC  GAAATGACCG  550
   AGTCTAACGT  TCTGGATAAA  GTTGCTCTGG  TTTATGGCCA  GATGAACGAG  600
15  CCACCAGGAA  ACCGTCTGCG  CGTTGCGCTG  ACCGGTCTGA  CTATGGCTGA  650
   AAAATTCCGT  GACGAAGGCC  GTGACGTACT  GCTGTTTCGT  GATAACATCT  700
   ATCGTTATAC  CCTGGCCGGT  ACTGAAGTTT  CAGCACTGCT  GGGTCGTATG  750
   CCTTCTGCGG  TAGGTTATCA  GCCAACACTG  GCCGAAGAAA  TGGGTGTTCT  800
   TCAGGAACGT  ATCACGTCAA  CCAAACCGG  TTCAATCACT  TCCGTA      896
20

```

2) INFORMATION FOR SEQ ID NO: 391

```

25  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 829 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear
30

```

```

(ii) MOLECULE TYPE: Genomic DNA

```

```

(vi) ORIGINAL SOURCE:

```

```

35  (A) ORGANISM: Trabulsiella guamensis
      (B) STRAIN: ATCC 49490

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 391

```

40  TTCCCTCAGG  ATGCCGTACC  GCGCGTGTAC  GATGCTCTTG  AGGTTATGAA  50
   TGGTAGTGAG  CGTCTGGTGC  TGGAAGTTCA  GCAGCAGCTC  GGTGGTGGTA  100
   TCGTACGTAC  TATCGCCATG  GGTTCTTCCG  ACGGTCTGCG  TCGTGGTCTG  150
   GATGTAAAAG  ATCTCGAGCA  TCCGATCGAA  GTCCCGGTAG  GTAAAGCAAC  200
   GCTGGGTCGT  ATCATGAACG  TGCTGGGTCA  GCCGATCGAT  ATGAAAGGCG  250
   ACATCGGCGA  AGAAGAGCGT  TGGGCTATCC  ACCGCGCAGC  ACCGTCCTAC  300
45  GAAGAGCTGT  CCAGCTCTCA  GGAAGTGTCT  GAAACCGGCA  TCAAAGTTAT  350
   CGACCTGATG  TGTCGGTTCG  CGAAGGGCGG  TAAAGTCGGT  CTGTTCCGGT  400
   GTGCGGGTGT  AGGTAAAACC  GTAAACATGA  TGGAGCTGAT  TCGTAACATC  450
   GCGATCGAGC  ACTCCGGTTA  CTCTGTGTTT  GCGGGCGTGG  GTGAACGTAC  500
   TCGTGAGGGT  AACGACTTCT  ACCACGAAAT  GACCGACTCC  AACGTTCTGG  550
50  ACAAAGTATC  CCTGGTGTAT  GGACAGATGA  ACGAGCCGCC  GGGAAACCGT  600
   CTGCGCGTTG  CACTGACCGG  TCTGACCATG  GCTGAGAAGT  TCCGTGACGA  650
   AGGTCGTGAC  GTTCTGCTGT  TCGTCGATAA  CATCTACCGT  TACACCCTGG  700
   CGGGTACTGA  AGTATCTGCA  CTGCTGGGCC  GTATGCCTTC  AGCGGTAGGT  750
   TACCAGCCGA  CCCTGGCGGA  AGAGATGGGT  GTTCTTCAGG  AACGTATCAC  800
55  CTCAACCAA  ACCGGTTCTA  TCACCTCCG

```

2) INFORMATION FOR SEQ ID NO: 392

```

60

```


(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yersinia bercovieri*
 (B) STRAIN: ATCC 43970

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 392

```

15 CGAATTCCCC CAAGACGCTG TACCAAAAGT GTACAACGCC CTTGAGGTTG      50
   AAGGCACAGC TCAGAAGCTG GTGCTGGAAG TTCAGCAACA GCTGGGCGGT      100
   GGTGTTGTTC GTTGTATCGC AATGGGCTCT TCCGATGGTC TGAGCCGCGG      150
   GTTGAAAGTC ATCAACCTGG AACACCCAAT TGAAGTGCCG GTGGGTAAAT      200
   CAACTCTGGG CCGTATCATG AACGTATTGG GTGACCCAAT CGACATGAAA      250
20 GGTCTTATCG GTGAAGAAGA GCGTTGGGCA ATCCACCGCG AAGCGCCTTC      300
   TTACGAAGAG CTGTCCAGCT CGCAAGATCT GTTAGAAACC GGTATCAAGG      350
   TAATGSGATCT GATTTGTCCG TTCTGCTAAGG GCGGTAAAGT CGGTCTGTTC      400
   GGTGGTGCGG GTGTGGGTAA AACAGTCAAC ATGATGGAGC TGATTTCGTAA      450
   TATTGCGATT GAGCACTCAG GTTATTCTGT ATTTGCCGGT GTGGGTGAGC      500
25 GTACTCGTGA GGGTAACGAC TTCTACCACG AGATGACTGA CTCCAACGTT      550
   CTGGACAAAG TATCCTTGGT TTATGGCCAG ATGAATGAGC CACCAGGTAA      600
   CCGTCTGCGC GTTGCCTGTA CCGGCTTGAC CATGGCGGAG AAATTCCGTG      650
   ATGAAGGTCG TGATGTACTG TTATTCATCG ATAACATCTA TCGTTATACC      700
   CTGGCCGGTA CAGAGGTATC TGCACGTGTA GGTCTGTATG CATCAGCGGT      750
30 AGGTATATCAG CCAACGCTGG CAGAAGAGAT GGGTGTGTTG CAGGAACGTA      800
   TCACTTCCAC CAAGACGGGT TCAATCACCT CCGTA                      835

```

35 2) INFORMATION FOR SEQ ID NO: 393

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 812 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yersinia enterocolitica*
 (B) STRAIN: ATCC 9610

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 393

```

50 GCTGTACCAA AAGTGTACAA CGCCCTTGAG GTTGAAGGCG CAGCTGAGAA      50
   GCTGGTGCTG GAAGTTCAGC AACAGCTGGG CGGTGGTGTT GTTCGTTGTA      100
   TCGCAATGGG CTCTTCCGAT GGTCTGAGCC GTGGGTGAA AGTCATCAAC      150
   CTGGAACACC CAATTGAAGT GCCTGTGGGC AAGTCAACTC TGGGCCGTAT      200
55 CATGAACGTA TTGGGTGACC CAATCGACAT GAAAGGTCCT ATCGCGGAAG      250
   AAGAGCGTTG GGCAATCCAT CGTGAAGCGC CTTCTTACGA AGATCTTGCC      300
   AGCTCGCAAG ACTTGTTAGA AACC GGATATC AAGGTAATGG ACTTGATTTG      350
   TCCGTTTCGCT AAGGGCGGTA AAGTCGGTCT GTTCGGTGGT GCGGGTGTAG      400
   GTAAAACGGT AAACATGATG GAGCTTATTC GTAACATTGC GATTGAGCAC      450
60 TCAGGTTATT CCGTATTTGC TGGCGTGGGT GAGCGTACTC GTGAGGGTAA      500

```

```

CGACTTCTAC CACGAGATGA CTGACTCCAA CGTTCCTGGAC AAAGTATCCT 550
TGGTTTATGG CCAAATGAAT GAGCCACCAG GTAACCGTCT GCGCGTTGCA 600
CTGACCGGCT TGACCATGGC GGAGAAATTC CGTGATGAAG GTCGTGACGT 650
ATTGCTGTTC ATCGATAACA TCTATCGCTA TACCTTAGCC GGTACGGAAG 700
5 TTTCCGCACT GCTGGGTCGT ATGCCATCTG CCGTAGGTTA CCAGCCAACG 750
CTGGCAGAAG AGATGGGTGT GTTGCAGGAA CGTATTACTT CCACCAAGAC 800
GGGTTCAATC AC 812

```

10

2) INFORMATION FOR SEQ ID NO: 394

(i) SEQUENCE CHARACTERISTICS:

```

15 (A) LENGTH: 802 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

20

(vi) ORIGINAL SOURCE:

```

    (A) ORGANISM: Yersinia frederiksenii
    (B) STRAIN: ATCC 33641

```

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 394

```

AAAGTGTACA ACGCCCTTGA GGTGAAGGT ACTGCTGAGA AGTTAGTACT 50
GGAAGTTCAG CAACAGCTGG GCGGTGGTGT TGCTCGTTGT ATCGCCATGG 100
GCTCTTCCGA TGGTTTGAGC CGCGGGTTGA AAGTTGTCAA CCTGGAACAC 150
30 CCAATTGAAG TACCGGTTGG TAAATCAACT CTGGGCCGTA TCATGAACGT 200
ATTGGGTGAC CCAATCGACA TGAAAGGTCC TATCGGTGAA GAAGAGCGTT 250
GGGCAATCCA CCGCGAAGCG CCTTCTTACG AAGAGCTTGC CAGCTCGCAA 300
GATCTGTTAG AAACCGGTAT CAAGGTAATG GATCTGATTT GCCCGTTCGC 350
TAAAGGCGGT AAAGTCGGTC TGTTCGGTGG TCGGGGTGTA GGTAAAACGG 400
35 TAAACATGAT GGAGCTGATC CGTAATATCG CGATCGAGCA CTCAGGTTAT 450
TCCGTATTTG CGGGTGTTGG TGAACGTACC CGTGAGGGTA ACGACTTCTA 500
CCACGAGATG ACTGACTCCA ACGTTCCTGGA CAAAGTATCC TTGGTTTATG 550
GCCAGATGAA TGAGCCACCA GGTAACCGTC TTCGCGTTGC ACTGACCGGT 600
CTGACCATGG CGGAGAAATT CCGTGATGAA GGTCTGTGAC TATTGCTGTT 650
40 CATCGATAAC ATCTATCGTT ATACCTTGGC CGGTACGGAA GTATCCGCAC 700
TGCTGGGTCTG TATGCCATCT GCGGTAGGCT ATCAGCCAAC GCTGGCAGAA 750
GAGATGGGTG TGTTGCAGGA ACGTATTACT TCCACCAAGA CGGGTTCAAT 800
CA

```

45

2) INFORMATION FOR SEQ ID NO: 395

(i) SEQUENCE CHARACTERISTICS:

```

50 (A) LENGTH: 806 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

55 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

```

    (A) ORGANISM: Yersinia intermedia
    (B) STRAIN: ATCC 29909

```

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 395

```

5  GCTGTACCAA GAGTGTACAA CGCCCTTGAG GTTGAAGGCA CTGCTGAGAA 50
   GCTGGTGCTG GAAGTTCAGC AACAGCTAGG CCGTGGTGTT GTTCGTTGTA 100
   TCGCAATGGG CTCTTCCGAT GGTCTGAGCC GCGGGTTGAA AGTCATCAAC 150
   CTGGAACACC CAATTGAAGT GCCGGTTGGT AAATCAACTC TGGGCCGTAT 200
   CATGAACGTA TTGGGTGACC CAATCGACAT GAAAGGTCCT ATCGGTGAAG 250
   AAGAGCGTTG GGCAATCCAC CGCGAAGCGC CTTCTTACGA AGAGCTTGCC 300
   AGCTCACAAG ATTTGTTAGA AACCGGTATC AAAGTAATGG ACTTGATTG 350
10 CCCGTTTCGCT AAGGGCGGTA AAGTGGGTCT GTTCGGTGGT GCGGGTGTAG 400
   GTAAACAGT AAACATGATG GAGCTTATTC GTAACATCGC GATTGAGCAC 450
   TCAGGTTATT CTGTATTTGC TGGTGTGGGT GAGCGTACTC GTGAGGGTAA 500
   CGACTTCTAC CACGAGATGA CTGACTCCAA CGTTCTGGAC AAAGTATCCT 550
   TGGTGTATTG CCAGATGAAT GAGCCACCAG GTAACCGTCT GCGCGTTGCA 600
15 CTGACCGGCC TGACCATGGC GGAGAAATTC CGTGATGAAG GTCGTGACGT 650
   ACTGTTGTTT ATCGATAACA TCTATCGCTA TACCTTGGCC GGTACGGAAG 700
   TATCCGCACT GCTGGGTCGT ATGCCATCAG CGGTAGGCTA CCAGCCAACG 750
   CTGGCAGAAG AGATGGGTGT GTTGCAGGAA CGTATTACGT CCACCAAGAC 800
   GGGTTC 806
20

```

2) INFORMATION FOR SEQ ID NO: 396

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 806 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yersinia pseudotuberculosis*
 35 (B) STRAIN: ATCC 29833

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 396

```

40 GCTGTACCAA AAGTGTACAA CGCCCTTGAG GTAGAAGGCA CAACTGAAAA 50
   GTTAGTGCTG GAAGTTCAGC AACAGTTGGG CCGTGGTGTT GTTCGTTGTA 100
   TCGCAATGGG CTCTTCCGAT GGTCTGAGCC GTGGGTTGAA AGTAACCAAC 150
   CTGGAACACC CGATCGAAGT ACCGGTTGGT AAAGCGACCC TTGGCCGTAT 200
   CATGAACGTA TTGGGTGAAC CAATCGACAT GAAAGGTCCT ATCGGTGAAG 250
   AAGAGCGTTG GGCAATCCAT CGCGAAGCGC CTTCTTATGA AGAGCTTGCT 300
45 AGCTCACAAG ATCTGTTAGA AACCGGTATC AAGGTTATGG ACCTGATTG 350
   TCCGTTTGCT AAGGGCGGTA AAGTCGGTCT GTTCGGTGGT GCGGGTGTAG 400
   GTAAACAGT AAACATGATG GAGCTGATCC GTAACATCGC GATCGAGCAC 450
   TCTGGGTATT CTGTATTTGC CGGTGTAGGT GAGCGTACCC GTGAGGGTAA 500
   TGACTTCTAC CATGAAATGA CTGACTCCAA CGTTTTGGAC AAAGTATCCT 550
50 TGGTTTACGG CCAGATGAAT GAGCCACCAG GTAACCGTCT ACGCGTTGCA 600
   CTGACCGGCC TGACCATGGC GGAGAAATTC CGTGATGAAG GTCGTGACGT 650
   ACTGCTGTTT ATCGATAATA TCTATCGTTA TACCCTAGCT GGTACGGAAG 700
   TATCCGCATT GCTGGGTCGT ATGCCATCAG CGGTAGGTTA TCAGCCAACA 750
   CTGGCTGAAG AGATGGGTGT GTTGCAGGAA CGTATTACTT CCACTAAGAC 800
55 GGGTTC 806

```

2) INFORMATION FOR SEQ ID NO: 397

60

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yersinia rohdei*
 (B) STRAIN: ATCC 43380

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 397

```

15  TTCCCCCAAG ACGCTGTACC AAAAGTGTAC AACGCCCTTG AGGTTGAAGG      50
    TGCAGCTGAG AAGCTTGTGC TGGAAGTTCA GCAGCAGCTG GGCGGTGGTG      100
    TTGTTTCGTTG TATCGCAATG GGCTCTTCCG ATGGTTTGAG CCGTGGGTTG      150
    AAAGTTATCA ACCTGGAACA CCCAATTGAA GTGCCAGTTG GTAAATCAAC      200
    TCTGGGCCGT ATCATGAACG TATTGGGTGA CCCAATCGAC ATGAAAGGCC      250
20  CTATCGGTGA AGAAGAGCGT TGGGCAATCC ACCGTGAAGC GCCTTCTTAC      300
    GAAGAGCTTG CCAGCTCGCA AGATCTGTTA GAAACCGGTA TCAAGGTAAT      350
    GGATCTGATT TGTCCGTTCG CTAAGGGCGG TAAAGTCGGT CTGTTTCGGTG      400
    GTGCGGGTGT TGGTAAAACA GTAAACATGA TGGAGCTTAT TCGTAACATC      450
    GCGATTGAGC ACTCAGGTTA TTCTGTATTT GCCGGGGTAG GTGAACGTAC      500
25  TCGTGAGGGT AACGACTTCT ACCACGAGAT GACTGACTCC AACGTTCTGG      550
    ACAAAGTATC CTTGGTTTAT GGCCAGATGA ATGAGCCACC AGGTAACCGT      600
    CTGCGCGTTG CACTGACCGG CTTGACCATG GCGGAAAAAT TCCGTGATGA      650
    AGGCCGTGAC GTATTGCTGT TCATCGATAA CATTTATCGT TATACCCTAG      700
    CCGGTACGGA AGTATCCGCA CTGCTGGGTC GTATGCCATC TCGCGTAGGC      750
30  TATCAGCCAA CACTGGCAGA AGAGATGGGT GTGTTGCAGG AACGTATTAC      800
    TTCCACTAAG ACGGGTTCAA TCACCTCCG      829
  
```

2) INFORMATION FOR SEQ ID NO: 398

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 819 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yokenella regensburgei*
 (B) STRAIN: ATCC 35313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 398

```

50  ATGCCGTACC GCGCGTGTA GATGCTCTTG AGGTACAAAA TGGTAACGAG      50
    AAAGTGGTGC TGGAAGCTCA GCAGCAGCTC GGCGGCGGTA TCGTGCGTAC      100
    TATCGCCATG GGTTCCTCCG ACGGTCTGCG TCGTGGTCTG GAAGTTAAAG      150
    ACCTCGAGCA CCCGATCGAA GTCCCGGTAG GTAAAGCAAC CCTGGGCCGT      200
55  ATCATGAACG TCCTGGGTCA GCCGATCGAC ATGAAAGGCG ACATCGGTGA      250
    AGAAGAGCGT TGGGCTATCC ACCGCGCAGC ACCTTCCTAT GAAGAGCTGT      300
    CCAGCTCTCA GGAAGTGTG GAAACCGGTA TCAAAGTAAT GGATCTGATC      350
    TGCCCGTTTC CTAAGGGTGG TAAAGTCGGT CTGTTCCGGT GTGCGGGTGT      400
    AGGTAAAACG GTAAACATGA TGGAGCTTAT CCGTAACATC GCGATTGAGC      450
60  ACTCCGGTTA CTCTGTGTTT GCAGGCGTGG GTGAACGTAC TCGTGAGGGT      500
  
```

	AACGACTTCT	ACCACGAAAT	GACCGACTCC	AACGTACTGG	ATAAAGTATC	550
	CCTGGTGTAC	GGCCAGATGA	ACGAGCCGCC	GGGAAACCGT	CTGCGCGTTG	600
	CGCTGACCGG	CCTGACCATG	GCTGAGAAAT	TCCGTGACGA	AGGCCGTGAC	650
	GTTCTGCTGT	TCGTCGATAA	CATCTACCGT	TATACCCTGG	CCGGTACGGA	700
5	AGTATCCGCA	CTGCTGGGTC	GTATGCCTTC	TGCGGTAGGT	TATCAGCCAA	750
	CTCTGGCGGA	AGAGATGGGT	GTTCTTCAGG	AACGTATCAC	CTCTACCAAA	800
	ACCGGTTCTA	TCACCTCCG				819

10

2) INFORMATION FOR SEQ ID NO: 399

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 1097 bases
15	(B)	TYPE: Nucleic acid
	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

	(A)	ORGANISM: <i>Yarrowia lipolytica</i>
	(B)	STRAIN: ATCC 38295

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 399

	AAGCTTAAGG	CTGAGCGAGA	GCGAGGTATC	ACCATTGATA	TCGCTCTCTG	50
	GAAGTTCCAG	ACCCCTAAGT	ACTACGTCAC	CGTTATTGAT	GCTCCCGGTC	100
	ACCGAGATTT	CATCAAGAAC	ATGATTACCG	GTACTTCCCA	GGCTGACTGC	150
30	GCCATCCTCA	TCATTGCTGG	TGGTGTTGGT	GAGTTCGAGG	CTGGTATCTC	200
	CAAGGATGGT	CAGACECGAG	AGCACGCCCT	GCTCGCTTTC	ACCCTCGGTG	250
	TTAAGCAGCT	CATTGTTGCT	ATCAACAAGA	TGGACTCCGT	CAAGTGGTCT	300
	CAGGATCGAT	ACCTCGAGAT	TTGCAAGGAG	ACTGCCAACT	TCGTCAAGAA	350
	GGTCGGTTAC	AACCCCAAGG	CTGTCCCCTT	CGTCCCCATT	TCCGGATGGA	400
35	ACGGTGACAA	CATGATCGAG	CCCTCTACCA	ACTGTGACTG	GTACAAGGGA	450
	TGGACCAAGG	AGACCAAGGC	CGGCGAGATC	AAGGGTAAGA	CCCTCCTCGA	500
	GGCCATTGAT	GCCATTGAGC	CCCCCGTGCG	ACCCACGAC	AAGCCCCTCC	550
	GACTTCCCCT	CCAGGATGTC	TACAAGATCG	GTGGTATCGG	CACAGTGCCC	600
	GTTGGCCGAG	TCGAGACCGG	TGTTATCAAG	GCCGGTATGG	KTGTTACCTT	650
40	CGCTCCCGCC	AACGTGACCA	CTGAGGTCAA	GTCTGTGAG	ATGCACCACG	700
	AGATCCTCCC	CGATGGAGGT	TTCCCCGGTG	ACAACGTCGG	TTTCAACGTC	750
	AAGAACGTTT	CCGTCAAGGA	TATCCGACGA	GGTAACGTTG	CTGGTGACTC	800
	CAAGAACGAC	CCCCCAAGG	GCTGCGACTC	TTTCAACGCT	CAGGTCATTG	850
	TTCTTAACCA	CCCCGGTCAG	ATCGGTGCTG	GTTACGCTCC	CGTCCTTGAT	900
45	TGCCCACTG	CCCACATTGC	TTGCAAGTTC	GACACCCTGA	TCGAGAAGAT	950
	CGACCGACGA	ACCGGTAAGA	AGATGGAGGA	CTCCCCAAG	TTCATCAAGT	1000
	CTGGTGATGC	TGCCATTGTC	AAGATGGTTC	CCTCCAAGCC	CATGTGTGTC	1050
	GAGGCCTTCA	CTGAGTACCC	CCCTCTTGGT	CGATTGCGCC	TCCGAGA	1097

50

2) INFORMATION FOR SEQ ID NO: 400

(i) SEQUENCE CHARACTERISTICS:

55	(A)	LENGTH: 1233 bases
	(B)	TYPE: Nucleic acid
	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

60 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Absidia corymbifera*
 (B) STRAIN: ATCC 46775

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 400

CAAGCTTAAG GCTGAACGTG AGCGTGGTAT CACCATCGAT ATCGCTCTCT 50
 GGAAGTTCGA GACTCCCAAG TACCACGTTA CCGTCATTGA TGCCCCTGGC 100
 10 CATCGTGATT TCATCAAGAA CATGATTACT GGTACTTCCC AAGCTGACTG 150
 CGGTATCTTG ATTATTGCTG CTGGTACTGG TGAATTCGAA GCTGGTATCT 200
 CCAAGGATGG TCAAACCCGT GAACACGCTT TGCTTGCTTT CACCCTTGGT 250
 GTCCGTCAAT TGATTGTCGC TATCAACAAG ATGGATTCCA CCAAGTACTC 300
 TGAGGCCCGT TACAACGAAA TTGTCAAGGA AGTCTCCACC TTCATCAAGA 350
 15 AGATTGGTTT CAACCCCAAG TCCGTTCCCTT TCGTCCCTAT CTCTGGCTGG 400
 AACGGTGACA ACATGTTGGA GGARTCCACC AACATGCCTT GGTTCAAGGG 450
 ATGGAACAAG GAGACTAAGG CTGGTGCCAA GACYGGCAAG ACCCTTCTTG 500
 AAGCCATTGA CAACATTGAT CCCCCTGTTC GTCCTTCCGA CAAGCCCCTT 550
 CGTCTTCCCC TTCAAGATGT CTACAAGATC GGTGGTATTG GTACAGTTCC 600
 20 TGTCGGTCGT GTTGAGACTG GTGTCATCAA GCCTGGTATG GTTGTACCT 650
 TCGCTCCCGC TAACGTCACC ACTGAAGTCA AGTCCGTYGA AATGCACCAC 700
 GAGCAACTTG CTGAAGGTGT TCCCGGTGAC AACGTCGGTT TCAACGTCAA 750
 GAACGTTTCC ATCAAGGATA TCCGCCGTGG TAACGTYTGC TCTGACTCCA 800
 AGAACGACCC CGCCAAGGAA TCCGCTTCCT TCACCGCTCA AGTTATTGTC 850
 25 TTGAACCACC CTGGTCARAT TGGTGCTGGT TACTCTCCTG TCTTGATTG 900
 CCACACTGCT CACATTGCAT GCAAGTTCTY TKAGCTTCTT KAGAAGATCG 950
 ATYGTCGTTT CGGTAAGTAA ATANTTTGGT TTRGGATATG GGTATTGGGC 1000
 TTAATCTYTG GATTTTGCCT CAATTGCTCC TTCCTTGATC TTTCTCGATT 1050
 ACTTTTGTAT CATTGTCTAA TCCAAACCTT TTCCATTTYA TTGAAAACAG 1100
 30 GTAAGAAGTT GGAAGACTCC CCCAAGTTCG TCAAGWSYGG TGAAGTCTGCY 1150
 ATCGTCAAGA TGGTTCCTTC CAAGCCCATG TCGGTTGAAG CCTACACTGA 1200
 ATATCCTCCT CTGGTTCGTT TCGCTGTCCG TGA 1233

35

2) INFORMATION FOR SEQ ID NO: 401

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1151 bases
 40 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Alternaria alternata*
 (B) STRAIN: ATCC 62099

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 401

CAAGTTGAAG GCCGAGCGTG AGCGTGGTAT CACCATCGAC ATTGCTCTCT 50
 GGAAGTTCGA GACTCCCAAG GTTAGTACCC CTCTGCCTAC TACATCAAGT 100
 TCTTTACAAT GCTAACATGT TGTACTCAGT ACTATGTCAC CGTCATTGAC 150
 55 GCCCCCGGTC ACCGTGATTT CATCAAGAAC ATGATCACTG GTACCTCCCA 200
 GGCCGACTGC GCTATTCTCA TCATTGCCGC CGGTACTGGT GAGTTCGAGG 250
 CTGGTATCTC CAAGGATGGC CAGACTCGTG AGCACGCTCT CCTCGCTTAC 300
 ACCCTCGGTG TCAAGCAGCT CATCGTTGCC ATCAACAAGA TGGACACCAC 350
 CAAGTGGTCC GAGGAGCGTT ACCAGGAGAT CATCAAGGAG ACCTCCAAC 400
 60 TCATCAAGAA GGTGCGCTAC AACCCTCAAGC ACGTTCCCTT CGTCCCCATC 450

	TCCGGTTTCA	ACGGTGACAA	CATGATTGAG	GCCTCATCCA	ACTGCCCCTG	500
	GTACAAGGGT	TGGGAGAAGG	AGACCAAGGC	CAAGGCCACT	GGTAAGACCC	550
	TCCTCGAGGC	CATCGACGCC	ATCGACCCTY	CCAGCCGTCC	CACCGACAAG	600
	CCCCTCCGTC	TTCCCCCTYCA	GGATGTTTAC	AAGATTGGTG	GTATTGGCAC	650
5	GGTGCCCCTG	GGTCGTGTCG	AGACCGGTAT	CATCAAGGCC	GGTATGGTCG	700
	TCACCTTCGC	CCCCGCTGGT	GTCACCACTG	AAGTCAAGTC	CGTCGAGATG	750
	CACCACGAGC	AGCTCACCGA	GGGTGTCCCC	GGTGACAACG	TCGGCTTCAA	800
	CGTCAAGAAC	GTCTCCGTCA	AGGAGATCCG	TCGTGGTAAC	GTTGCCGGTG	850
	ACTCCAAGAA	CGACCCCCCC	AAGGGTGCCG	AGTCCTTCAA	CGCCCAGGTC	900
10	ATCGTCCTCA	ACCACCCCTG	TCAGGTCGGT	GCTGGTTACG	CCCCAGTCCT	950
	CGACTGCCAC	ACCGCCCCACA	TTGCTTGCAA	GTTCTCTGAG	CTCCTCGAGA	1000
	AGATTGACCG	CCGTACCGGA	AAGTCTGTTG	AGAACTCTCC	CAAGTTCATC	1050
	AAGTCCGGTG	ACGCCGCCAT	CGTCAAGATG	GTTCCCTCCA	AGCCCATGTG	1100
	CGTTGAGGCT	TTCAC TGACT	ACCCTCCTCT	CGGTCGTTTC	GCTGTCCGTG	1150
15	A					1151

2) INFORMATION FOR SEQ ID NO: 402

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1283 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus flavus*
 (B) STRAIN: ATCC 26947

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 402

35	CAAGCTCAAG	TCCGAGCGTG	AGCGTGGTAT	CACCATCGAT	ATCGCCCTCT	50
	GGAAGTTCCA	GACCTCCAAG	TATGAGGTCA	CCGTCATTGG	TAAGCATTTG	100
	AGTTCCAACC	TACGTTGCCC	AACATTTACA	GTCATCTAAC	AAAGTTCAAT	150
	AGATGCCCCC	GGTCACCGTG	ACTTCATCAA	GAACATGATC	ACTGGTACTT	200
	CCCAGGCTGA	CTGCGCTATC	CTCATCATTG	CCTCCGGTAC	TGGTGAATTC	250
40	GAGGCTGGTA	TCTCCAAGGA	TGGTCAGACC	CGTGAGCACG	CTCTGCTCGC	300
	TTTCACCTC	GGTGTCCGTC	AGCTCATCGT	TGCCCTCAAC	AAGATGGACA	350
	CCTGCAAGTG	GTCTCAGGAT	CGTTACAACG	AAATCGTTAA	GGAGACTTCC	400
	AACTTCATCA	AGAAGGTCGG	ATACAACCCC	AAGAGCGTTC	CTTTCGTCCC	450
	CATCTCCGGT	TTCAACGGTG	ACAACATGAT	TGAGGCCTCC	ACCAACTGCC	500
45	CCTGGTACAA	GGGTTGGGAG	AAGGAGACCA	AGGCTGGCAA	GTCCACCGGT	550
	AAGACCCTTC	TCGAGGCCAT	CGATGCCATC	GAGCCCCCCG	TCCGTCCCAC	600
	CGACAAGCCT	CTCCGTCTTC	CCCTYCAGGA	TGTCTACAAG	ATCTCTGGTA	650
	TCGGTACTGT	GCCCGTCGGT	CGTGTCGAGA	CTGGTGTGAT	CAAGCCTGGT	700
	ATGGTCGTTA	CTTTCGCTCC	TGCCAACGTG	ACCACTGAAG	TCAAGTCCGT	750
50	TGAAATGCAC	CACCAGCAGC	TCCAGGCCGG	TAACCCCGGT	GACAACGTTG	800
	GTTTCAACGT	CAAGAACGTC	TCCGTCAAGG	AAGTCCGCCG	TGGTAACGTT	850
	GCCGGTGACT	CCAAGAACGA	CCCCCCTGCT	GGCTGCGATT	CCTTCAACGC	900
	CCAGGTCATC	GTCTTAAACC	ACCCCGGTCA	GGTCGGCAAC	GGTTACGCTC	950
	CCGTCTGGA	CTGCCACACC	GCTCACATTG	CTTGCAAGTT	CGCTGAGCTC	1000
55	TTTGAGAAGA	TTGACCGCCG	TACCGGTAAA	TCTGTTGAGG	ACAAGCCCAA	1050
	GTTTCATCAAG	TCTGGTGATG	CTGCCATCGT	CAAGATGATT	CCCTCCAAGC	1100
	CCATGTGTGT	GGAGTCTTTC	ACTGACTTCC	CCCCTCTTGG	TCGTTTCGCT	1150
	GTCCGTGACG	TAAGTTTTTC	CCTCTTGACT	ATCTTCACAA	TTTTTTCACAT	1200
	ATTTTCACGC	CTCGTCCCAC	TCTTTTTCCT	CCCTTCCTCT	TTGGTTCCCC	1250
60	TTTTTGCCTG	CAAGTTCTCT	ATAGCTAACA	TGA		1283

2) INFORMATION FOR SEQ ID NO: 403

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1103 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus fumigatus*
 (B) STRAIN: DAL95

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 403

```

20  TCCGAGCGTG AGCGTGGTAT CACCATCGAC ATTGCCCTCT GGAAGTTCCA      50
    GACTCCCAAG TATGAGGTCA CTGTCATCGG TAAGCTCGAC TCGCCCCGAT      100
    ATGTTTGGT GCTGTAGCTA ACACGATCTG AAGATGCCCC CGGTCACCGT      150
    GACTTCATCA AGAACATGAT CACTGGTACC TCCCAGGCTG ACTGCGCTAT      200
    CCTCATCATT GCCTCCGGTA CTGGTGAGTT CGAGGCTGGT ATCTCCAAGG      250
25  ATGGCCAGAC CCGTGAGCAC GCTCTGCTGG CTTTCACCCT CGGTGTCAAG      300
    CAGCTCATCG TCGCCCTCAA CAAGATGGAC ACCTGCAAGT GGTCCGAGGA      350
    TCGTTACAAC GAAATTGTCA AGGAAACCTC CAACTTCATC AAGAAGGTCG      400
    GCTACAACCC CAAGGCCGTT CCCTTCGTCC CCATCTCTGG CTTCAACGGT      450
    GACAACATGC TTGAGCCCTC CTCCAACCTG CCCTGGTACA AGGGATGGGA      500
30  GAAGGAGACC AAGGCCGCCA AGGTCACTGG TAAGACCCTC ATCGAGGCCA      550
    TCGACGCCAT TGAGCCCCCT GTCCGTCCCT CCAACAAGCC CCTCGGTCTT      600
    CCCCTCCAGG ATGTCTACAA GATCTCTGGT ATCGGAACGG TCCCTGTCGG      650
    CCGTGTCGAG ACCGGTATCA TCAAGCCCGG CATGGTCGTC ACCTTCGCCC      700
    CCGCCAACGT CACCACTGAA GTCAAGTCCG TCGAGATGCA CCACCAGCAG      750
35  CTCAGGAGG GTGTCCCCGG TGACAACGTC GGTTCACACG TCAAGAACGT      800
    TTCCGTCAAG GAAGTCCGCC TTGGTAACGT CTGCGGTGAC TCCAAGAACG      850
    ATCCCCCTCA GGGTGCTGCC TCCTTCAACG CCCAGGTCAT CGTCCTCAAC      900
    CACCCCGGTC AGGTCGGCGC TGGTTACGCC CCCGTCCTCG ACTGCCACAC      950
    TGCCACATT GCTTGCAAGT TCTCTGAGCT GCTTGAGAAG ATTGACCGCC      1000
40  GTACCGGCAA GTCTGTTGAG AACAACCCCA AGTTCATCAA GTCCGGTGAT      1050
    GCCGCCATCG TGAAGATGGT TCCTTCCAAG CCCATGTGTG TCGAGTCCTT      1100
    CAC                                                                1103
  
```

2) INFORMATION FOR SEQ ID NO: 404

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1149 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus fumigatus*
 (B) STRAIN: WSA-172

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 404

445

	AAGCTCAAGT	CCGAGCGTGA	GCGTGGTATC	ACCATCGACA	TTGCCCTCTG	50
	GAAGTTCCAG	ACTCCCAAGT	ATGAGGTCAC	TGTCATCGGT	AAGCTCGACT	100
	CGCCCCGATA	TGTTTTGGTG	CTGTAGCTAA	CACGATCTGA	AGATGCCCCC	150
5	GGTCACCGTG	ACTTCATCAA	GAACATGATC	ACTGGTACCT	CCCAGGCTGA	200
	CTGCGCTATC	CTCATCATTG	CCTCCGGTAC	TGGTGAGTTC	GAGGCTGGTA	250
	TCTCCAAGGA	TGGCCAGACC	CGTGAGCACG	CTCTGCTGGC	TTTCACCCTC	300
	GGTGTC AAGC	AGCTCATCGT	CGCCCTCAAC	AAGATGGACA	CCTGCAAGTG	350
	GTCCGAGGAT	CGTTACAACG	AAATTGTCAA	GGAAACCTCC	AACTTCATCA	400
10	AGAAGGTCGG	CTACAACCCC	AAGGCCGTTC	CCTTCGTCCC	CATCTCTGGC	450
	TTCAACGGTG	ACAACATGCT	TGAGCCCTCC	TCCAAC TGCC	CCTGGTACAA	500
	GGGATGGGAG	AAGGAGACCA	AGGCCGGCAA	GGTCACTGGT	AAGACCCTCA	550
	TCGAGGCCAT	CGACGCCATT	GAGCCCCCTG	TCCGTCCCTC	CAACAAGCCC	600
	CTCCGTCTTC	CCCTCCAGGA	TGTCTACAAG	ATCTCTGGTA	TCGGAACGGT	650
15	CCCTGTTCGGC	CGTGTGAGGA	CCGGTATCAT	CAAGCCCGGC	ATGGTCGTCA	700
	CCTTCGCCCC	CGCCAACGTC	ACCACTGAAG	TCAAGTCCGT	CGAGATGCAC	750
	CACCAGCAGC	TCCAGGAGGG	TGTCCCCGGT	GACAACGTCG	GTTTCAACGT	800
	CAAGAACGTT	TCCGTCAAGG	AAGTCCGCCC	TGGTAACGTC	TGCGGTGACT	850
	CCAAGAACGA	TCCCCCTCAG	GGTGCTGCCT	CCTTCAACGC	CCAGGTCATC	900
20	GTCTCTCAACC	ACCCCGGTCA	GGTCGGCGCT	GTTACGCCC	CCGTCTCTGA	950
	CTGCCACACT	GCCCACATTG	CTTGCAAGTT	CTCTGAGCTG	CTTGAGAAGA	1000
	TTGACCGCCG	TACCGGCAAG	TCTGTTGAGA	ACAACCCCAA	GTTTCATCAAG	1050
	TCCGGTGATG	CCGCCATCGT	GAAGATGGTT	CCTTCCAAGC	CCATGTGTGT	1100
25	CGAGTCCTTC	ACTGACTACC	CCCCTCTGGG	TCGTTTCGCC	GTCCGTGAC	1149

2) INFORMATION FOR SEQ ID NO: 405

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1151 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Aspergillus niger*
 (B) STRAIN: ATCC 9508

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 405

	CAAGCTCAAG	TCCGAGCGTG	AGCGTGGTAT	CACCATCGAC	ATTGCCCTCT	50
45	GGAAGTTCCA	GACTGGCAAG	TATGAGGTCA	CCGTCATTGG	TATGTACTCA	100
	CAGAGTTCTC	TTTTTCATCAA	AGCAATATAC	TAACGTCCAT	CATAGACGCC	150
	CCCGGTCACC	GTGACTTCAT	CAAGAACATG	ATCACTGGTA	CCTCCCAGGC	200
	TGACTGCGCT	ATCCTCATCA	TTGCCTCCGG	TACTGGTGAG	TTCGAGGCTG	250
	GTATCTCCAA	GGATGGCCAG	ACTCGTGAGC	ACGCTCTGCT	TGCTTTCACC	300
50	CTCGGTGTCC	GCCAGCTCAT	CGTTGCCCTC	AACAAGATGG	ACACCTGCAA	350
	GTGGTCCGAG	GACCGTTACA	ACGAAATCGT	TAAGGAGACC	TCCAAC TTCA	400
	TCAAGAAGGT	CGGATACAAC	CCCAAGGGTG	TTCC TTTCTG	CCCCATCTCC	450
	GGTTTCAACG	GTGACAACAT	GCTCGAGCCC	TCCCCCAACT	GCCCCTGGTA	500
	CAAGGGTTGG	GAGAAGGAGA	CCAAGGCCGG	CAAGGTCACC	GGTAAGACCC	550
55	TCCTTGAGGC	CATCGACGCC	ATCGAGCCCC	CCGTCCGTCC	CTCCAACAAG	600
	CCCCTCCGTC	TTCCCCTCCA	GGATGTCTAC	AAGATCTCCG	GTATTGGAAC	650
	TGTTCCCGTC	GGTCGTGTCG	AGACCGGTAT	CATTGCCCTC	GGTATGGTCG	700
	TGACCTTCGC	TCCCGCCAAC	GTCACCACTG	AAGTCAAGTC	CGTTGAGATG	750
	CACCACCAGC	AGCTCAAGGA	AGGTGTCCCC	GGTGACAACG	TTGGTTTCAA	800
60	CGTCAAGAAC	GTTTCCGTCA	AGGAGGTTCC	CCGTGGTAAC	GTTGCCCGTG	850

```

ACTCCAAGAA CGACCCCCCT CTTGGCTGTG AGAGCTTCAC CGCCCAGGTC 900
ATCGTCCTCA ACCACCCCGG TCAGGTCGGC GCTGGTTACG CTCCCGTCCT 950
GGACTGCCAC ACTGCTCACA TTGCTTGCAA GTTCGCTGAG CTCCTTGAGA 1000
AGATTGACCG CCGTACCGGA AAGTCTGTTG AATCTTCCCC CAAGTTCATC 1050
5 AAGTCCGGTG ACGCTGCCAT CGTCAAGATG ATTCCCTCCA AGCCCATGTG 1100
TGTGAGGCT TTTACTGACT ACCCCCCTCT TGGTCGTTTC GCCGTCCGCG 1150
A 1151

```

10

2) INFORMATION FOR SEQ ID NO: 406

(i) SEQUENCE CHARACTERISTICS:

```

15 (A) LENGTH: 1093 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

```

    (A) ORGANISM: Blastoschizomyces capitatus
    (B) STRAIN: ATCC 10663

```

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 406

```

GCTTAAAGCT GAACGTGAAC GTGGTATCAC CATTGATATC GCTCTCTGGA 50
AGTTTCGAAAC TCCTAAGTAC TACGTTACTG TTATTGATGC TCCAGGTCAC 100
CGTGATTTCA TCAAGAACAT GATTACTGGT ACTTCCCAAG CCGATTGCGC 150
30 CATTCTTATC ATTGCTGCCG GTGTCGGTGA ATTCGAAGCT GGTATCTCCA 200
AGGAAGGTCA AACGAGAGAA CACGCTCTTC TCGCTTTCAC CCTTGGTGTC 250
AGACAACCTA TCATTGCCAT CAACAAGATG GACTCTGTCA AGTGGGACCA 300
AAAGAGATAC GAAGAAATCG TCAAGGAGGC TTCCAACCTC GTCAAGAAGG 350
TTGGTTACAA CCCCAAGTCT GTTCCATTCG TTCCTATCTC TGGTTGGAAC 400
35 GGTGACAACA TGTGGAACC TACCACCAAC GCCCCATGGT ACAAGGGATG 450
GACCAAGGAA ACCAAGGCTG GTGCCACTAA GGGTATGACT CTTATTGAAG 500
CCATTGACGC CATTGAACCA CCAGTAAGAC CATCCGACAA GCCACTCCGT 550
CTCCCCTCC AAGATGTTTA CAAGATTGGT GGTATCGGAA CTGTGCCAGT 600
CGGCCGTGTC GAAACCGGTA TCATCAAGGC CGGTATGGTC GTTACCTTTG 650
40 CTCCACCAAT GGTCACAACT GAAGTTAAGT CCGTTGAAAT GCACCACGAA 700
CAACTTGCTC AAGGTAACCC AGGTGACAAC GTTGTTTCA ACGTCAAGAA 750
CGTTTCCGTT AAGGAAATCA GACGTGGTAA CGTCTGTGGT GACTCCAAGA 800
ACGATCCACC AAAGGGCTGC GAATCTTTCA ACGCTCAAGT TATCGTCTTG 850
AACCACCCTG GTCAAATCTC TGTTGGTTAC TCTCCAGTTC TCGATTGCCA 900
45 CACTGCCCAC ATTGCTTGCA GATTCGACGA ACTCCTTGAA AAGATCGACC 950
GTCGTTCTGG TAAGAAGATT GAAGACTCTC CAAAGTTTGT CAAGTCTGGT 1000
GATGCCGCTA TCGTCAAGAT GATCCCAACC AAGCCAATGT GCGTTGAAAC 1050
CTTCACTGAA TACCCACCAC TTGGTCGTTT CGCCGTCCGT GAT 1093

```

50

2) INFORMATION FOR SEQ ID NO: 407

(i) SEQUENCE CHARACTERISTICS:

```

55 (A) LENGTH: 1101 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

60 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida albicans*
 (B) STRAIN: ATCC 10231

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 407

	CTTGGACAAA	TTGAAGGCTG	AAAGAGAAAG	AGGTATCACC	ATTGATATCG	50
	CTTTGTGGAA	ATTCGAAACT	CCAAAATACC	ACGTTACCGT	CATTGATGCT	100
10	CCAGGTCACA	GAGATTTTCAT	CAAGAATATG	ATCACTGGTA	CTTCTCAAGC	150
	TGATTGTGCT	ATTTTGTATTA	TTGCTGGTGG	TACTGGTGAA	TTCGAAGCCG	200
	GTATTTCTAA	GGATGGTCAA	ACCAGAGAAC	ACGCTTTGTT	GGCTTACACT	250
	TTGGGTGTCA	AACAATTGAT	TGTTGCTGTC	AACAAGATGG	ACTCTGTCAA	300
	ATGGGACAAA	AACAGATTG	AAGAAATCAT	CAAGGAAACC	TCCAACCTCG	350
15	TCAAGAAGGT	TGGTTACAAC	CCAAAGACTG	TTCCATTYGT	TCCAATCTCT	400
	GGTTGGAATG	GTGACAACAT	GATTGAACCA	TCCACCAACT	GTCCATGGTA	450
	CAAGGGTTGG	GAAAAGGAAA	CCAAATCCGG	TAAAGTTACT	GGTAAGACCT	500
	TGTTAGAAGC	TATTGACGCT	ATTGAACCAC	CAACCAGACC	AACCGACAAA	550
	CCATTGAGAT	TGCCATTGCA	AGATGTTTAC	AAGATCGGTG	GTATTGGTAC	600
20	TGTGCCAGTC	GGTAGAGTTG	AACTGGGTAT	CATCAAAGCC	GGTATGGTTG	650
	TTACTTTTCGC	CCCAGCTGGT	GTTACCACTG	AAGTCAAATC	CGTTGAAATG	700
	CATCACGAAC	AATTGGCTGA	AGGTGTTCCA	GGTGACAATG	TTGGTTTCAA	750
	CGTTAAGAAC	GTTTCCGTTA	AAGAAATTAG	AAGAGGTAAC	GTTTGTGGTG	800
	ACTCCAAGAA	CGATCCACCA	AAGGGTTGTG	ACTCTTTCAA	TGCCCCAAGTC	850
25	ATTGTTTTTGA	ACCATCCAGG	TCAAATCTCT	GCTGGTTACT	CTCCAGTCTT	900
	GGATTGTCAC	ACTGCCCACA	TTGCTTGTA	ATTCGACACT	TTGGTTGAAA	950
	AGATTGACAG	AAGAACTGGT	AAGAAATTGG	AAGAAAATCC	AAAATTCGTC	1000
	AAATCCGGTG	ATGCTGCTAT	CGTCAAGATG	GTCCCAACCA	AACCAATGTG	1050
	TGTTGAAGCT	TTCACTGACT	ACCCACCATT	AGGTAGATTC	GCTGTCAGAG	1100
30	A					1101

2) INFORMATION FOR SEQ ID NO: 408

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1089 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida albicans*
 (B) STRAIN: ATCC 18804

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 408

50	GAAGGCTGAA	AGAGAAAGAG	GTATCACCAT	TGATATCGCT	TTGTGGAAAT	50
	TCGAAACTCC	AAAATACCAC	GTTACCGTCA	TTGATGCTCC	AGGTCACAGA	100
	GATTTTCATCA	AGAATATGAT	CACTGGTACT	TCTCAAGCTG	ATTGTGCTAT	150
	TTTGATTATT	GCTGGTGGTA	CTGGTGAATT	CGAAGCCGGT	ATTTCTAAGG	200
	ATGGTCAAAC	CAGAGAACAC	GCTTTGTTGG	CTTACACTTT	GGGTGTCAAA	250
55	CAATTGATTG	TTGCTGTCAA	CAAGATGGAC	TCTGTCAAAT	GGGACAAAAA	300
	CAGATTTGAA	GAAATCATCA	AGGAAACCTC	CAACTTCGTC	AAGAAGGTTG	350
	GTTACAACCC	AAAGACTGTT	CCATTTCGTT	CAATCTCTGG	TTGGAATGGT	400
	GACAACATGA	TTGAACCATC	CACCAACTGT	CCATGGTACA	AGGGTTGGGA	450
	AAAGGAAACC	AAATCCGGTA	AAGTTACTGG	TAAGACCTTG	TTAGAAGCTA	500
60	TTGACGCTAT	TGAACCACCA	ACCAGACCAA	CCGACAAACC	ATTGAGATTG	550

```

5  CCATTGCAAG ATGTTTACAA GATCGGTGGT ATTGGTACTG TGCCAGTCGG 600
   TAGAGTTGAA ACTGGTATCA TCAAAGCCGG TATGGTTGTT ACTTTCGCCC 650
   CAGCTGGTGT TACCACTGAA GTCAAATCCG TTGAAATGCA TCACGAACAA 700
   TTGGCTGAAG GTGTTCCAGG TGACAATGTT GGTTCACACG TTAAGAACGT 750
   TTCCGTTAAA GAAATTAGAA GAGGTAACGT TTGTGGTGAC TCCAAGAACG 800
   ATCCACCAAA GGGTTGTGAC TCTTTCAATG CCCAAGTCAT TGTTTTGAAC 850
   CATCCAGGTC AAATCTCTGC TGGTTACTCT CCAGTCTTGG ATTGTCACAC 900
   TGCCACATT GCTTGTAAT TCGACACTTT GGTGAAAAG ATTGACAGAA 950
   GAACTGGTAA GAAATTGGAA GAAATCCAA AATTCGTCAA ATCCGGTGAT 1000
10 GCTGCTATCG TCAAGATGGT CCCAACCAA CCAATGTGTG TTGAAGCTTT 1050
   CACTGACTAC CCACCATTAG GTAGATTCGC TGTCAGAGA 1089

```

15 2) INFORMATION FOR SEQ ID NO: 409

(i) SEQUENCE CHARACTERISTICS:

```

20 (A) LENGTH: 1101 bases
   (B) TYPE: Nucleic acid
   (C) STRANDEDNESS: Double
   (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

```

   (A) ORGANISM: Candida albicans
   (B) STRAIN: ATCC 56884

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 409

```

30 CTTGGACAAA TTGAAGGCTG AAAGAGAAAG AGGTATCACC ATTGATATCG 50
   CTTTGTGGAA ATTCGAAACT CCAAATACC ACGTTACCGT CATTGATGCT 100
   CCAGGTCACA GAGATTTTCAT CAAGAATATG ATCACTGGTA CTTCTCAAGC 150
   TGATTGTGCT ATTTTGATTA TTGCTGGTGG TACTGGTGAA TTCGAAGCCG 200
35 GTATTTCTAA GGATGGTCAA ACCAGAGAAC ACGCTTTGTT GGCTTACACT 250
   TTGGGTGTCA AACAATTGAT TGTTGCTGTC AACAAGATGG ACTCTGTCAA 300
   ATGGGACAAA AACAGATTTG AAGAAATCAT CAAGGAAACC TCCAACCTCG 350
   TCAAGAAGGT TGGTTACAAC CCAAAGACTG TTCCATTTCGT TCCAATCTCT 400
   GGTTGGAATG GTGACAACAT GATTGAACCA TCCACCAACT GTCCATGGTA 450
40 CAAGGGTTGG GAAAAGGAAA CCAAATCCGG TAAAGTTACT GGTAAGACCT 500
   TGTTAGAAGC TATTGACGCT ATTGAACCAC CAACCAGACC AACCGACAAA 550
   CCATTGAGAT TGCCATTGCA AGATGTTTAC AAGATCGGTG GTATTGGTAC 600
   TGTGCCAGTC GGTAGAGTTG AAATGGTAT CATCAAAGCC GGTATGGTTG 650
   TTACTTTCGC CCCAGCTGGT GTTACCACTG AAGTCAAATC CGTTGAAATG 700
45 CATCACGAAC AATTGGCTGA AGGTGTTCCA GGTGACAATG TTGGTTTCAA 750
   CGTTAAGAAC GTTCCGTTA AAGAAATTAG AAGAGGTAAC GTTTGTGGTG 800
   ACTCCAAGAA CGATCCACCA AAGGGTTGTG ACTCTTCAA TGCCCAAGTC 850
   ATTGTTTTGA ACCATCCAGG TCAAATCTCT GCTGGTTACT CTCCAGTCTT 900
   GGATTGTCAC ACTGCCCACA TTGCTTGTA AATCGACACT TTGGTTGAAA 950
50 AGATTGACAG AAGAACTGGT AAGAAATTGG AAGAAAATCC AAAATTCGTC 1000
   AAATCCGGTG ATGCTGCTAT CGTCAAGATG GTCCCAACCA AACCAATGTG 1050
   TGTGAAGCT TTTACTGACT ACCCACCATT AGGTAGATTC GCTGTCAGAG 1100
   A

```

55

2) INFORMATION FOR SEQ ID NO: 410

(i) SEQUENCE CHARACTERISTICS:

```

60 (A) LENGTH: 1102 bases

```

(B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida albicans*
 (B) STRAIN: ATCC 60193

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 410

	CTTGGACAAA	TTGAAGGCTG	AAAGAGAAAG	AGGTATCACC	ATTGATATCG	50
	CTTTGTGGAA	ATTCGAAACT	CCAAAATACC	ACGTTACCGT	CATTGATGCT	100
15	CCAGGTCACA	GAGATTTTCAT	CAAGAATATG	ATCACTGGTA	CTTCTCAAGC	150
	TGATTGTGCT	ATTTTGATTA	TTGCTGGTGG	TACTGGTGAA	TTCGAAGCCG	200
	GTATTTCTAA	GGATGGTCAA	ACCAGAGAAC	ACGCTTTGTT	GGCTTACACT	250
	TTGGGTGTCA	AACAATTGAT	TGTTGCTGTC	AACAAGATGG	ACTCTGTCAA	300
	ATGGGACAAA	AACAGATTTG	AAGAAATCAT	CAAGGAAACC	TCCAACCTCG	350
20	TCAAGAAGGT	TGGTTACAAC	CCAAAGACTG	TTCCATTCGT	TCCAATCTCT	400
	GGTTGGAATG	GTGACAACAT	GATTGAACCA	TCCACCAACT	GTCCATGGTA	450
	CAAGGGTTGG	GAAAAGGAAA	CCAAATCCGG	TAAAGTTACT	GGTAAGACCT	500
	TGTTAGAAGC	TATTGACGCT	ATTGAACCAC	CAACCAGACC	AACCGACAAA	550
	CCATTGAGAT	TGCCATTGCA	AGATGTTTAC	AAGATCGGTG	GTATTGGTAC	600
25	TGTGCCAGTC	GGTAGAGTTG	AAACTGGTAT	CATCAAAGCC	GGTATGGTTG	650
	TTACTTTTCGC	CCCAGCTGGT	GTTACCACTG	AAGTCAAATC	CGTTGAAATG	700
	CATCACGAAC	AATTGGCTGA	AGGTGTTCCA	GGTGACAATG	TTGGTTTCAA	750
	CGTTAAGAAC	GTTTCCGTTA	AAGAAATTAG	AAGAGGTAAC	GTTTGTGGTG	800
	ACTCCAAGAA	CGATCCACCA	AAGGGTTGTG	ACTCTTTCAA	TGCCCAAGTC	850
30	ATTGTTTTTGA	ACCATCCAGG	TCAAATCTCT	GCTGGTTACT	CTCCAGTCTT	900
	GGATTGTCAC	ACTGCCCACA	TTGCTTGTA	ATTTCGACACT	TTGGTTGAAA	950
	AGATTGACAG	AAGAACTGGT	AAGAAATTGG	AAGAAAATCC	AAAATTCGTC	1000
	AAATCCGGTG	ATGCTGCTAT	CGTCAAGATG	GTCCCAACCA	AACCAATGTG	1050
	TGTTGAAGCT	TTCCTGACT	ACCCACCATT	AGGTAGATTC	GCTGTCAGAG	1100
35	AT					1102

2) INFORMATION FOR SEQ ID NO: 411

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1102 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

50 (A) ORGANISM: *Candida albicans*
 (B) STRAIN: ATCC 90028

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 411

55	CTTGGACAAA	TTGAAGGCTG	AAAGAGAAAG	AGGTATCACC	ATTGATATCG	50
	CTTTGTGGAA	ATTCGAAACT	CCAAAATACC	ACGTTACCGT	CATTGATGCT	100
	CCAGGTCACA	GAGATTTTCAT	CAAGAATATG	ATCACTGGTA	CTTCTCAAGC	150
	TGATTGTGCT	ATTTTGATTA	TTGCTGGTGG	TACTGGTGAA	TTCGAAGCCG	200
	GTATTTCTAA	GGATGGTCAA	ACCAGAGAAC	ACGCTTTGTT	GGCTTACACT	250
60	TTGGGTGTCA	AACAATTGAT	TGTTGCTGTC	AACAAGATGG	ACTCTGTCAA	300

```

5  ATGGGACAAA AACAGATTTG AAGAAATCAT CAAGGAAACC TCCAAC TTCG 350
   TCAAGAAGGT TGGTTACAAC CCAAAGACTG TTCCATTTCG TCCAATCTCT 400
   GGTGGAATG GTGACAACAT GATTGAACCA TCCACCAACT GTCCATGGTA 450
   CAAGGGTTGG GAAAAGGAAA CCAAATCCGG TAAAGTTACT GGTAAGACCT 500
   TGTTAGAAGC TATTGACGCT ATTGAACCAC CAACCAGACC AACCGACAAA 550
   CCATTGAGAT TGCCATTGCA AGATGTTTAC AAGATCGGTG GTATTGGTAC 600
   TGTGCCAGTC GGTAGAGTTG AAAC TGGTAT CATCAAAGCC GGTATGGTTG 650
   TTACTTTCGC CCCAGCTGGT GTTACCACTG AAGTCAAATC CGTTGAAATG 700
   CATCACGAAC AATTGGCTGA AGGTGTTCCA GGTGACAATG TTGGTTTCAA 750
10 CGTTAAGAAC GTTTCCTTA AAGAAATTAG AAGAGGTAAC GTTTGTGGTG 800
   ACTCCAAGAA CGATCCACCA AAGGGTTGTG ACTCTTTCAA TGCCCAAGTC 850
   ATTGTTTTGA ACCATCCAGG TCAAATCTCT GCTGGTTACT CTCCAGTCTT 900
   GGATTGTCAC ACTGCCCACA TTGCTTGTA AATTCGACACT TTGGTTGAAA 950
   AGATTGACAG AAGAACTGGT AAGAAATTGG AAGAAAATCC AAAATTCGTC 1000
15 AAATCCGGTG ATGCTGCTAT CGTCAAGATG GTCCCAACCA AACCAATGTG 1050
   TGTGAAGCT TTCACTGACT ACCCACCATT AGGTAGATTC GCTGTCAGAG 1100
   AT 1102

```

20

2) INFORMATION FOR SEQ ID NO: 412

(i) SEQUENCE CHARACTERISTICS:

```

25 (A) LENGTH: 1101 bases
   (B) TYPE: Nucleic acid
   (C) STRANDEDNESS: Double
   (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

30

- (vi) ORIGINAL SOURCE:

```

   (A) ORGANISM: Candida dubliniensis
   (B) STRAIN: NCPF 3108

```

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 412

```

   CTTGGATAAA TTGAAGGCTG AAAGAGAAAG AGGTATCACC ATTGATATCG 50
   CTTTGTGGAA ATTCGAAACT CCAAAATACC ACGTTACCGT CATTGATGCT 100
   CCAGGTCACA GAGATTTTCAT CAAGAACATG ATCACTGGTA CTTCTCAAGC 150
40 TGATTGTGCT ATTTTGATTA TTGCTGGTGG TACTGGTGAA TTCGAAGCCG 200
   GTATTTCTAA GGATGGTCAA ACCAGAGAAC ACGCTTTGTT GGCTTACACT 250
   TTGGGTGTCA AACAATTGAT TGTTGCTGTC AACAAGATGG ACTCTGTCAA 300
   ATGGGACAAA AACAGATTTG AAGAAATCAT CAAGGAAACC TCTAACTTCG 350
   TCAAGAAGGT TGGTTACAAC CCAAAGACTG TTCCATTTCG TCCAATCTCT 400
45 GGTGGAATG GTGACAACAT GATTGAAGCT TCCACCAACT GTCCATGGTA 450
   CAAGGGTTGG GAAAAGGAAA CCAAATCCGG TAAAGTTACT GGTAAGACCT 500
   TGTTAGAAGC TATTGATGCT ATTGAACCAC CAACCAGACC AACCGACAAA 550
   CCATTGAGAT TGCCATTGCA AGATGTTTAC AAGATCGGTG GTATTGGTAC 600
   TGTGCCAGTC GGTAGAGTTG AAAC TGGTGT CATTAAAGCC GGTATGGTTG 650
50 TCACTTTTGC CCCAGCTGGT GTTACCACTG AAGTCAAATC CGTTGAAATG 700
   CATCACGAAC AATTGGCTGA AGGTGTTCCA GGTGACAATG TTGGTTTCAA 750
   CGTTAAGAAAT GTTCTGTCA AAGAAATTAG AAGAGGTAAC GTTTGTGGTG 800
   ACTCCAAGAA CGATCCACCA AAGGGTTGTG ACTCTTTCAA TGCCCAAGTC 850
   ATTGTCTTGA ACCATCCAGG TCAAATCTCT GCTGGTTACT CTCCAGTCTT 900
55 GGATTGTCAC ACTGCCCACA TTGCTTGTA AATTCGACACT TTGGTTGAAA 950
   AGATTGACAG AAGAACTGGT AAGAAATTGG AAGAAAATCC AAAATTCGTC 1000
   AAATCCGGTG ACGCTGCTAT YGTCAAGATG GTCCCAACCA AACCAATGTG 1050
   TGTGAAGCT TTCACTGACT ACCCACCATT AGGTAGATTC GCTGTCAGAG 1100
   A 1101

```

60

2) INFORMATION FOR SEQ ID NO: 413

5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1098 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Candida catenulata*
 15 (B) STRAIN: ATCC 10565

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 413

20	GGACAAGCTT AAGGCTGAGC GTGAGAGAGG TATCACCATT GACATTGCCT	50
	TGTGGAAGTT CGAGACTCCC AAGTACCACG TCACTGTCAT TGACGCCCCC	100
	GGTCACAGAG ATTTTCATCAA GAACATGATC ACTGGTACCT CGCAGGCTGA	150
	CTGTGCTATC TTGATCATTTG CTTCCGGTGT CGGTGAGTTC GAGGCTGGTA	200
	TCTCCAAGGA CGGTCAGACC CGTGAGCACG CCTTGTTGGC CTACACCTTG	250
	GGTGTC AAGC AGTTGATCGT TGCCATCAAC AAGATGGACT CCGTCAAGTG	300
25	GGACAAGAAC AGATTCGAGG AGATTGTCAA GGAGACCACC AACTTCGTCA	350
	AGAAGGTTGG TTACAACCCC AAGGCTGTCC CCTTCGTCCC CATCTCTGGC	400
	TGGAACGGTG ACAACATGAT TGAGGCCTCC ACCAACTGCC CCTGGTACAA	450
	GGGCTGGGAG AAGGAGACCA AGGCCGGTAA GTCTACCGGT AAGACCTTGT	500
	TGGAGGCCAT TGACGCCATT GAGCCCCCTA CCAGACCCAC CGACAAGCCC	550
30	TTGAGATTGC CCTTGCAGGA TGTCTACAAG ATCGGTGGTA TTGGTACGGT	600
	GCCCGTCGGC CGTGTGAGGA CCGGTGTCAT CAAGCCCGGT ATGGTCGTCA	650
	CCTTCGCCCC CGCTGGGTGC ACCACTGAAG TCAAGTCCGT CGAGATGCAC	700
	CACGAGCAGT TGTCCGAGGG TGTCCCCGGT GACAACGTTG GTTTCAACGT	750
	CAAGAACGTC TCTGTTAAGG AGATCAGACG TGGTAAACGTC TCGGGTGA	800
35	CCAAGAACGA CCCCCCATG GGTGCTCTT CTTTCAACGC CCAGGTATATC	850
	GTGTTGAACC ACCCCGGTCA GATCTCTGCC GGTACTCTC CCGTCTTGGA	900
	CTGCCACACC GCCACATTG CTTGCAAGTT CGCCGAGTTG ATCGAGAAGA	950
	TTGACAGACG TACCGGTAAG TCCATGGAGG CTAACCCCAA GTTCGTCAAG	1000
	TCTGGTGACG CCGCCATCGT CAAGATGGAG CCCACTAAGC CCATGTGTGT	1050
40	TGAGGCCTTC ACTGACTTCC CTCCTTTGGG TAGATTCGCC GTCAGAGA	1098

2) INFORMATION FOR SEQ ID NO: 414

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1102 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 50 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Candida dubliniensis*
 55 (B) STRAIN: NCPF 3949

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 414

60	CTTGGATAAA TTGAAGGCTG AAAGAGAAAG AGGTATCACC ATTGATATCG	50
----	--	----

```

CTTTGTGGAA ATTGCGAACT CCAAAATACC ACGTTACCGT CATTGATGCT 100
CCAGGTCACA GAGATTTTCAT CAAGAACATG ATCACTGGTA CTTCTCAAGC 150
TGATTGTGCT ATTTTGATTA TTGCTGGTGG TACTGGTGAA TTCGAAGCCG 200
GTATTTCTAA GGATGGTCAA ACCAGAGAAC ACGCTTTGTT GGCTTACACT 250
5 TGGGTGTCA AACAATTGAT TGTTGCTGTC AACAAGATGG ACTCTGTCAA 300
ATGGGACAAA AACAGATTCG AAGAAATCAT CAAGGAAACC TCTAACTTCG 350
TCAAGAAGGT TGGTTACAAC CCAAAGACTG TTCCATTTCGT TCCAATCTCT 400
GGTTGGAATG GTGACAACAT GATTGAAGCT TCCACCAACT GTCCATGGTA 450
CAAGGGTTGG GAAAAGGAAA CCAATCCGG TAAGGTTACT GGTAAGACCT 500
10 TGTTAGAAGC TATTGATGCT ATTGAACCAC CAACCAGACC AACCGACAAA 550
CCATTGAGAT TGCCATTGCA AGATGTTTAC AAGATCGGTG GTATTGGTAC 600
TGTGCCAGTC GGTAGAGTTG AAAGTGGTGT CATTAAAGCC GGTATGGTTG 650
TCACTTTTGC CCCAGCTGGT GTTACCACTG AAGTCAAATC CGTTGAAATG 700
CATCACGAAC AATTGGTTGA AGGTGTTCCA GGTGACAATG TTGGTTTCAA 750
15 CGTTAAGAAT GTTCTGTCA AAGAAATTAG AAGAGGTAAC GTTTGTGGTG 800
ACTCCAAGAA CGATCCACCA AAGGGTTGTG ACTCTTTCAA TGCCCAAGTC 850
ATTGTCTTGA ACCATCCAGG TCAAATCTCT GCTGGTTAYT CTCCAGTCTT 900
GGATTGTCAC ACTGCCACA TTGCTTGTA AATCGACACT TTGGTTGAAA 950
AGATTGACAG AAGAACTGGT AAGAAATTGG AAGAAAATCC AAAATTCGTC 1000
20 AAATCCGGTG ACGCTGCTAT YGTCAAGATG GTCCCAACCA AACCAATGTG 1050
TGTTGAAGCT TTTACTGACT ACCCACCATT AGGTAGATTC GCTGTCAGAG 1100
AT 1102

```

25

2) INFORMATION FOR SEQ ID NO: 415

(i) SEQUENCE CHARACTERISTICS:

```

30 (A) LENGTH: 1102 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

35

(vi) ORIGINAL SOURCE:

```

    (A) ORGANISM: Candida dubliniensis
    (B) STRAIN: CBS 7987

```

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 415

```

CTTGATAAA TTGAAGGCTG AAAGAGAAAG AGGTATCACC ATTGATATCG 50
CTTTGTGGAA ATTGCGAACT CCAAAATACC ACGTTACCGT CATTGATGCT 100
CCAGGTCACA GAGATTTTCAT CAAGAACATG ATCACTGGTA CTTCTCAAGC 150
45 TGATTGTGCT ATTTTGATTA TTGCTGGTGG TACTGGTGAA TTCGAAGCCG 200
GTATTTCTAA GGATGGTCAA ACCAGAGAAC ACGCTTTGTT GGCTTACACT 250
TTGGGTGTCA AACAATTGAT TGTTGCTGTC AACAAGATGG ACTCTGTCAA 300
ATGGGACAAA AACAGATTYG AAGAAATCAT CAAGGAAACC TCTAACTTCG 350
TCAAGAAGGT TGGTTACAAC CCAAAGACTG TTCCATTTCGT TCCAATCTCT 400
50 GGTGGAATG GTGACAACAT GATTGAAGCT TCCACCAACT GTCCATGGTA 450
CAAGGGTTGG GAAAAGGAAA CCAATCCGG TAAGGTTACT GGTAAGACCT 500
TGTTAGAAGC TATTGATGCT ATTGAACCAC CAACCAGACC AACCGACAAA 550
CCATTGAGAT TGCCATTGCA AGATGTTTAC AAGATCGGTG GTATTGGTAC 600
TGTGCCAGTC GGTAGAGTTG AAAGTGGTGT CATTAAAGCC GGTATGGTTG 650
55 TCACTTTTGC CCCAGCTGGT GTTACCACTG AAGTCAAATC CGTTGAAATG 700
CATCACGAAC AATTGGTTGA AGGTGTTCCA GGTGACAATG TTGGTTTCAA 750
CGTTAAGAAT GTTCTGTCA AAGAAATTAG AAGAGGTAAC GTTTGTGGTG 800
ACTCCAAGAA CGATCCACCA AAGGGTTGTG ACTCTTTCAA TGCCCAAGTC 850
ATTGTCTTGA ACCATCCAGG TCAAATCTCT GCTGGTTAYT CTCCAGTCTT 900
60 GGATTGTCAC ACTGCCACA TTGCTTGTA AATCGACACT TTGGTTGAAA 950

```


AGATTGACAG	AAGAACTGGT	AAGAAATTGG	AAGAAAATCC	AAAATTCGTC	1000
AAATCCGGTG	ACGCTGCTAT	YGTCAAGATG	GTCCCAACCA	AACCAATGTG	1050
TGTTGAAGCT	TTCCTGACT	ACCCACCATT	AGGTAGATTC	GCTGTCAGAG	1100
AT					1102

5

2) INFORMATION FOR SEQ ID NO: 416

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1094 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

20 (A) ORGANISM: *Candida famata*
 (B) STRAIN: ATCC 62894

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 416

AATTGAAGGC	TGAAAGAGAA	AGAGGTATCA	CCATTGATAT	CGCTTTATGG	50
AAATTCGAAA	CTCCAAAATA	CCACGTTACC	GTTATTGATG	CTCCAGGTCA	100
CAGAGATTTT	ATCAAGAACA	TGATTACTGG	TACTTCTCAA	GCTGATTGTG	150
CTATTTTTRAT	TATTGCTGGT	GGTGTCGGTG	AATTCGAAGC	CGGTATCTCT	200
AAGGATGGTC	AAACCAGAGA	ACACGCTTTA	TTGGCTTACA	CCTTAGGTGT	250
TAGACAATTG	ATTGTTGCCG	TCAACAAGAT	GGACTCTGTT	AAATGGGACA	300
AGGCTAGATT	CGAAGAAATC	ATCAAGGAAA	CCTCTAACTT	CGTCAAGAAG	350
GTTGGTTACA	ACCCTAAGAC	TGTTCCCTTC	GTGCCAATTT	CTGGATGGAA	400
CGGTGACAAC	ATGATTGAAG	CCTCCACCAA	CTGTCCATGG	TACAAGGGTT	450
GGGAAAAGGA	AACCAAGGCT	GGTAAATCTA	CTGGTAAGAC	TTTGTTAGAA	500
GCCATTGATG	CCATTGAACC	ACCAACCAGA	CCAACCGAAA	AGCCATTGAG	550
ATTACCATTA	CAAGATGTCT	ACAAGATCGG	TGGTATTGGT	ACTGTGCCAG	600
TCGGTAGAGT	TGAAACCGGT	GTTATCAAGG	GTGGTATGGT	TGTTACCTTT	650
GCCCCAGCCG	GTGTCCTAC	CGAAGTCAAA	TCCGTTGAAA	TGCACCACGA	700
ACAATTAGCT	GAAGGTGTTT	CAGGTGACAA	TGTTGGTTTC	AACGTCAAGA	750
ACGTTTCCGT	TAAGGAAATC	AGAAGAGGTA	ACGTTTGTGG	TGACTCCAAG	800
AACGACCCAC	CAAAGGGTGC	TGAATCTTTC	ACCGCTCAAG	TTATTGTCTT	850
GAACCAACCA	GGTCARATCT	CTGCTGGTTA	CTCTCCAGTC	TTAGATTGTC	900
ACACCGCCCA	CATTGCTTGT	AAATTCGATG	CTTTACTCGA	AAAGATTGAC	950
AGAAGATCCG	GTAAGAAATT	AGAAGACGAA	CCAAAATTCG	TCAAGTCCGG	1000
TGATGCTGCT	ATCGTCAAGA	TGGTCCCAAC	CAAACCAATG	TGTGTTGAAG	1050
CTTTCCTACT	GAATCCACCA	TTAGGTAGAT	TCGCTGTTAG	AGAT	1094

50

2) INFORMATION FOR SEQ ID NO: 417

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1101 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

60 (A) ORGANISM: *Candida glabrata*

(B) STRAIN: ATCC 66032

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 417

```

5  TTTGGACAAG TTGAAGGCTG AAAGAGAAAG AGGTATCACT ATCGATATCG      50
   CTTTGTGGAA GTTCGAAACT CCAAAGTACC ACGTYACCGT TATCGATGCT      100
   CCAGGTCACA GAGATTTTCAT CAAGAACATG ATTACTGGTA CTTCTCAAGC      150
   TGACTGTGCT ATCTTGATTA TTGCTGGTGG TGTCGGTGAA TTCGAAGCYG      200
   GTATCTCCAA GGATGGTCAA ACCAGAGAAC ACGCTCTATT GGCTTTTCACC      250
10  CTAGGTGTTA GACAATTGAT TGTYGCTGTC AACAAAGATGG ACTCTGTCAA      300
   GTGGGATGAA TCCAGATTCG CTGAAATCGT TAAGGAAACC TCCAACCTCA      350
   TCAAGAAGGT CGGTTACAAC CCAAAGACTG TTCCATTCTG CCAATCTCT      400
   GGTGGAACG GTGACAACAT GATTGAAGCC ACCACCAACG CTTCTTGCTA      450
   CAAGGGTTGG GAAAAGGAAA CCAAGGCTGG TGTCGTCAAG GGTAAGACCT      500
15  TGTGGAAGC CATTGACGCT ATCGAACCAC CAACCAGACC AACTGACAAG      550
   CCATTGAGAT TGCCATTGCA AGATGCTCTAC AAGATCGGTG GTATCGGTAC      600
   GGTGCCAGT GGTAGAGTCG AAACCGGTGT CATCAAGCCA GGTATGGTTG      650
   TTACCTTCGC CCCAGCTGGT GTTACCACTG AAGTCAAGTC CGTTGAAATG      700
   CACCAGAAC AATTGACTGA AGGTTTGCCA GGTGACAACG TTGGTTTCAA      750
20  CGTTAAGAAC GTTTCGTTA AGGAAATCAG AAGAGGTAAT GTCTGTGGTG      800
   ACTCCAAGAA CGACCCACCA AAGGCTGCTG CTTCTTTCAA CGCTACCGTC      850
   ATTGTCTTGA ACCACCCAGG TCAAACTCTCT GCTGGTTACT CTCCAGTTTT      900
   GGACTGTCAC ACCGCCACA TTGCTTGTA GTCGAAGAA TTGTTGGAAA      950
   AGAACGACAG AAGATCCGGT AAGAAGTTGG AAGACTCTCC AAAGTTCTTG      1000
25  AAGTCCGGTG ACGCTGCTTT GGTAAAGTTC GTTCCATCCA AGCCAATGTG      1050
   TGTGAAGCT TTCTCCGACT ACCCACCATT GGGTAGATTC GCTGTCAGAG      1100
   A

```

30 2) INFORMATION FOR SEQ ID NO: 418

(i) SEQUENCE CHARACTERISTICS:

```

35  (A) LENGTH: 1080 bases
   (B) TYPE: Nucleic acid
   (C) STRANDEDNESS: Double
   (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

```

   (A) ORGANISM: Candida guilliermondii
   (B) STRAIN: ATCC 6260

```

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 418

```

   AGAGAAAGAG GTATCACCAT TGACATTGCT TTGTGGAAAT TCGAGACTCC      50
   AAAGTACCAC GTTACYGTCA TTGATGCCCC AGGTCACAGA GATTTCATCA      100
   AGAACATGAT CACTGGTACT TCTCAAGCTG ACTGTGCTAT TTTGATTATT      150
50  GCTGGTGGTA CCGGTGAATT CGAAGCTGGT ATCTCTAAGG ATGGTCAAAC      200
   CAGAGAGCAC GCTTTGTTGG CTTACACCTT GGGTGTTAGA CAATTGATTG      250
   TTGCTGTCAA CAAGATGGAC TCCGTCAART GGGACAAGAA CAGATTYAGAG      300
   GAAATCATCA AGGAAACCTC TAACTTCGTC AAGAAGGTTG GTTACAACCC      350
   TAAGACTGTG CCATTCGTTT CTATCTCTGG ATGGAAYGGT GACAACATGA      400
55  TTGAGGCTTC TACCAACTGT CCTTGGTACA AGGGATGGGA GAAGGAGACC      450
   AAGGCTGGTA AGTCCACCGG TAAGACTTTG TTGGAGGCCA TTGACGCCAT      500
   TGAGCCACCT CAAAGACCAA CCGACAAGCC ATTGAGATTG CCATTGCAAG      550
   ATGTYTACAA GATTGGTGGT ATTGGAACGG TGCCAGTCGG TAGAGTTGAA      600
   ACCGGTATCA TYAAGGCCGG TATGGTTGTT ACCTTTGCCC CAGCTGGTGT      650
60  YACCACTGAA GTCAAGTCCG TGGAAATGCA CCACGAACAA TTGGTTGAAG      700

```

	GTGTTCCAGG	TGACAATGTT	GGTTTCAACG	TTAAGAACGT	TTCCGTTAAG	750
	GAAATTAGAA	GAGGTAACGT	TTGTGGTGAC	TCCAAGAACG	ACCCACCAAA	800
	GGGTTGTGAC	TCTTTCACCG	CTCAAGTTAT	TGTGTTGAAC	CACCCTGGTC	850
	AAATCTCTGC	TGGTTACTCT	CCAGTTTTTG	ACTGTCACAC	CGCCCACATT	900
5	GCTTGTAAT	TCGACACCTT	GTTGGAGAAG	ATTGACAGAA	GAACCGGTAA	950
	GAAGATGGAG	GACAACCCCA	AGTTTGTCAA	GTCCGGTGAC	GCTTCTATCG	1000
	TCAAGATGGT	GCCATCCAAG	CCAATGTGTG	TTGAGGCTTT	CACCGACTAC	1050
	CCACCATTGG	GAAGATTTCG	CGTCAGAGAC			1080

10

2) INFORMATION FOR SEQ ID NO: 419

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 751 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida haemulonii*
 (B) STRAIN: ATCC 22991

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 419

	TCTGTCAAGT	GGGACAAGGC	CAGATACGAG	GAAATCGTCA	AGGAGACCTC	50
	TAACCTTCGTC	AAGAAGGTTG	GTTACAACCC	TAAGACTGTT	CCATTTCGTCC	100
30	CAATCTCTGG	TTGGAACGGT	GACAACATGA	TTGAGGCTTC	TACCAACTGT	150
	GACTGGTACA	AGGGTTGGGA	GAAGGAGACC	AAGTCTGGTA	AGTCCACCGG	200
	TAAGACCTTG	TTGGAGGCCA	TTGACGCCAT	TGAGCCACCA	ACCAGACCAA	250
	CCGACAAGCC	ATTGAGATTG	CCATTGCAGG	ATGTCTACAA	GATTGGTGGT	300
	ATCGGAACTG	TGCCAGTCGG	CAGAGTTGAG	ACCGGTGTTA	TCAAGGCCCG	350
35	TATGGTTGTC	ACCTTCGCCC	CAGCTGGTGT	CACCACTGAA	GTCAAGTCTG	400
	TCGAGATGCA	CCACGAGCAG	TTGCCAGAGG	GTGTCCCAGG	TGACAACGTT	450
	GGTTTCAACG	TCAAGAACGT	TTCCGTTAAG	GAAATCAGAA	GAGGTAACGT	500
	CTGTGGTGAC	TCCAAGCAGG	ACCCACCAAA	GGGCTGTGAC	TCTTTCACCG	550
	CTCAGGTTAT	TGTGTTGAAC	CACCCAGGTC	AGATCTCTTC	TGGTTACTCT	600
40	CCAGTTTTTG	ACTGTCACAC	TGCCCACATT	GCTTGTAAGT	TCGACACCTT	650
	GGTTGAGAAG	ATCGACAGAA	GAACCGGTAA	GAAGTTGGAA	GATGAGCCAA	700
	AGTTCATCAA	GTCCGGTGAC	GCTGCTATCG	TCAAGATGGT	CCCAACCAAG	750
	C					751

45

2) INFORMATION FOR SEQ ID NO: 420

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 1102 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida inconspicua*
 (B) STRAIN: ATCC 16783

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 420

	TCTTGACAAG	TTAAAGGCTG	AAAGAGAAAG	AGGTATCACT	ATTGATATTG	50
	CTTTATGGAA	ATTCGAAACT	CCAAAGTATC	ACGTTACCGT	CATTGATGCT	100
5	CCAGGTCACA	GAGATTTTCAT	TAAGAACATG	ATTACTGGTA	CTTCTCAAGC	150
	AGATTGTGCT	ATTTTGATTA	TTGCTGGTGG	TGTCGGTGAA	TTCGAAGCTG	200
	GTATTTCCAA	GGATGGTCAA	ACTAGAGAAC	ACGCTTTATT	AGCATTCCACC	250
	TTAGGTGTTA	AGCAATTGAT	TGTTGCTATC	AACAAGATGG	ATTCTGTAA	300
	GTGGGATGAA	AAGAGATTTG	AAGAAATTGT	CAAGGAAACC	CAAAACTTCA	350
10	TCAAGAAGGT	TGGTTACAAC	CCAAAGACTG	TTCCATTTCGT	TCCAATTTCT	400
	GGTTGGAATG	GTGACAACAT	GATTGAACCA	TCTTCTAACT	GTCCATGGTA	450
	CAAGGGTTGG	ACTAAGGAAA	CCAAGGCAGG	TGTTGTCAAG	GGTAAGACCT	500
	TATTAGAAGC	TATTGATGCT	ATTGAACCAC	CTGTCAGACC	AACTGATAAG	550
	CCATTAAGAT	TACCATTACA	AGATGTTTAC	AAGATTGGTG	GTATTGGTAC	600
15	TGTGCCAGTC	GGTAGAGTTG	AAACCGGTAT	TATTAAGCCA	GGTATGGTTG	650
	TTGTTTTTCGC	ACCATCTGGT	GTTACCACTG	AAGTCAAGTC	CGTTGAAAATG	700
	CACCATGAAC	AATTAGAAGA	AGGTGTCCCA	GGTGACAATG	TTGGTTTCAA	750
	CGTCAAGAAC	GTCTCTGTTA	AGGATATCAA	GAGAGGTAAC	GTTTGTGGTG	800
	ACTCCAAGAA	TGACCCACCA	CAAGGTTGTG	CTTCCTTCAA	TGCTCAAGTC	850
20	ATTGTCTTGA	ACCACCCTGG	TCAAATTTCT	GCTGGTTACT	CTCCAGTTTT	900
	AGATTGTCAC	ACTGCCCACA	TTGCATGTAA	ATTCGATGAA	TTAATTGAAA	950
	AGATTGACAG	AAGAACTGGT	AAGTCCGTTG	AAGACCATCC	AAAGTCTGTT	1000
	AAGTCTGGTG	ATGCAGCTAT	CGTTAAGATG	GTTCCAACCA	AGCCAATGTG	1050
	TGTTGAAGCT	TTCCTGAAT	ACCCACCATT	AGGTAGATTC	GCAGTCAGAG	1100
25	AT					1102

2) INFORMATION FOR SEQ ID NO: 421

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1099 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida kefyr*
- (B) STRAIN: ATCC 28838

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 421

45	TGGACAAGTT	AAAGGCTGAA	AGAGAAAGAG	GTATCACCAT	CGATATCGCT	50
	TTGTGGAAGT	TCGAAACTCC	AAAGTACCAA	GTTACCGTTA	TCGATGCTCC	100
	AGGTCACAGA	GATTTTCATCA	AGAACATGAT	TACTGGTACT	TCTCAAGCTG	150
	ACTGTGCTAT	CTTGATTATT	GCTGGTGGTG	TCGGTGAATT	CGAAGCCGGT	200
	ATCTCCAAGG	ATGGTCAAAC	CAGAGAACAC	GCTTTGTTGG	CTTACACCTT	250
50	GGGTGTTAGA	CAATTGATTG	TTGCTATCAA	CAAGATGGAC	TCTGTTAAGT	300
	GGGATGAATC	TCGTTACCAA	GAAATTGTTA	AGGAAACCTC	CAACTTCATC	350
	AAGAAGGTCG	GTTACAACCC	AAAGAATGTT	CCATTTCGTCC	CAATCTCTGG	400
	TTGGAACGGT	GACAACATGA	TTGAAGCCAC	CACCAACGCT	CCATGGTACA	450
	AGGGTTGGGA	AAGGAAACC	AAGGCTGGTA	CCGTCAAGGG	TAAGACCTTG	500
55	TTGGAAGCTA	TTGACGCTAT	CGAACCACCA	ACCAGACCAA	CTGACAAGCC	550
	ATTGAGATTG	CCATTGCAAG	ATGTCTACAA	GATCGGTGGT	ATTGGTACTG	600
	TGCCAGTCGG	TAGAGTCGAA	ACCGGTGTCA	TCAAGCCAGG	TATGGTTGTT	650
	ACCTTCGCC	CAGCCGGTGT	CACTACCGAA	GTTAAGTCCG	TCGAAATGCA	700
	CCACGAACAA	TTGGAAGAAG	GTCTACCAGG	TGACAACGTC	GGTTTCAACG	750
60	TCAAGAACGT	TTCCGTAAAG	GAAATCAGAA	GAGGTAACGT	CTGTGGTGAC	800

	TCCAAGAACG	ATCCACCAAA	GGCTGCTGCT	TCTTTCAACG	CCACTGTTAT	850
	CGTCTTGAAC	CACCCAGGTC	AAATCTCTGC	TGGTTACTCT	CCAGTTTTTG	900
	ATTGTACAC	TGCTCACATT	GCTTGTAAGT	TCGACGAATT	GTTGGAAAAG	950
	AACGACAGAA	GATCCGGTAA	GAAGTTGGAA	GACTCTCCAA	AGTTCTTGAA	1000
5	GTCTGGTGAC	GCTGCTTTGG	TTAAGTTCGT	TCCATCTAAG	CCAATGTGTG	1050
	TTGAAGCATT	CTCTGACTAC	CCACCATTGG	GTAGATTTCG	TGTCAGAGA	1099

10 2) INFORMATION FOR SEQ ID NO: 422

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 1095 bases
	(B)	TYPE: Nucleic acid
15	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

	(A)	ORGANISM: <i>Candida krusei</i>
	(B)	STRAIN: ATCC 34135

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 422

25	AAGTTAAAGG	CAGAAAGAGA	AAGAGGTATC	ACTATTGATA	TTGCTTTATG	50
	GAAGTTYGAA	ACTCCAAART	ACCACGTTAC	CGTTATTGAT	GCTCCAGGTC	100
	ACAGAGATTT	CATCAAGAAC	ATGATTACCG	GTAATTCTCA	AGCTGATTGT	150
	GCTATTTTGA	TTATTGCTGG	TGGTGTCGGT	GAATTCGAAG	CTGGTATCTC	200
30	CAAGGATGGT	CAAACTAGAG	AACACGCTCT	ATTGGCTTTC	ACCTTAGGTG	250
	TTAGACAATT	GATTGTTGCT	ATCAACAAGA	TGGATTCCGT	TAARTGGGAT	300
	GAAAACAGAT	TTGAAGAAAT	TGTCAAGGAA	ACCCAAAAC	TCATCAAGAA	350
	GGTTGGTTAC	AACCCAAAGA	CTGTTCCATT	CGTTCCAATY	TCTGGTTGGA	400
	ATGGTGACAA	CATGATTGAA	GCATCCACCA	ACTGTCCATG	GTACAAGGGT	450
35	TGGACTAAGG	AAACCAAGGC	AGGTGTTGTT	AAGGGTAAGA	CCTTATTAGA	500
	AGCAATCGAT	GCTATTGAAC	CACCTGTCAG	ACCAACCGAA	AAGCCATTAA	550
	GATTACCATT	ACAAGATGTT	TACAAGATTG	GTGGTATTGG	TACTGTGCCA	600
	GTCGGTAGAG	TCGAAACCGG	TGTCATTAAG	CCAGGTATGG	TTGTCACTTT	650
	TGCTCCAGCA	GGTGTACCA	CCGAAGTCAA	GTCCGTTGAA	ATGCACCATG	700
40	AACAATTAGA	ACAAGGTGTT	CCAGGTGATA	ACGTTGGTTT	CAACGTTAAG	750
	AACGTTTCTG	TCAAGGATAT	CAAGAGAGGT	AACGTTTGTG	GTGACTCCAA	800
	GAACGACCCA	CCAATGGGTG	CAGCTTCCTT	CAATGCTCAA	GTCATTGTCT	850
	TGAACCACCC	TGGTCAAATT	TCCGCTGGTT	ACTCTCCAGT	CTTGGATTGT	900
	CACACTGCCC	ACATTGCATG	TAAGTTCGAC	GAATTAATCG	AAAAGATTGA	950
45	CAGAAGAACT	GGTAAGTCTG	TTGAAGACCA	TCCAAAGTCY	GTCAAGTCTG	1000
	GTGATGCAGC	TATCGTCAAG	ATGGTCCCAA	CCAAGCCAAT	GTGTGTTGAA	1050
	GCTTTCACTG	AATAYCCACC	ATTAGGTAGA	TTCGCAGTCA	GAGAT	1095

50

2) INFORMATION FOR SEQ ID NO: 423

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 1104 bases
55	(B)	TYPE: Nucleic acid
	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida lambica*
 (B) STRAIN: ATCC 24750

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 423

```

CTTGGACAAG CTTAAGGCTG AAAGAGAAAG AGGTATCACC ATTGATATCG      50
CTTTATGGAA GTTCGAAACT CCAAAGTACC ACGTTACCGT CATTGACGCT      100
CCAGGTCACA GAGATTTTCAT CAAGAACATG ATTACTGGTA CCTCTCAAGC      150
10 AGATTGTGCT ATTTTRATYA TTGCTGGTGG TGTCGGTGAA TTCGAAGCTG      200
GTATCTCTAA GGATGGTCAA ACCAGAGAAC ACGCTCTTCT TGCATTCACT      250
CTTGGTGTTA GACAATTGAT TGTTGCTATC AACAAGATGG ACTCTGTCAA      300
GTGGGACGAA TCCAGATTCG ATGAAATTTG TAAGGAAACC GCWAACTTCA      350
TCAAGAAGGT TGGTTACAAC CCAAAGACTG TTCCATTTCGT CCAATCTCT      400
15 GGTGGAACG GTGACAACAT GATTGAACCA TCTGCTAACT GTCCATGGTA      450
CAAGGGATGG ACTAAGGAAA CCAAGGCTTC CGGTGTCGTC AAGGGTAAGA      500
CCCTTCTTGA AGCAATTGAT GCTATTGAGC CACCTGTCAG ACCAACTGAC      550
AAGGCTTTGA GATTGCCATT RCAAGATGTC TACAAGATTG GTGGTATTGG      600
TACTGTGCCA GTCGGTAGAG TTGAAACCGG TATCATCAAG CCAGGTATGA      650
20 TTGTCGTTTT CGCTCCAACC GGTGTTACTA CTGAAGTTAA GTCCGTTGAA      700
ATGCACCATG AACAATTAGA AGAAGGTGTC CCAGGTGACA ATGTTGGTTT      750
CAACGTCAAG AACGTCTCTG TTAAGGATAT TAAGAGAGGT AACGTCTGTG      800
GTGACTCCAA GAACGACCCA CCAATGGGTT GTGCTTCCTT CAATGCTCAA      850
GTCATTGTTC TTAACCACCC AGGTCAAATT TCTGCTGGTT ACTCACCAGT      900
25 TCTTGACTGT CACACTGCCC ACATTGCATG TAAGTTCGAY GAATTACTCG      950
AAAAGATTGA CAGAAGAACC GGTAAGGCTA CTGAAGACCA TCCAAAGTCT      1000
GTCAAGTCTG GTGATGCAGC TATCGTCAAG ATGGTTCCAA CCAAGCCAAT      1050
GTGTGTYGAA GCTTTCACTG ACTACCCACC ATTAGGTAGA TTCGCTGTYA      1100
GAGA                                                                1104

```

30

2) INFORMATION FOR SEQ ID NO: 424

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1098 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida lusitanae*
 (B) STRAIN: ATCC 66035

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 424

```

GGACAAGTTG AAGGCTGAGA GAGAAAGAGG TATCACCATC GATATCGCTT      50
50 TGTGGAAGTT CGAGACTCCA AAGTACCACG TTACCGTCAT TGACGCTCCA      100
GGTCACAGAG ATTTTCATCA GAACATGATC ACTGGTACTT CCCAAGCTGA      150
CTGTGCTATC TTGATTATCG CTGGTGGTGT CGGTGAGTTC GAAGCCGGTA      200
TCTCTAAGGA CGGTCAAACC AGAGAGCAGC CTTTGTGTGGC TTACACCTTG      250
GGTGTCGAAGC AGTTGATTGT TGCTGTCAAC AAGATGGACT CCGTCAAGTG      300
55 GGACCAATCT AGATTCGAGG AAATCATCAA GGAAACCTCT AACTTCGTCA      350
AGAAGGTTGG TTACAACCCT AAGACTGTTC CATTCGTCCC AATCTCTGGT      400
TGGAACGGTG ACAACATGAT TGAGCCATCY ACCAACTGCC CATGGTACAA      450
GGGTGTTGGGAG AAGGAGACCA AGTCYGGTAA GTCCACCGGT AAGACCTTGT      500
TGGAGGCCAT TGACGCCATT GAGCACCTT CGAGACCAAC CGACAAGCCA      550
60 TTGAGATTGC CATTGCAAGA TGTCTACAAG ATYGGTGGTA TTGGTACTGT      600

```

	GCCAGTCGGT	AGAGTTGAGA	CCGGTGTTCAT	CAAGGCCGGT	ATGGTTGTCA	650
	CCTTTGCTCC	AGCTGGTGTC	ACCACTGAAG	TCAAGTCCGT	GGAAATGCAC	700
	CACGAACAAT	TGGCTGAGGG	TGTCCCAGGT	GACAACGTTG	GTTTCAACGT	750
	CAAGAACGTT	TCCGTCAAGG	AAATCAGAAG	AGGTAACGTC	TGTGGTGAAT	800
5	CCAAGAACGA	CCCACCAAAG	GCTGCTGCTT	CYTTCACTGC	TCAAGTYATY	850
	GTCTTGAACC	ACCCAGGTCA	AATCTCCTCY	GGTTACTCTC	CAGFYTTGGA	900
	CTGTCACT	GCYCACATTG	CTTGTAAGTT	CGACACCTTG	ATTGAGAAGA	950
	TCGACAGAAG	AACYGGTAAG	AAGTTGGAAG	AAGAGCCAAA	GTTTCATCAAG	1000
	TCYGGTGACG	CTGCTATCGT	CAAGATGGTC	CCAACCAAGC	CAATGTGYGT	1050
10	YGAAGCTTTC	ACCGACTACC	CACCATTGGG	TAGATTCGCT	GTCAGAGA	1098

2) INFORMATION FOR SEQ ID NO: 425

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1101 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida norvegensis*
 (B) STRAIN: ATCC 22977

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 425

30	TCTTGACAAG	TTAAAGGCTG	AAAGAGAAAG	AGGTATCACT	ATTGATATTG	50
	CTTTATGGAA	ATTCGAAACT	CCAAAATACC	ACGTTACCGT	TATTGATGCT	100
	CCAGGTCACA	GAGATTTTCAT	TAAGAACATG	ATTACTGGTA	CTTCCCAAGC	150
	TGATTGTGCT	ATCTTAATTA	TTGCTGGTGG	TGTCGGTGAA	TTCGAAGCTG	200
	GTATCTCCAA	GGATGGTCAA	ACCAGAGAAC	ACGCTTTATT	AGCATTCACC	250
35	TTAGGTGTTA	AGCAATTAAT	TGTTGCTATC	AACAAGATGG	ACTCTGTAA	300
	GTGGGATGAA	AAGAGATTTG	AAGAAATTGT	CAAGGAAACC	CAAAACTTCA	350
	TCAAGAAGGT	TGGTTACAAC	CCAAAGACTG	TTCCATTTCG	TCCAATTTCT	400
	GGTTGGAATG	GTGACAACAT	GATTGAACCA	TCTACTAACT	GTCCATGGTA	450
	CAAGGGTTGG	ACTAAGGAAA	CCAAGGCAGG	TGTTGTTAAG	GGTAAGACCT	500
40	TATTAGAAGC	TATTGATGCT	ATTGAACCAC	CTGTCAGACC	AACTGACAAG	550
	CCATTAAGAT	TACCATTACA	AGATGTTTAC	AAGATTGGTG	GTATTGGTAC	600
	TGTGCCAGTC	GGTAGAGTTG	AAACCGGTGT	TATTAAGCCA	GGTATGGTTG	650
	TTGTTTTTCG	ACCATCTGGT	GTTACCACTG	AAGTCAAGTC	CGTTGAAATG	700
	CACCATGAAC	AATTAGAACA	AGGTGTCCCA	GGTGACAATG	TTGGTTTCAA	750
45	CGTCAAGAAC	GTCTCTGTTA	AGGATATTAA	GAGAGGTAAC	GTTTGTGGTG	800
	ACTCCAAGAA	CGACCCACCA	CAAGGTTGTG	CTTCCTTCAA	TGCTCAAGTC	850
	ATTGTCTTGA	ACCACCTTGG	TCAAATTTCT	GCAGGTTACT	CTCCAGTTTT	900
	AGATTGTCAC	ACTGCCCACA	TTGCATGTAA	GTTCGATGAA	TTAATCGAAA	950
	AGATTGACAG	AAGAACTGGT	AAGTCCGTTG	AAGACCATCC	AAAGTCTGTT	1000
50	AAGTCTGGTG	ATGCAGCTAT	CGTTAAGATG	GTTCCAACCA	AGCCAATGTG	1050
	TGTTGAAGCT	TTCACTGAAT	ACCCACCATT	AGGTAGATTC	GCAGTCAGAG	1100
	A					1101

2) INFORMATION FOR SEQ ID NO: 426

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1095 bases
 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida parapsilosis*
(B) STRAIN: ATCC 90018

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 426

CAAATTGAAG	GCTGAAAGAG	AAAGAGGTAT	CACCATTGAT	ATCGCTTTGT	50
GGAAATTCGA	AACTCCAAAA	TACCATGTTA	CTGTTATTGA	TGCTCCAGGT	100
CACAGAGATT	TCATCAAGAA	TATGATTACT	GGTACTTCTC	AAGCTGATTG	150
TGCTATTTTG	ATTATTGCTG	GTGGTACTGG	TGAATTCGAA	GCTGGTATCT	200
CTAAGGATGG	TCAAACCAGA	GAACACGCTT	TGTTGGCTTA	CACCTTGGGT	250
GTTAAGCAAT	TGATTGTTGC	CATCAACAAG	ATGGACTCAG	TCAAATGGGA	300
CAAGAACAGA	TACGAAGAAA	TTGTCAAGGA	AACTTCCAAC	TTCGTCAAGA	350
AGGTTGGTTA	CAACCCTAAA	GCTGTCCCAT	TCGTCCCAAT	CTCTGGTTGG	400
AACGGTGACA	ATATGATTGA	ACCATCAACC	AACTGTCCAT	GGTACAAGGG	450
TTGGGAAAAG	GAAACTAAAG	CTGGTAAGGT	TACCGGTAAG	ACCTTGTGTTG	500
AAGCTATCGA	TGCTATCGAA	CCACCAACCA	GACCAACTGA	CAAGCCATTG	550
AGATTGCCAT	TGCAAGATGT	CTACAAGATT	GGTGGTATTG	GAAGCTGTGCC	600
AGTTGGTAGA	GTTGAAACCG	GTATCATCAA	GGCTGGTATG	GTTGTTACTT	650
TTGCCCCAGC	TGGTGTTACC	ACTGAAGTCA	AGTCCGTTGA	AATGCACCAC	700
GAACAATTGA	CTGAAGGTGT	CCCAGGTGAC	AATGTTGGTT	TCAACGTCAA	750
GAACGTTTCA	GTTAAGGAAA	TCAGAAGAGG	TAACGTTTGT	GGTGACTCCA	800
AGAACGATCC	ACCAAAGGGA	TGTGAYTCCT	TCAATGCTCA	AGTTATTGTC	850
TTGAACCACC	CAGGTCAAAT	CTCTGCTGGT	TACTCACCAG	TCTTGGATTG	900
TCACACTGCC	CACATTGCTT	GTAAATTCTG	CACTTTGATT	GAAAAGATTG	950
ACAGAAGAAG	CGGTAAGAAA	TTGGAAGATG	AACCAAAATT	CATCAAGTCC	1000
GGTGATGCTG	CYATCGTCAA	GATGGTCCCA	ACCAAGCCAA	TGTGTGTTGA	1050
AGCTTTTCACT	GACTACCCAC	CATTGGGAAG	ATTCGCTGTT	AGAGA	1095

2) INFORMATION FOR SEQ ID NO: 427

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 752 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida rugosa*
(B) STRAIN: ATCC 96275

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 427

CTCCGTC AAG	TGGTCTC AGT	CTCGTTTCGA	GGAGATCGTC	AAGGAGGTTT	50
CCAACTTCAT	CAAGAAGGTT	GGTTACAAGC	CCGATGAGGT	TCCTTTTCGTC	100
CCCATCTCTG	GCTGGAACGG	CGACAACATG	CTTGAGCCCT	CCACCAACTG	150
CCCCTGGTAC	AAGGGATGGA	CCAAGAAGAC	CAAGAAGGGT	GAGGTCAAGG	200
GTAAGACTCT	TCTCGAGGCC	ATTGACGCCA	TCGAGCCCCC	CTCCCGTCCT	250
ACCGACAAGC	CCCTCCGCTT	GCCTCTTCAG	GATGTCTACA	AGATCGGCGG	300
TATCGGTACG	GTACCTGTCTG	GCCGTGTCGA	GACCGGTATC	ATCAAGCCCCG	350
GCATGGTCTG	CACTTTCGCC	CCCGCTGGTG	TCACCACTGA	AGTGAAGTCC	400

5 GTCGAGATGC ACCACGAGCA GATCCCCGAG GGTCTCCCCG GTGACAACGT 450
 CGGTTTCAAC GTCAAGAACG TTACCGTCAA GGATATCCGC CGTGGTAACG 500
 TCTGCGGTGA CTCCAAGAAC GACCCCCCA AGGGCTGCTC TTCCTTCACT 550
 GCCCAGGTCA TCGTTTTCAA CCACCCCGGT CAGATCTCCA ACGGTACTC 600
 CCCCCTTTTG GACTGCCACA CCGCCACAT TGCCTGCCGC TTCGACGAGA 650
 TCCAGTCCAA GATGGACCGT CGTACTGGTA AGACCCTTGA GGAGAACCCC 700
 AAGTTCATCA AGGCTGGTGA CTCCGCTATC GTCAAGATGG TTCCCTCCAA 750
 GC 752

10

2) INFORMATION FOR SEQ ID NO: 428

- 15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1093 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 20 (ii) MOLECULE TYPE: Genomic DNA
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Candida sphaerica*
 (B) STRAIN: ATCC 2504
 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 428

AGTTAAAGGC TGAAAGAGAA AGAGGTATCA CCATCGATAT CGCTTTGTGG 50
 AAGTTCGAAA CTCCAAAGTA CCAAGTTACC GTTATCGATG CTCCAGGTCA 100
 30 CAGAGATTTT ATCAAGAACA TGATTACTGG TACTTCTCAA GCTGACTGTG 150
 CTATCTTGAT TATTGCTGGT GGTGTCGGTG AATTCGAAGC CCGGTATCTCC 200
 AAGGATGGTC AAACCAGAGA ACACGCTTTG TTGGCTTTCA CCTTGGGTGT 250
 TAGACAATTG ATTGTTGCTG TTAACAAGAT GGATTCCGTT AAGTGGGATG 300
 AATCTCGTTT CCAAGAAATT GTCAAGGAAA CCTCTAATT CATCAAGAAG 350
 35 GTCGGTTACA ACCCAAAGAC TGTTCCATT GTCCCAATCT CTGGTTGGAA 400
 CCGTGACAAC ATGATTGAAG CCACCACCAA TGCTTCATGG TACAAGGGTT 450
 GGGAAAAGGA AACCAGTCC GGTGTCGTCA AGGGTAAGAC CTTGTTGGAA 500
 GCTATTGACG CTATCGAACC ACCATCCAGA CCAACTGACA AGCCATTGAG 550
 ATTGCCATTG CAAGATGTCT ACAAGATTGG TGGTATCGGA ACTGTGCCAG 600
 40 TCGGTAGAGT CGAAACCGGT GTTATCAAGC CAGGTATGAT TGTACCTTT 650
 GCCCCAGCCG GTGTTACTAC TGAAGTTAAG TCCGTCGAAA TGCACCACGA 700
 ACAATTGGAA GAAGGTCTAC CAGGTGACAA CGTCGGTTTC AACGTCAAGA 750
 ACGTTTCCGT TAAGGAAATC AGAAGAGGTA ACGTCTGTGG TGACTCCAAG 800
 AACGATCCAC CAAAGGCTGC TGCTTCTTTC AACGCCACTG TTATCGTCTT 850
 45 GAACCATCCA GGTCAAATCT CTGCTGGTTA CTCTCCAGTT TTGGATTGTC 900
 AACTGCTCA CATGCTTGT AAGTTCGACG AATTGTTGGA AAAGAACGAT 950
 AGAAGATCCG GTAAGAAGTT GGAAGACTCT CCAAAGTTCT TGAAGTCCGG 1000
 TGATGCTGCT TTGGTTAAGT TCGTTCCATC TAAGCCAATG TGTGTTGAAG 1050
 50 CCTTCTCTGA CTACCCACCT CTAGGTAGAT TCGCTGTCAG AGA 1093

2) INFORMATION FOR SEQ ID NO: 429

- 55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1094 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 60 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida tropicalis*
 (B) STRAIN: ATCC 13803

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 429

	AAATTGAAGG	CTGAAAGAGA	AAGAGGTATC	ACCATTGATA	TCGCTTTGTG	50
10	GAAATTCGAA	ACTCCAAAAT	ACCACGTTAC	CGTTATTGAT	GCTCCAGGTC	100
	ACAGAGATTT	CATCAAGAAC	ATGATTACTG	GTAATTCCCA	AGCTGATTGT	150
	GCTATTTTGA	TTATTGCTGG	TGGTACTGGT	GAATTCCAAG	CTGGTATTTT	200
	TAAAGATGGT	CAAACCAGAG	AACACGCTTT	GTTGGCTTAC	ACCTTGGGTG	250
	TCAAACAATT	GATTGTTGCT	GTCAACAAGA	TGGACTCTGT	TAAATGGGAC	300
15	AAAAACAGAT	TTGAAGAAAT	TATCAAGGAA	ACTTCTAACT	TCGTCAAGAA	350
	GGTTGGTTAC	AACCCTAAGG	CTGTTCCATT	CGTTCCAATC	TCTGGTTGGA	400
	ATGGTGACAA	CATGATTGAA	GCTTCTACCA	ACTGTCCATG	GTACAAGGGT	450
	TGGGAAAAAG	AAACCAAGGC	TGGTAAGGTT	ACCGGTAAGA	CTTTGTTGGA	500
	AGCCATTGAT	GCTATTGAAC	CACCTTCAAG	ACCAACTGAC	AAGCCATTGA	550
20	GATTGCCATT	GCAAGATGTT	TACAAGATTG	GTGGTATTGG	TACTGTGCCA	600
	GTCGGTAGAG	TTGAAACTGG	TGTCATCAAA	GCCGGTATGG	TTGTTACTTT	650
	CGCCCCAGCT	GGTGTTACCA	CTGAAGTCAA	ATCCGTCGAA	ATGCACCACG	700
	AACAATTGGC	TGAAGGTGTC	CCAGGTGACA	ATGTTGGTTT	CAACGTTAAG	750
	AACGTTTCTG	TTAAAGAAAT	TAGAAGAGGT	AACGTTTGTG	GTGACTCCAA	800
25	GAACGATCCA	CCAAAGGGTT	GTGACTCTTT	CAACGCTCAA	GTTATTGTCT	850
	TGAACCACCC	AGGTCAAATC	TCTGCTGGTT	ACTCTCCAGT	CTTGGATTGT	900
	CACACTGCTC	ATATTGCTTG	TAAATTCGAC	ACCTTGGTTG	AAAAGATTGA	950
	CAGAAGAACT	GGTAAGAAAT	TGGAAGAAAA	TCCAAAATTC	GTCAAATCCG	1000
	GTGATGCTGC	TATTGTCAAG	ATGGTTCCAA	CCAAACCAAT	GTGTGTTGAA	1050
30	GCTTTCACTG	ACTACCCACC	ATTAGGTAGA	TTGCTGTCA	GAGA	1094

2) INFORMATION FOR SEQ ID NO: 430

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1095 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida utilis*
 (B) STRAIN: Csp 388

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 430

50	CAAGCTTAAA	GCTGAGAGAG	AGAGAGGTAT	CACTATCGAC	ATTGCTCTCT	50
	GGAAGTTCGA	GACTCCAAAG	TACCACGTTA	CTGTCATTGA	TGCCCCAGGT	100
	CACAGAGATT	TCATCAAGAA	CATGATTACT	GGTACCTCCC	AGGCTGACTG	150
	TGCTATTCTT	ATCATTGCCG	GTGGTGTTGG	TGAGTTCGAG	GCTGGTATCT	200
	CTAAGGATGG	TCAGACCAGA	GAGCACGCTT	TGCTCGCTTT	CACCTTGGT	250
55	GTTAGACAGA	TGATTGTTGC	TATCAACAAG	ATGGACTCTG	TCAAGTGGGA	300
	CGAGAAGAGA	TTCGAGGAGA	TCGTTAAGGA	GACCTCTAAC	TTCATCAAGA	350
	AGGTGTTGTTA	CAACCCAAAG	ACTGTTCCAT	TTGTCCCAAT	TTCTGTTGG	400
	AACGGTGACA	ACATGATTGA	GGCCTCTACC	AACGTGTCAT	GGTACAAGGG	450
	TTGGGAGAAG	GAGACCAAGG	CTGGTGTTGT	CAAGGGTAAG	ACCTTGCTCG	500
60	ATGCCATTGA	CGCCATTGAG	CCACCAACAA	GACCAACTGA	CAAGCCATTG	550

	AGATTGCCAC	TCCAGGATGT	CTACAAGATT	GGTGGTATCG	GAACTGTTCC	600
	AGTCGGTAGA	GTCGAGACCG	GTGTCATCAA	GCCAGGTATG	GTTGTTACCT	650
	TTGCCCCATC	CGGTGTCACC	ACTGAGGTTA	AGTCCGTCGA	GATGCACCAC	700
	GAGCAGCTTG	CTGAGGGTAT	CCCAGGTGAC	AACGTTGGTT	TCAACGTTAA	750
5	GAACGTCTCT	GTTAAGGAGA	TCAGAAGAGG	TAACGTTGCC	GGTGACTCCA	800
	AGAACGACCC	ACCACAGGGT	GCTGAGTCCT	TCAACGCTCA	GGTCATTGTC	850
	TTGAACCACC	CAGGTCAGAT	CTCTGCTGGT	TACTCTCCAG	TTTTGGACTG	900
	TCACACCGCC	CACATTGCTT	GTAAGTTCTC	TGAGCTTTTG	GAGAAGATTG	950
	ACAGAAGATC	CGGTAAGTCC	CTTGAGGCCT	CTCCAAAGTT	CGTCAAGTCT	1000
10	GGTGATGCCG	CTATCGTCAA	GATGGTTCCA	TCCAAGCCAT	TGTGTGTTGA	1050
	GGCCTTCACT	GACTACCCAC	CACTCGGTAG	ATTCGCTGTC	AGAGA	1095

15 2) INFORMATION FOR SEQ ID NO: 431

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1085 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida viswanathii*
 (B) STRAIN: ATCC 28269

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 431

30	GCTGAAAGAG	AAAGAGGTAT	CACCATCGAT	ATCGCTTTGT	GGAAATTCGA	50
	AACTCCAAAR	TACCACGTTA	CCGTCATTGA	YGCTCCAGGT	CACAGAGATT	100
	TCATCAAGAA	CATGATYACT	GGTACTTCTC	AAGCTGATTG	TGCTATYTTG	150
	ATTATCGCTG	GTGGTACTGG	TGAATTCGAA	GCTGGTATYT	CTAAGGATGG	200
35	TCAAACCAGA	GAACACGCTT	TGTTGGCCTA	CACCTTGGGT	GTCAAGCAAT	250
	TGATTGTTGC	TGTCAACAAG	ATGGACTCTG	TCAAATGGGA	CAAGAACAGA	300
	TTCGAAGAAA	TCATCAAGGA	AACCTCCAAC	TTCGTCAAGA	AGGTTGGTTA	350
	CAACCCAAAG	ACTGTTCCAT	TCGTCCCAAT	CTCTGGTTGG	AACGGTGACA	400
	ACATGATTGA	AGCCTCCACC	AACTGCCCCAT	GGTACAAGGG	TTGGGAAAAG	450
40	GAAACCAAGG	CTGGTAAGGT	TACCGGTAAG	ACTTTGTTGG	AAGCCATTGA	500
	CGCTATCGAA	CCACCAACCA	GACCAACTGA	CAAGCCATTG	AGATTGCCAT	550
	TGCAAGATGT	CTACAAGATT	GGTGGTATCG	GAACGTGACC	AGTCGGTAGA	600
	GTTGAAACTG	GTGTCATCAA	GGCCGGTATG	GTTGTCACTT	TYGCCCCAGC	650
	TGGTGTTACC	ACTGAAGTCA	AGTCCGTTGA	AATGCACCAC	GAACAATTGG	700
45	CTGAAGGTGT	CCCAGGTGAC	AACGTTGGTT	TCAACGTCAA	GAACGTTTCC	750
	GTCAAGGAAA	TCAGAAGAGG	TAACGTCTGT	GGTGACTCCA	AGAACGACCC	800
	ACCAAAGGGT	TGTGASTCTT	TCAACGCTCA	AGTCATTGTC	TTGAACCACC	850
	CAGGTCAAAAT	CTCTGCTGGT	TACTCTCCAG	TCTTGGATTG	TCACACTGCC	900
	CACATTGCTT	GTAAGTTTGA	CACCTTGGTT	GAAAAGATTG	ACAGAAGAAC	950
50	CGGTAAGAAG	TTGGAAGAAA	ACCAAAGTT	TGTCAAGTCC	GGTGACGCTG	1000
	CTATCGTCAA	GATGGTCCCA	ACCAAGCCAA	TGTGTGTTGA	AGCYTTCACT	1050
	GACTACCCAC	CATTGGGTAG	ATTCGCTGTC	AGAGA		1085

55

2) INFORMATION FOR SEQ ID NO: 432

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1072 bases
 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida zeylanoides*
(B) STRAIN: ATCC 7351

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 432

	AGGTATTACC	ATTGACATTG	CCTTGTGGAA	GTTTCGAGACC	CCCAAGTACC	50
	AGGTCACCGT	CATTGACGCT	CCTGGCCACA	GAGATTTTCAT	TAAGAACATG	100
	ATCACTGGTA	CCTCCCAGGC	TGACTGTGCC	ATCTTGATCA	TTGCTGGTGG	150
15	TGTTGGTGAG	TTTCGAGGCTG	GTATCTCCAA	GGATGGCCAG	ACCAGAGAGC	200
	ACGCCTTGCT	TGCCTACACC	TTGGGTGTCA	AGCAATTGAT	TGTTGCTGTC	250
	AACAAGATGG	ACTCCGTCAA	GTGGGACAAG	AACAGATTCG	AGGAGATTGT	300
	CAAGGAGACC	TCCAACCTCG	TCAAGAAGGT	TGGCTACAAC	CCCAAGACTG	350
	TCCCCTTCGT	TCCCATCTCC	GGTTGGAACG	GTGACAACAT	GATTGAGGCC	400
20	TCCACCAACT	GCCCTTGGTA	CAAGGGTTGG	GAGAAGGAGA	CCAAGGCCGG	450
	TAAGGTCACT	GGTAAGACCT	TGTTGGAGGC	TATTGACGCC	ATTGAGCCCC	500
	CCACCAGACC	CACCGACAAG	CCCTTGAGAT	TGCCCTTGCA	GGATGTCTAC	550
	AAGATTGGTG	GTATTGGAAC	GGTGCCCGTT	GGCAGAGTTG	AGACCGGCAT	600
	CATCAAGGCC	GGTATGGTTG	TCACCTTTGC	CCCCGCTGGT	GTCACACTG	650
25	AAGTGAAGTC	TGTCGAGATG	CACCACGAGC	AATTGGCTGA	GGGTGTCCCA	700
	GGTGACAATG	TTGGTTTCAA	CGTGAAGAAC	GTTTCCGTTA	AGGAGATCAG	750
	AAGAGGTAAC	GTTTGCGGTG	ACTCCAAGAA	CGACCCCCC	AAGGCTGCTG	800
	CTTCTTTCAA	CGCCCAGGTT	ATCGTCTTAA	ACCACCCCCG	TCAAATCTCT	850
	GCTGGTTACT	CTCCGGTTTT	GGATTGCCAC	ACTGCCCCA	TTGCTTGCGAG	900
30	ATTTCGACCAG	TTGATTGAGA	AGATCGACAG	AAGAACCGGT	AAGAAGATGG	950
	AGGACGACCC	TAAGTTCATC	AAGTCCGGTG	ACGCTGCCAT	CGTCAAGATG	1000
	GTTCTTTCCA	AGCCCATGTG	TGTTGAGGCC	TTCACTGACT	ACCCTCCCTT	1050
	GGGTCGTTTC	GCTGTCAGAG	AC			1072

2) INFORMATION FOR SEQ ID NO: 433

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 751 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Coccidioides immitis*
(B) STRAIN: Silveira

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 433

	AGCACCAACT	GGTCCGAGCC	TCGTTTCAAC	GAAATCGTCA	AGGAAGTCTC	50
	CAACTTCATC	AAGAAGGTG	GATACAACCC	CAAGGCTGTT	CCATTCGTCC	100
55	CCATCTCTGG	TTTCGAAGGT	GACAACATGA	TTCAACCCTC	CACCAACGCT	150
	CCTTGGTACA	AGGGCTGGAA	CAAGGAGACC	GCCTCTGGCA	AGCACACTGG	200
	CAAGACCCTC	CTCGACGCCA	TTGATGCCAT	CGACCCCCCA	ACCCGCCCCA	250
	CCGAGAAGCC	CCTCCGTCTC	CCACTTCAGG	ATGTGTACAA	GATCTCTGGT	300
	ATCGGAACAG	TCCCAGTCGG	CCGTGTGCGAA	ACCGGTGTTA	TCAAGCCTGG	350
60	TATGGTTGTG	ACCTTCGCTC	CTTCCAACGT	CACCACTGAA	GTCAAGTCCG	400

TCGAAATGCA CCACCAGCAG CTCACCCAGG GTAACCCTGG TGACAACGTT 450
 GGCTTCAACG TCAAGAACGT CTCTGTCAAG GAAGTCCGCC GCGGTAACGT 500
 CGCTGGTGAC TCCAAGAACG ACCCACCAAA GGGCTGCGAC TCCTTCAACG 550
 CCCAGGTCAT CGTCCTCAAC CACCCTGGTC AAGTCGGTGC TGGTTATGCC 600
 5 CCAGTCCTTG ACTGCCACAC TGCCACATT GCTTGCAAGT TCTCCGAGCT 650
 CCTCGAGAAG ATCGACCGCC GTACCGGTAA ATCCGTTGAG AACACCCCA 700
 AGTTCATCAA GTCTGGTGAT GCCGCTATCG TCAAGATGGT TCCATCCAAG 750
 C 751

10

2) INFORMATION FOR SEQ ID NO: 434

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 1146 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cryptococcus albidus*
 (B) STRAIN: ATCC 66030

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 434

AAGCTCAAGG CCGAGCGAGA GCGAGGTATC ACCATCGACA TCGCCTTGTTG 50
 GAAGTTCGAG ACCCCCAAGT ACAATGTCAC CGTCATTGAC GCGCCCGGTC 100
 30 ACCGAGACTT CATCAAGAAC ATGATCACC GATACCTCGCA GGCCGACTGT 150
 GCCATCCTCA TCATCGCCTC CGGTATCGGA GAGTTCGAGG CTGGTATCTC 200
 CAAGGACGGT CAGACCCGAG AGCACGCCCT TTTGGCCTTC ACCCTCGGTG 250
 TCCGACAGCT CATCATTGCC ATCAACAAGA TGGACACCTG CAAGGTTAGT 300
 TCGCAGGTCC TGGTCTCTGT ACGAATCTTG CTGACCCCTT TTACAGTGGT 350
 35 CCGAAGACCG ATACAACGAA ATCGTCAAGG AGGCTTCCGG TTTTCATCAAG 400
 AAGGTCGGAT ACAACCCCAA GACCGTTCCC TTCGTCCCCA TCTCCGGATG 450
 GCACGGAGAC AACATGTTGG AGGAGTCCAC CAACATGCCC TGGTACAAGG 500
 GATGGCACAA GGAGTCCAAG GCCCGTGTTG TCAAGGAAA GACCTTGCTC 550
 GAGGCCATCG ACGCCATCGA GCGCCCTACC CGACCTTCCG ACAAGCCCTT 600
 40 GCGATTGCC CTCCAGGATG TCTACAAGAT CCGTGGTATC GGTACGGTGC 650
 CCGTCGGTCG AGTCGAGACC GGTGTCATCA AGGCTGGTAT GGTTCGTCACC 700
 TTCGCCCTCG CCAACGTCAC CACCGAAGTC AAGTCCGTCG AAATGCACCA 750
 CGAACAGCTC GCTGAGGGTG TTCCCGGTGA CAACGTCGGT TTCAACGTCA 800
 AGAACGTTTC CGTCAAGGAC ATCCGACGAG GAAACGCTG CTCCGACTCG 850
 45 AAGAACGACC CCGCTATGGA GTCTGCTTCC TTCAACGCTC AGGTCATTGT 900
 CTTGAACCAC CCGGGTCAGA TCGGTGCCGG CTACTCCCCC GTTTTGGAAT 950
 GCCACACCGC TCACATTGCC TGCAAGTTCC CTGAGCTCGT TGAGAAGATC 1000
 GACCGACGAA CCGGTAAGGT CATGGAGGCC GCGCCCAAGT TCGTCAAGTC 1050
 CGGTGACGCC GCCATCGTCA AGTTGATCCC GTCCAAGCCC ATGTGTGTCG 1100
 50 AGTCCTACTC CGAGTACCCC CCCTTGGGTC GATTCGCCGT CCGAGA 1146

2) INFORMATION FOR SEQ ID NO: 435

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 1095 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 60 (D) TOPOLOGY: Linear

(ii)MOLECULE TYPE: Genomic DNA

(vi)ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Exophiala jeanselmei*
 (B) STRAIN: ATCC 64755

(xi)SEQUENCE DESCRIPTION: SEQ ID NO: 435

```

10 CAAGCTGAAG GCCGAGCGTG AGCGTGGTAT CACCATCGAT ATCGCCTTGT      50
   GGAAGTTCGA GACTCCCAAG TACTATGTCA CTGTCATCGA CGCCCCTGGT      100
   CATCGTGACT TTATCAAGAA CATGATCACT GGTACTTCCC AGGCTGACTG      150
   CGCCATTCTC ATCATTGCCG CCGGTACTGG TGAATTTCGAA GCCGGTATCT      200
   CCAAGGATGG TCAGACTCGT GAGCACGCTC TGCTCGCCTA CACCCTGGGT      250
15 GTCAAGCAGC TCATTGTGCG CATCAACAAG ATGGACACCA CCAAGTGGTC      300
   CGAGGATCGT TTCAACGAAA TCATCAAGGA GACTTCCAGC TTCATCAAGA      350
   AGGTCGGCTA CAACCCCAAG TCCGTTCCCT TCGTCCCCAT CTCCGGCTTC      400
   AACGGTGACA ACATGATCGA TGTCTCCACC AACTGCCCCCT GGTACAAGGG      450
   CTGGGAGAAG GAGACCAAGG CTGGCAAGGC CTCTGGCAAG ACTCTCCTCG      500
20 AGGCCATCGA CGCCATCGAC CCCCCCACTC GTCCCACCGA CAAGCCTCTC      550
   CGTCTTCCTC TCCAGGATGT CTACAAGATC TCTGGTATCG GAACGGTGCC      600
   CGTCGGTCGT GTTGAGACTG GTGTCAATCA GGCCGGTATG GTCGTTACCT      650
   TCGCTCCTGC CAACGTCACC ACTGAAGTCA AGTCCGTCGA AATGCACCAC      700
   GAACAACCTCG CCGAGGGTGT TCCAGGTGAC AACGTTGGTT TCAACGTCAA      750
25 GAACGTCTCC GTCAAGGAGG TTCGTCGTGG AAACGTCTGC GGTGACTCCA      800
   AGAACGACCC ACCCAAGGGT GCTGATTCCT TCAACGCCCA GGTCAATCGTC      850
   TTGAACCACC CTGGTCAAGT CGGTGCTGGC TACGCCCCAG TGTGATTG      900
   CCACACTGCC CACATTGCTT GCAAGTTCTC TGAGCTTCTC GAGAAGATTG      950
   ACCGCCGTAC CGGTAAATCC ATCGAAAACA ACCCCAAGTT CATCAAGTCT      1000
30 GGTGACGCTG CCATCGTCAA GATGGTTCCC AGCAAGCCCA TGTGTGTTGA      1050
   GGCTTCACT GACTACCCAC CTCTTGGTGCG TTTCGCCGTC CGTGA          1095

```

35 2) INFORMATION FOR SEQ ID NO: 436

(i)SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 1113 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii)MOLECULE TYPE: Genomic DNA

45 (vi)ORIGINAL SOURCE:

- (A) ORGANISM: *Fusarium oxysporum*
 (B) STRAIN: WSA-212

(xi)SEQUENCE DESCRIPTION: SEQ ID NO: 436

```

50 AAGCTCAAGG CCGAGCGTGA GCGTGGTATC ACCATCGATA TTGCTCTCTG      50
   GAAGTTCGAG ACTCCTCGCT ACTATGTCAC CGTCATTGGT ATGTTGTCGC      100
   TCATGCTTCA TTCTACTTCT CTTCGTAATA ACACATCACT CAGACGCTCC      150
   CGGTCAACCGT GATTTTCATCA AGAACATGAT CACTGGTACT TCCCAGGCCG      200
55 ATTGCGCCAT TCTCATCATT GCCGCCGGTA CTGGTGAGTT CGAGGCTGGT      250
   ATCTCCAAGG ATGGCCAGAC CCGTGAGCAC GCTCTTCTTG CCTACACCTT      300
   TGGTGTCAAG AACCTCATCG TCGCCATCAA CAAGATGGAC ACCACCAAGT      350
   GGTCTGAGGC CCGTTACCAG GAGATCATCA AGGAGACCTC CTCTTTCATC      400
   AAGAAGGTCG GCTACAACCC CAAGGCTGTC GCTTTCGTCC CCATCTCCGG      450
60 TTCAACGGT GACAACATGC TTACCCCTC CACCAACTGC CCCTGGTACA      500

```

AGGGTTGGGA GCGTGAGATC AAGTCCGGCA AGCTCACTGG CAAGACCCTC 550
 CTCGAGGCCA TTGACTCCAT CGAGCCCCCC AAGCGTCCCG TTGACAAGCC 600
 CCTTCGTCTT CCCCTTCAGG ATGTCTACAA GATCGGTGGT ATTGGAACGG 650
 TTCCCGTCGG CCGTATCGAG ACTGGTGTCA TCAAGCCCGG TATGGTCGTT 700
 5 ACCTTCGCTC CTTCCAACGT CACCACTGAA GTCAAGTCCG TCGAGATGCA 750
 CCACGAGCAA CTCACTGAGG GCCAGCCCGG TGACAACGTT GGTTTCAACG 800
 TGAAGAACGT CTCCGTCAAG GACATCCGAC GTGGTAACGT CGCTGGTGAC 850
 TCCAAGAACG ACCCCCCTAT GGGTGCCGCT TCTTTCACCG CCCAGGTCAT 900
 CGTCCTCAAC CACCCCGGTC AGGTCGGTGC TGGTTACGCT CCCGTCCTCG 950
 10 ATTGTCACAC TGCCACATT GCCTGCAAGT TCGCCGAGAT CCAGGAGAAG 1000
 ATCGACCGCC GAACCGGTAA GGCTACTGAG GCCGCCCCCA AGTTCATCAA 1050
 GTCTGGTGAC TCCGCCATCG TCAAGATGGT TCCCTCCAAG CCCATGTGTG 1100
 TTGAGGCTTT CAC 1113

15

2) INFORMATION FOR SEQ ID NO: 437

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 726 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Geotrichum* spp.
 (B) STRAIN: LEV-4

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 437

GGTCCGAGGA CAGATTCAAC GAGATTGTCA AGGAGACTTC CAACTTCATC 50
 AAGAAGGTTG GTTAYAACCC CAAGACTGTT GCTTTCGTCC CCATCTCTGG 100
 35 TTGGAACGGT GACAACATGA TTGAGCCCTC CACCAACTGC CCCTGGTACA 150
 AGGGATGGCA GAAGGAGACC AAGGCTGGTG TCACTAAGGG TAAGACCCTC 200
 CTTGAGGCCA TCGATGCCAT TGAGCCCCCT GTCAGACCTT CCGACAAGCC 250
 CCTCCGTCTT CCCCTCCAGG ATGTCTACAA GATCGGTGGT ATCGGAACTG 300
 TGCCCGTCGG CCGTGTCGAA ACCGGTGTCA TCAAGGCCGG TATGGTCGTC 350
 40 ACCTTCGCCC CCGCTGGTGT CACCACTGAA GTCAAGTCCG TCGAGATGCA 400
 CCACGAGCTC CTCACTGAGG GTCTCCCCGG TGACAACGTT GGTTTCAACG 450
 TCAAGAACGT CTCCGTTAAG GATATCAGAC GTGGTAACGT CTGCGGTGAC 500
 TCCAAGAACG ATCCCCCCTA GGCTTGCGCT TCTTTCAACG CCCAGGTCAT 550
 TATCTTCAAC CACCCTGGTC AGATCTCTGC TGGATACTCT CCCGTCCTTG 600
 45 ATTGCCACAC CGCCCATATT GCTTGCAAGT TCGACACTTT GATCGAGAAG 650
 ATTGACCGTC GTACTGGTAA GAAGACTGAG GACTCCCCCA AGTTCGTCAA 700
 GGCCGGTGAT GCTGCTATCG TCAAGA 726

50

2) INFORMATION FOR SEQ ID NO: 438

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 754 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Histoplasma capsulatum*
 (B) STRAIN: G186A5

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 438

```

CACCACCAAG TGGTCCGAGT CCCGTTTCAA CGAAATCATC AAGGAGGTTT      50
CCAACCTTCAT CAAGAAGGTC GGATATAACC CCAAGGCTGT TCCCTTCGTG      100
CCAATCTCTG GTTTCGAGGG TGACAACATG ATTGAACCCT CCCCCAACTG      150
10 CACATGGTAC AAGGGCTGGA ACAAGGAGAC TGCCCTCTGGC AAGTCTTCTG      200
GTAAACCCT TCTCGATGCC ATTGACGCCA TTGAACCCCC AACCCGTCCT      250
ACCGATAAGC CCCTCCGTCT TCCCCTCCAG GATGTGTACA AAATCTCTGG      300
TATTGGCACT GTTCCCGTCT GACGTGTTGA GACTGGTGTC ATCAAGCCCG      350
GTATGGTCGT GACTTTCGTCT CCCTCCAACG TCACCACTGA AGTCAAGTCC      400
15 GTCGAAATGC ACCACCAACA ACTCCAGGCT GGTACCCTG GCGACAACGT      450
CGGCTTCAAC GTCAAGAACG TTTCAAGTCAA GGAAGTCCGC CGTGGCAACG      500
TTGCTGGCGA CTCCAAAAAT GATCCCCCTA AGGGCTGCGA ATCCTTCAAT      550
GCCCAGGTCA TCGTCCTTAA CCACCCCGGC CAGGTTGGCG CTGGTTATGC      600
CCCAGTCCTC GACTGCCACA CTGCCCACAT TGCTTGCAAG TTCTCTGAGC      650
20 TTATTGAGAA GATCGACCGC CGTACCGGAA AGTCTGTTGA GAACAACCCC      700
AAGTTCATCA AGTCTGGTGA TGCTGCTATC GTCAAGATGG TTCCCTCCAA      750
GCCC
  
```

25 2) INFORMATION FOR SEQ ID NO: 439

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 743 bases
 30 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Issatchenkia orientalis*
 (B) STRAIN: ATCC 6258

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 439

```

TGGGATGAAA ACAGATTTGA AGAAATTGTC AAGGAAACCC AAAACTTCAT      50
CAAGAAGGTT GGTTACAACC CAAAGACTGT TCCATTCTGT CCAATCTCTG      100
GTTGGAATGG TGACAACATG ATTGAAGCAT CCACCAACTG TCCATGGTAC      150
45 AAGGGTTGGA CTAAGGAAAC CAAGGCAGGT GTTGTTAAGG GTAAGACCTT      200
ATTAGAAGCA ATCGATGCTA TTGAACCACC TGTCAGACCA ACCGAAAAGC      250
CATTAAGATT ACCATTACAA GATGTTTACA AGATTGGTGG TATTGGTACT      300
GTGCCAGTCG GTAGAGTCGA AACC GGTTGTC ATTAAGCCAG GTATGGTTGT      350
CACTTTTGCT CCAGCAGGTG TCACCACCGA AGTCAARTCC GTTGAAATGC      400
50 ACCATGAACA ATTAGAACAA GGTGTTCCAG GTGATAACGT TGGTTTCAAC      450
GTTAAGAACG TCTCTGTCAA GGATATCAAG AGAGGTAACG TTTGTGGTGA      500
CTCCAAGAAC GACCCACCAA TGGGTGCAGC TTCYTTCAAT GCTCAAGTCA      550
TTGTCTTGAA CCACCCTGGT CAAATTTCCG CTGGTTACTC TCCAGTCTTG      600
GATTGTCACA CTGCCACAT TGCAATGTAAG TTCGACGAAT TAATCGAAAA      650
55 GATTGACAGA AGAAGTGGTA AGTCTGTTGA AGACCATCCA AAGTCYGTCA      700
AGTCTGGTGA TGCAGCTATC GTCAAGATGG TCCCAACCAA GCC      743
  
```

60 2) INFORMATION FOR SEQ ID NO: 440

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1091 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Malassezia furfur*
 (B) STRAIN: ATCC 42132

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 440

```

15 CAAGCTCAAG GCTGAGCGTG AGCGTGGTAT CACCATCGAC ATTGCTCTGT      50
   GGAAGTTCGA GACCCCTAAG TACCACGTTA CCGTCATTGA CGCTCCTGGT      100
   CACCGTGACT TCATCAAGAA CATGATTACG GGTACCTCGC AGGCTGACTG      150
   CGCTATCCTC ATCATTGCCG GTGGTACCGG TGAGTTCGAG GCTGGTATCT      200
20 CGAAGGACGG TCAGACCCGT GAGCACGCTC TGCTCGCTTT CACCCTGGGT      250
   GTGCGTCAGC TCATTGTGGC CGTCAACAAG ATGGACACCA CCAAGTACTC      300
   GGAGGACCGC TTCAACGAGA TTGTCCGCGA AGTGTGGAAC TTCATCAAGA      350
   AGGTCGGTTT CAACCCCAAG ACTGTTGCCT TCGTCCCAT CTCGGGCTGG      400
   CACGGTGACA ACATGATCGA GGCCACCACC AACATGCCTT GGTACAAGGG      450
25 CTGGGAGAAG GAGACCAAGT CGGGCAAGGT CACTGGTAAG ACTCTGCTGG      500
   ACGCCATCGA CGCCATCGAG CCCCCGACCC GCCCACTGA CAAGCCCCTG      550
   CGTCTCCCTC TGCAGGATGT GTACAAGATC GGTGGTATCG GTACTGTCCC      600
   TGTCGGTCGT GTTGAGACCG GTGTGATCAA GCCCGGTATG GTTGTGACCT      650
   TCGTCCCTC GAACGTCACC ACTGAAGTTA AGTCGGTTGA GATGCACCAC      700
30 GAGTCGCTCC CTGAGGGTCT CCCCAGGTGAC AACGTTGGTT TCAACGTGAA      750
   GAACGTCTCG GTTAAGGACA TTCGCCGTGG TAACGTTGCC TCGGACTCGA      800
   AGAACGACCC CGCTCAGGAG GCTGCTTCGT TCAACGCGCA GGTCAATTGTC      850
   ATGAACCACC CTGGTCAGAT CAGCAACGGT TACTCGCCCG TGCTTGACTG      900
   CCACACTGCG CACATTGCCT GCCGCTTCAA CAACATCCTC CAGAAGATCG      950
35 ACCGTCGCTC GGGTAAGGTG CTTGAGGAGA ACCCAAGTT CATCAAGTCG      1000
   GGTGACGCTG CCATGGTGGA GATGATCCCC ACCAAGCCCA TGTGTGTGGA      1050
   GTCGTTCAAC GAGTACCCCC CTCTGGGTCG TTTCGCTGTG C              1091

```

2) INFORMATION FOR SEQ ID NO: 441

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 749 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Malassezia pachydermatis*
 (B) STRAIN: ATCC 42756

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 441

```

60 ACCACCAAGT ACTCGGAGGA CCGCTTCAAC GAGATTATTC GCGAGACTTC      50
   GAACCTCATC AAGAAGGTCG GTTACAACCC GAAGACTGTT GCCTTCGTCC      100
   CGATCTCGGG CTGGCACGGT GACAACATGA TTGAGGCGAC CACCAACATG      150
   CCGTGGTACA AGGGCTGGGA GAAGGAGACC AAGTCGGGCA AGGCCACTGG      200

```

	TAAGACCCTT	CTGGACGCTA	TTGACGCCAT	TGAGCCGCCG	ACGCGCCCGA	250
	CCGACAAGCC	TCTCCGTCTT	CCTCTCCAGG	ATGTGTACAA	GATCGGTGGT	300
	ATCGGTACYG	TCCCCGGTCGG	CCGTGTTGAG	ACCGGTGTTA	TCAAGCCCGG	350
	TATGGTTGTG	ACCTTCGCTC	CGTCGAACGT	CACSACTGAA	GTTAAGTCGG	400
5	TCGAGATGCA	CCACGAGCAG	ATCCCTGAGG	GTCTTCCGGG	TGACAACGTT	450
	GGTTTCAACG	TGAAGAACGT	GTCCGGTCAAG	GACATTCGCC	GTGGTAACGT	500
	CGCTTCGGAC	TCGAAGAACG	ACCCGGCTCA	GGAGGCTGCC	TCGTTCAATG	550
	CTCAGGTCAT	TGTGATGAAC	CACCCTGGTC	AGATCAGCAA	CGGTTACTCG	600
	CCRGTGCTCG	ACTGCCACAC	TGCTCACATT	GCCTGCCGCT	TCAACAACAT	650
10	CCTCCAGAAG	ATCGACCGTC	GTTCGGGTAA	GGTTCTYGAA	GAGAACCCCA	700
	AGTTCATCAA	GTCGGGTGAC	GCTGCCATGG	TTGAGATGAT	CCCGACCAA	749

15 2) INFORMATION FOR SEQ ID NO: 442

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1150 bases
 (B) TYPE: Nucleic acid
 20 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Malbranchea filamentosa*
 (B) STRAIN: ATCC 48174

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 442

30	ACTGAAGGCC	GAGCGTGAGC	GTGGTATCAC	CATCGATATC	GCCCTCTGGA	50
	AGTTCGAGAC	CCCCAAGTAC	CATGTCACCG	TCATTGGTAC	GTTTCGACATG	100
	TTCGACCTTT	TGCCTAGTGT	CCCCTTCTAA	CCACAGTTTA	TAGACGCCCC	150
	TGGCCATCGT	GATTTTCGTCA	AGAACATGAT	CACTGGTACT	TCCCAGGCTG	200
35	ATTGCGCTAT	CCTCATCATT	GCTTCCGGCA	CTGGTGAATT	CGAGGCTGGT	250
	ATCTCCAAGG	ATGGCCAGAC	CCGTGAGCAC	GCTCTGCTTT	CCTTCACCCT	300
	CGGTGTTAGG	CAGCTCATTG	TCGCCCTCAA	CAAGATGGAC	ACTGTCAACT	350
	TCGCTGAGGC	CCGTTACAAC	GAGATTGTCA	AGGAAGTCTC	CAACTTCATC	400
	AAGAAGGTCG	GCTACAACCC	CAAGGCCGTT	CCTTTCGTCC	CCATCTCCGG	450
40	TTTTCGAGGT	TGACAACATGA	TCGAGGCCTC	CACCCGCATT	CCTTGGTACA	500
	AGGGCTGGAA	CAAGGAGACC	GCCAGTGGCA	AGAGCACCGG	CAAGACCCTY	550
	CTCGAGGCCA	TTGATGCCAT	CGAACCCCCG	GTCCGTCCCA	CCGACAAGCC	600
	CCTYCGTCTC	CCTCTTCAGG	ATGTGTACAA	GATCTCCGGT	ATTGGCACTG	650
	TTCTGTTCGG	TCGTGTTGAG	ACTGGTGTCA	TCAAGCCTGG	TATGGTCGTT	700
45	ACTTTCGCCC	CCGCCAACGT	CACCACTGAA	GTCAAGTCCG	TCGAGATGCA	750
	CCACCAGCAG	CTCCAGGCCG	GTAACCCCGG	TGACAACGTC	GGCTTCAACG	800
	TCAAGAACGT	TTCCGTCAAG	GAAGTCCGCC	GTGGCAACGT	TGCCCTCCGAC	850
	TCCAAGAACG	ACCCCGCCAA	GGGCTGCGAC	TCCTTCAACG	CCCAGGTCAT	900
	CGTCCTTAAC	CACCCCGGTC	AGGTCGGTGC	TGGATACGCT	CCCGTCCTCG	950
50	ATTGCCACAC	TGCCCACATT	GCTTGCAAGT	TCTCTGAGCT	TCTTGAGAAG	1000
	ATCGATCGCC	GTACCGGTAA	ATCCGTTGAG	GACCACCCCA	AGTTCATCAA	1050
	GTCTGGTGAT	GCCGCTATCG	TCAAGATGGT	TCCCTCCAAG	CCTATGTGCG	1100
	TTGAGGCTTT	CACTGACTAC	CCTCCCCTTG	GTCTGTTTCG	CGTCCGTGAC	1150

55

2) INFORMATION FOR SEQ ID NO: 443

(i) SEQUENCE CHARACTERISTICS:

- 60 (A) LENGTH: 1099 bases

(B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5 (ii)MOLECULE TYPE: Genomic DNA

(vi)ORIGINAL SOURCE:

(A) ORGANISM: *Metschnikowia pulcherrima*
 (B) STRAIN: DSM 70336

10

(xi)SEQUENCE DESCRIPTION: SEQ ID NO: 443

	GGACAAGTTG	AAGGCTGAGA	GAGAGAGAGG	TATCACCATC	GACATTGCCT	50
	TGTGGAAGTT	CGAGACTCCT	AAGTACCACG	TCACCGTYAT	TGACGCCCCA	100
15	GGTCACAGAG	ATTTTCATCA	GAACATGATC	ACTGGTACTT	CCCAGGCTGA	150
	CTGTGCTATC	TTGATTATCG	CYGGTGGTGT	TGGTGAGTTC	GAGGCTGGTA	200
	TCTCCAAGGA	TGGCCAGACC	AGAGAGCACG	CTTTGTTGGC	YTACACCTTG	250
	GGTGTTAGAC	ARTTGATTGT	TGCCGTC AAC	AAGATGGACT	CTGTCAAGTG	300
	GGACAAGAAC	AGATTTGAGG	AGATCATCAA	GGAGACCTCT	AACTTCGTCA	350
20	AGAAGGTTGG	TTACAACCTT	AAGACYGTGC	CATTCGTGCC	AATYTCTGGT	400
	TGGAACGGTG	ACAACATGAT	TGAGGCYTCC	ACTAACTGCC	CATGGTACAA	450
	GGGTTGGGAG	AAGGAGACCA	AGGCCGGTAA	GTCTWCCGGT	AAGACCTTGT	500
	TGGAGGCCAT	TGACGCCATT	GAGCCACCAA	CCAGACCTAC	CGACAAGGCC	550
	TTGAGATTGC	CTTTGCAGGA	TGTCTACAAG	ATCGGTGGTA	TCGGAACGGT	600
25	GCCAGTCGGC	CGTGTGAGGA	CCGGTGTGTC	TAAGGCCGGT	ATGGTTGTYA	650
	CCTTYGCCCC	AGCTGGTGTC	ACCACTGAGG	TCAAGTCCGT	CGAGATGCAC	700
	CACGAGCAGT	TGGTCGAGGG	TCTTCCAGGT	GACAAYGTTG	GTTTCAACGT	750
	CAAGAACGTC	TCCGTTAAGG	AGATCAGAAG	AGGTAACGTC	TGTGGTGACT	800
	CCAAGCAGGA	CCCACCAAAG	GGTGCCGCTT	CTTTCACCGC	YCAGGTTATT	850
30	GTGTTGAACC	ACCCTGGTCA	GATCTCCTCT	GGTTACTCTC	CAGTGTGGA	900
	CTGYCACACC	GCCCACATTG	CCTGTAARTT	CGACACCTTG	TTGGAGAAGA	950
	TTGACAGAAG	AACTGGTAAG	TCCTTGGAGT	CYGAGCCTAA	GTTCGTCAAG	1000
	TCYGGTGACG	CCGCCATTGT	CAAGATGGTG	CCAACCAAGC	CAATGTGTGT	1050
35	TGAGGCTTTC	ACCGACTACC	CACCTTTGGG	TAGATTCGCC	GTCAGAGAC	1099

2) INFORMATION FOR SEQ ID NO: 444

40 (i)SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1153 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii)MOLECULE TYPE: Genomic DNA

(vi)ORIGINAL SOURCE:

(A) ORGANISM: *Paecilomyces lilacinus*
 (B) STRAIN: ATCC 42570

50

(xi)SEQUENCE DESCRIPTION: SEQ ID NO: 444

	CAAGCTCAAG	GCCGAGCGTG	AGCGTGGTAT	CACCATCGAC	ATTGCCCTCT	50
55	GGAAGTTCGA	GACTCCCAAG	TACTATGTCA	CCGTCATTGG	TACGTCGACT	100
	CGCGCGAGAC	TGGTCGCAAT	TTCCACGTCG	CTAACGTGCT	TGAACAGACG	150
	CTCCCGGCCA	CCGTGCACTT	ATCAAGAACA	TGATCACTGG	TACCTCCAG	200
	GCTGACTGCG	CTATCCTCAT	TATCGCTGCC	GGCACTGGTG	AGTTCGAGGC	250
	TGGTATCTCC	AAGGATGGCC	AGACCCGTGA	GCACGCTCTG	CTCGCCTACA	300
60	CCCTCGGTGT	TAAGCAGCTC	ATCGTCGCTA	TCAACAAGAT	GGACACCACC	350

```

AAGTGGTCTG AGGCCCCGTTT CCAGGAGATC ATCAAGGAGA CCTCCAACTT 400
CATCAAGAAG GTCGGCTACA ACCCCAAGAC CGTCGCTTTC GTCCCCATCT 450
CTGGTTTCCA CGGCGACAAC ATGCTTTCCC CCTCCACCAA CTGCCCCTGG 500
TACAAGGGCT GGGAGAAGGA GACCAAGGCT GGCAAGTCCA CCGGCAAGAC 550
5 CCTCCTTGAG GCCATCGACT CCATCGAGCC CCCCAGCGC CCCAGCGACA 600
AGCCCCCTCCG CCTTCCCCTT CAGGATGTGT ACAAGATCGG CCGTATCGGC 650
ACAGTCCCTG TCGGCCGTAT CGAGACTGGT GTCATCAAGC CCGGCATGGT 700
CGTGACCTTC GCTCCTTCCA ACGTCACCAC CGAAGTCAAG TCCGTTGAGA 750
TGCACCACGA GCAGCTCTCC GAGGGTGTC CCGGTGACAA CGTCGGCTTC 800
10 AACGTCAAGA ACGTCTCCGT CAAGGAGATC CGTCGTGGCA ACGTCGCCCG 850
TGACTCCAAG AACGACCCCC CTCTGGGTGC CGCTTCTTTC GATGCCCAGG 900
TCATCGTCCT CAACCACCCC GGCCAGGTGC GTGCTGGCTA CGCCCCCGTC 950
CTCGACTGCC ACACCGCCCA CATTGCCGTG AAGTTCGCCG AGATCAAGGA 1000
GAAGATCGAC CGCCGTACCG GCAAGTCTGT CGAGTCCGCC CCAAGTTCA 1050
15 TCAAGTCTGG CGACTCTGCC ATCGTCAAGA TGATTCCCTC CAAGCCCATG 1100
TGC GTTGAGG CTTTCACCGA CTACCCTCCT CTGGGCCGCT TCGCCGTCCG 1150
TGA 1153

```

20

2) INFORMATION FOR SEQ ID NO: 445

(i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 763 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Paracoccidioides brasiliensis*
- (B) STRAIN: ATCC 32071

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 445

```

TACCACTAAG TGGTCCGAGA CCCGATTCAA TGAAATTATC AAGGAAGTCA 50
CCAATTTTCAT TAAGAAGGTC GGATATAACC CCAAGACTGT TCCTTTCGTT 100
CCCATTTCTG GTTTCGAGGG TGACAACATG ATCGAGCCCT CTGCCAACTG 150
40 CCCATGGTAC AAGGGCTGGT CCAAGGAGAC TGCTCAGGGC AAGTACTCTG 200
GCAAGACCCCT TCTTGAGGCC ATCGACGCCA TTGAGCCCCC CACCCGTCTT 250
ACCGATAAAC CTCTCCGTCT TCCCCTCCAG GATGTCTACA AGATCTCCGG 300
TATTGGCACT GTTCCTGTCT GACGTGTTGA GACTGGAGTC ATCAAGCCCCG 350
GTATGGTCGT GACCTTCGCT CCCGCCAACG TCACCACTGA AGTCAAGTCC 400
45 GTCGAAATGC ACCACCAGCA GCTTACCGCC GGTAACCCCG GTGACAACGT 450
CGGCTTCAAC GTCAAGAATG TTTCCGTCAA AGAAGTCCGC CGTGGTAAACG 500
TTGCCGGTGA CTCTAAGAAT GATCCCCCAA AGGGCTGCGA TTCCTTCAAT 550
GCCCAGGTCA TCGTCCTCAA CCACCCTGGT CAGGTGCGC CTGGTTATGC 600
CCCAGTCCTC GACTGCCATA CTGCCCACAT TGCCCTGCAA TTCGCTGAGC 650
50 TCCTTGAGAA GATTGATCGA CGAACCGGAA AGTCTGTTGA GAACAACCCC 700
AAGTTCATCA AGTCCGGTGA TGCTGCTATC GTCAAGATGA TTCCTTCCAA 750
GCCCATGTGC GTC 763

```

55

2) INFORMATION FOR SEQ ID NO: 446

(i) SEQUENCE CHARACTERISTICS:

60

- (A) LENGTH: 1346 bases
- (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Penicillium marneffei*
(B) STRAIN: ATCC 64101

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 446

	AAGCTCAAGG	CTGAGCGTGA	GCGTGGTATC	ACCATCGATA	TTGCTCTCTG	50
	GAAGTTCCAG	ACTGCCAAGT	ACGAGGTTAC	CGTCATTGAC	GCCCCCGGTC	100
	ACCGTGATTT	CATCAAGAAC	ATGATCACTG	GTACCTCCCA	GGCCGATTGC	150
15	GCTATTCTCA	TCATTGCCTC	TGGTACTGGT	GAATTCGAGG	CTGGTATCTC	200
	CAAGGATGGC	CAGACTCGTG	AGCACGCTCT	TTTGGCTTTC	ACCCTCGGTG	250
	TCCGTCAGCT	CATTGTTGCC	CTCAACAAGA	TGGACACTTG	CAAGTGGTCT	300
	CAGGGTGAGT	ACTCGTACCT	GCGTTTGGCC	TTGAATATCT	TACTAATGCA	350
	CCATAGATCG	TTACAACGAA	ATTGTCAAGG	AGACTTCCAA	CTTCATCAAG	400
20	AAGGTCGGAT	ACAACCCCAA	GAACGTTTCCT	TTTCGTTCTA	TCTCCGGTTT	450
	CAACGGTGAC	AACATGCTTG	AGCCCTCCCC	CAACTGCCCC	TGGTACAAGG	500
	GTTGGGAGAA	GGAGACCAAG	GCCGGTAAGG	TCACTGGTAA	GACCCCTCCTC	550
	GAGGCCATCG	ACGCCATTGA	GCCCCCTACC	CGTCCCGCCA	ACAAGGTTAG	600
	TCCCTCCTCG	ACTACTCAAA	CCCTCCTCAT	AAGTTCAGAT	TACTGACTCG	650
25	TTCACAGCCC	CTCCGTCTTC	CCCTCCAGRA	TGTCTACAAG	ATCGGTGGTA	700
	TTGGAACGGT	TCCCGTCGGT	CGTGTGAGA	CTGGTACCAT	CGTTCCTGGT	750
	ATGGTTGTCA	CCTTGTAAGT	CACTCTCCTC	GCTTATCCTA	CCTGAAATCA	800
	TCATGTGCTA	ACTTGACACT	CAGCGCTCCC	GCCAACGTCA	CCACTGAAGT	850
	CAAGAGTGTT	GAAATGCACC	ACCAGCAGCT	CACTGCCGGT	CAGCCCCGGTG	900
30	ACAACGTTGG	TTTCAACGTG	AAGAACGTCT	CCGTCAAGGA	AATCCGTCGT	950
	GGTAACGTTG	CTGGTGACAG	CAAGAACGAC	CCCCCTGCCG	GTGCTGCCTC	1000
	CTTCAACGCC	CAGGTCATCG	TCCTCAACCA	CCCCGGTCAG	GTCCGGTGCTG	1050
	GTTACGCCCC	AGTCCTCGAT	TGCCACACTG	CCCACATTGC	TTGCAAGTTC	1100
	GCTGAGCTCC	TCGAGAAGAT	TGACCGTCGT	ACCGGAAAGT	CTGTTGAGGA	1150
35	CCACCCCAAG	TTCATCAAGT	CCGGTGACGC	TGCCATCGTC	AAGATGATTC	1200
	CTTCCAAGCC	CATGTGTGTT	GAGGCTTTCA	CCGAGTACCC	TCCTCTCGGT	1250
	CGTTTCGCCG	TTTCGCGAGTA	AGTTTATCT	CCGTTGTCTA	TTTTCCATCC	1300
	TTCCCTTCTC	CTCCGTCTTC	CATATATACT	TTTTCAGTTA	TATGTG	1346

40

2) INFORMATION FOR SEQ ID NO: 447

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 1094 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Pichia anomala*
(B) STRAIN: ATCC 18205

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 447

	AAGTTAAAG	CTGAACGTGA	AAGAGGTATC	ACTATTGATA	TTGCTTTATG	50
	GAAATTTCGAA	ACTCCAAAAT	ACCATGTTAC	CGTTATTGAT	GCTCCAGGTC	100
60	ACAGAGATTT	CATCAAAAAT	ATGATTACTG	GTACTTCCCA	AGCTGATTGT	150

	GCTATYTTAA	TTATTGCCGG	TGGTATTGGT	GAATTCGAAG	CTGGTATCTC	200
	AAAAGATGGT	CAAACCAGAG	AACACGCTTT	NTTAGCTTAC	ACCTTAGGTG	250
	TTAAACAATT	GATTGTTGCT	ATCAACAAGA	TGGATTCCGT	TAAATGGGAT	300
	GAATCTCGTT	TCGAAGAAAT	TGTCAAGGAA	ACYTCAAAC	TTATCAAGAA	350
5	AGTTGGTTAC	AACCCAAAAA	CTGTTCCATT	CGTTCCAATC	TCAGGTTGGA	400
	ATGGTGATAA	CATGATTGAA	CCATCAWCTA	ACTGTCCATG	GTACAAAGGT	450
	TGGAAAAAAG	AAACCAAAGC	TGGTGAAGCT	AAAGGTAAAA	CTTTATTAGA	500
	AGCCATTGAT	GCTATTGACC	CACCATCAAG	ACCAACTGAT	AAACCATTAC	550
	GTTTACCATT	ACAAGATGTT	TACAARATTG	GTGGTATTGG	TACTGTGCCA	600
10	GTCGGTAGAG	TTGAAACCGG	TGTTATCAAA	CCAGGTATGG	TTGTTACCTT	650
	TGCCCCAGCT	GGTGTTACCA	CTGAAGTCAA	ATCTGTTGAA	ATGCATCATG	700
	AACAATTGAC	TGAAGGTTTA	CCAGGTGACA	ATGTTGGTTT	CAACGTTAAG	750
	AATGTTTCTG	TTAAAGAAAT	CCGTCGTGGT	AACGTCTGTG	GTGACTCTAA	800
	AAACGATCCA	CCAAAAGCTG	CTGAATCATT	CAATGCTCAA	GTTATTGTCT	850
15	TAAACCATCC	AGGTCAAATC	TCTGCTGGTT	ACTCTCCAGT	TTTAGATTGT	900
	CACACTGCTC	ACATTGCTTG	TAAATTTGAC	ACTTTAATTG	AAAAAATTGA	950
	CAGACGTACT	GGTAAGAAAT	TAGAAGAAGC	TCCAAAATTC	ATCAAATCAG	1000
	GTGATGCTGC	TATTGTTAAA	TTTGTTCAT	CAAAACCATT	ATCAGTTGAA	1050
	GCTTTCAC	ACTACCCACC	ATTAGGTCGT	TTGCTGTCA	GAGA	1094

2) INFORMATION FOR SEQ ID NO: 448

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1100 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pichia anomala*
 (B) STRAIN: ATCC 2149

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 448

	CTTAGATAAG	TTAAAAGCTG	AACGTGAAAG	AGGTATCACT	ATTGATATTG	50
40	CTTTATGGAA	ATTCGAAACT	CAAAAATACC	ATGTTACCGT	TATTGATGCT	100
	CCAGGTCACA	GAGATTTTCA	CAAAAATATG	ATTACTGGTA	CTTCCCAAGC	150
	TGATTGTGCT	ATMTTAATTA	TTGCCGGTGG	TATTGGTGAA	TTCGAAGCTG	200
	GTATCTCAAA	AGATGGTCAA	ACCAGAGAAC	ACGCTTTRTT	AGCTTACACC	250
	TTAGGTGTTA	AACAATTGAT	TGTTGCTATC	AACAAGATGG	ATTCCGTTAA	300
45	ATGGGATGAA	TCTCGTTTCG	AAGAAATTGT	CAAGGAAACY	TCAAACCTTA	350
	TCAAGAAAGT	TGGTACAACC	CAAAAAC	TCCATTTCGT	CCAATCTCAG	400
	GTTGGAATGG	TGATAACATG	ATTGAACCAT	CAACTAACTG	TCCATGGTAC	450
	AAAGGTTGGA	AAAAAGAAAC	CAAAGCTGGT	GAAGCTAAAG	GTAAAACCTT	500
	ATTAGAAGCC	ATTGATGCTA	TTGATCCACC	ATCAAGACCA	ACTGATAAAC	550
50	CATTACGTTT	ACCATTACAA	GATGTTTACA	ARATTGGTGG	TATTGGTACT	600
	GTGCCAGTGC	GTAGAGTTGA	AACCGGTGTT	ATCAAACCAG	GTATGGTTGT	650
	TACCTTTGCC	CCAGCTGGTG	TTACCACTGA	AGTCAAATCT	GTTGAAATGC	700
	ATCATGAACA	ATTGACTGAA	GGTTTACCAG	GTGACAATGT	TGGTTTCAAC	750
	GTTAAGAATG	TTTCTGTTAA	AGAAATCCGT	CGTGGTAACG	TCTGTGGTGA	800
55	CTCTAAAAAC	GATCCACCAA	AAGCTGCTGA	ATCATTCAAT	GCTCAAGTTA	850
	TTGTCTTAAA	CCATCCAGGT	CAAATCTCTG	CTGGTTACTC	TCCAGTTTAA	900
	GATTGTCACA	CTGCTCACAT	TGCTTGTAAG	TTTGACACTT	TAATTGAAAA	950
	AATTGACAGA	CGTACTGGTA	AGAAATTAGA	AGAAGCTCCA	AAATTCATCA	1000
	AATCAGGTGA	TGCTGCTATT	GTTAAATTTG	TTCCATCAAA	ACCATTATCA	1050
60	GTTGAAGCTT	TCACTGACTA	CCCACCATTA	GGTCGTTTCG	CTGTCAGAGA	1100

2) INFORMATION FOR SEQ ID NO: 449

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1201 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudallescheria boydii*
 (B) STRAIN: ATCC 44331

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 449

```

20 CAAGCTCAAG GCCGAGCGTG AGCGTGTTAT CACCATCGAT ATCGCCCTCT      50
   GGAAGTTCGA GACCCCCAAG TACCAGGTCA CCGTCATTGG TATGTCTTTG      100
   TGCTTTTGTG GCTTTTGTGT CCTGTGCTTC GCACAATTCC AGCCCTCGAT      150
   AATTATGAAC CTCGTACTAA TATGTCGTTT TCCCACTACC CACAGACGCC      200
   CCCGGCCATC GTGATTTTCAT CAAGAACATG ATTACTGGTA CCTCCCAGGC      250
25 TGATTGCGCC ATTCTCATCA TTGCCTCCGG TACTGGTGAG TTCGAGGCTG      300
   GCATCTCCAA GGATGGCCAG ACCCGTGAGC ACGCTCTTCT CGCCTTCACC      350
   CTCGGTGTCA AGAACCTCAT TGTTGCCATC AACAGATGG ACACCAACAA      400
   CTGGTCCGAG GACCGATACA AGGAGATCAT CAAGGAGACC TCCAACCTCA      450
   TCAAGAAGGT CGGCTACAAC CCCAAGGCCG TTCCTTTCGT CCCCATCTCC      500
30 GGTTTCCACG GAGACAACAT GCTTACCCCC TCCACCAACT GCCCCTGGTA      550
   CAAGGGTTGG GTCCGTGAGG TCAAGGGTAA CACCCTTACC GGCAAGACCC      600
   TTCTCGAGGC CATCGACTYC ATCGAGCCCC CCAAGCGTCC CACCGAGAAG      650
   CCCCTCCGTC TTCCCCTTCA GGACGTCTAC AAGATCGGTG GTATTGGCAC      700
   TGTGCCCGTC GGCCGTATCG AGACCGGTAT CCTCAAGCCC GGTATGGTCG      750
35 TCACCTTCGC TCCCTCCAAC GTCACCACTG AAGTCAAGTC CGTCGAGATG      800
   CACCACGAGC AGCTTACCGA GGGTGTCCCC GGTGACAACG TTGGTTTCAA      850
   CGTGAAGAAC GTCTCCGTCA AGGATATCCG CCGTGGCAAC GTCTGCGGTG      900
   ACTCCAAGAA CGACCCCCCC GCTGCTGCCG CCTCTTTCCA GGCCCAGGTC      950
   ATTGTCCTCA ACCACCCCGG CCAGATCGGT GCTGGTTACG CTCCCCTTCT      1000
40 TGACTGCCAC ACTGCCCCA CA TTGCTTGCAA GTTCGCCGAG CTCCTTGAGA      1050
   AGATCGACCG CCGTACCGGT AAGTCGGTCG AGAACAACCC CAAGTTCGTC      1100
   AAGTCTGGTG ATGCCGCCAT CGTCAAGATG GTTCCCTCCA AGCCCATGTG      1150
   TGTGAGTCC TTCACCGAGT ACCCCCCTCT CGGTCGTTT CCGTCCGTG      1200
A

```

2) INFORMATION FOR SEQ ID NO: 450

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1095 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Rhizopus oryzae*
 (B) STRAIN: ATCC 56015

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 450

	CAAGCTTAAG	GCTGAACGTG	AACGTGGTAT	CACCATCGAT	ATTGCTCTCT	50
5	GGAAGTTCGA	AACCCCCAAG	TACCAAATTA	CCGTTATTGA	TGCTCCCGGT	100
	CACCGTGATT	TCATCAAGAA	CATGATTACC	GGTACTTCTC	AAGCCGATTG	150
	TGCTATTCTT	ATCATTGCTG	GTGGTACTGG	TGAATTCGAA	GCTGGTATCT	200
	CCAAGGATGG	TCAAACCCGT	GAACACGCC	TTTTGGCTTT	CACTCTCGGT	250
	GTCCGTCAAT	TGATTGTTGC	TGTCAACAAG	ATGGATACCA	CCAAGTGGTC	300
10	CGAAGCTCGT	TTCAACGAAA	TYGTCAAGGA	AGTTTCTTCC	TTCATCAAGA	350
	AGATTGGTTA	CAACCCCAAG	TCTGTTCCCT	TCGTCCCCAT	CTCTGGTTGG	400
	CACGGTGACA	ACATGTTGGA	AGAATCTACC	AACATGCCCT	GGTACAAGGG	450
	ATGGAACAAG	GAAACCAAGG	CTGGTGCCAA	GTCTGGTAAG	ACCCTCTTGG	500
	ATGCCATTGA	CAACATTGAC	CCTCCTACCC	GTCCTGTTGA	CAAGCCTCTC	550
15	CGTCTTCCTC	TTCAAGATGT	TTACAAGATT	GGTGGTATCG	GTACTGTCCC	600
	CGTCGGTTCG	GTCGAAACTG	GTGTCATCAA	GGCTGGTATG	GTTGTCACCT	650
	TCGCTCCTGC	TGCTGTCACC	ACTGAAGTTA	AGTCCGTCGA	AATGCACCAC	700
	GAAACCCCTCA	CTGAAGGTCT	CCCCGGTGAC	AACGTCGGTT	TCAACGTCAA	750
	GAACGTCTCC	GTCAAGGATA	TCCGTCGTGG	TAACGCTCTGT	TCTGACTCCA	800
20	AGAACGACCC	CGCCAAGGAA	GCCGGTTCCT	TCACCGCTCA	AGTCATTATC	850
	TTGAACCACC	CTGGTCAAAT	TGGTGCTGGT	TACGCTCCYG	TTTTGGATTG	900
	TCACACTGCT	CACATTGCCT	GTAAGTTCGC	TGAATTGATC	GAAAAGATTG	950
	ACAGACGTT	CGGTAAGTCC	TTGGAAGCTA	CTCCCAAGTT	CGTCAAGTCT	1000
	GGTGACTCTG	CCATCGTCAA	GATGATCCCC	TCCAAGCCCA	TGTGTGTTGA	1050
25	AGCTTACACT	GACTACCCTC	CTCTCGGTCTG	TTTCGCTGTT	CGTGA	1095

2) INFORMATION FOR SEQ ID NO: 451

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1092 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Rhodotorula minuta*
 (B) STRAIN: ATCC 10658

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 451

45	GCTGAAGGCC	GAGCGAGAGC	GTGGTATCAC	CATCGATATC	GCTCTATGGA	50
	AGTTCGAGAC	CCCCAAGTAC	AACGTCACCG	TCATTGACGC	TCCAGGACAT	100
	CGTGATTTC	TCAAGAGTGA	GTAAACCATA	ACATCAAACA	GTGTTGCAAA	150
	CATCAGCTAA	TGCATGTTAT	GCGTCCAGAC	ATGATTACTG	GTAATTCCCA	200
	GGCCGATTGC	GCTATTCTCA	TCATCGCCAC	CGGTGTTGGT	GAGTTCGAGG	250
50	CTGGTATCTC	CAAGGATGGC	CAGACCCGAG	AGCACGCCCT	TCTCGCCTTC	300
	ACCCTCGGTG	TCAGACAGCT	CATCGTTGCC	TTGAACAAGA	TGGACTCGGT	350
	CAAGGTAGGC	TAACCTCACA	ACGTCGGCTT	CCCATCATTC	ATTCACCTAC	400
	CTGTCTTGTC	TTCCACCCTC	CAGTTCTCCG	AGTCCCGATA	CGATGAAATC	450
	GTCAAGGAGA	CATCCGGTTT	CATCAAGAAG	GTCGGATTCT	ACCCCAAGGG	500
55	TGTTCCCTTC	GTCCCCATCT	CAGGATGGCA	CGGAGACAAC	ATGATCGAGG	550
	AGTCCACCAA	CATGCCTTGG	TACAAGGGAT	GGAAGAAGAC	CACCAAGACC	600
	GGCGAGTACA	AGGGAAAGAC	CCTGCTCGAG	GCCATCGACT	CCATCGAGCC	650
	CCCCACCCGT	CCTACCGACA	AGCCTCTCCG	ACTTCCCCTC	CAGGATGTCT	700
	ACAAGATTGG	TGGTATCGGA	ACAGTGCCAG	TCGGACGAGT	CGAGACTGGT	750
60	ACCATCAAGG	CTGGTATGGT	CGTCACCTTC	GCTCCTTCAG	CTGTCACCAC	800

	CGAAGTCAAG	TCTGTTGAGA	TGCACCACGA	GCAGCTCGAG	GCTGGTCTTC	850
	CAGGTGACAA	CGTCGGATTC	AACATCAAGA	ACGTTTCAGT	CAAGGATATC	900
	CGAAGAGGAA	ACGTCTGCGG	TGACTCCAAG	AACGATCCCC	CCAAGGAGGC	950
	TGCTTCCTTC	ACCGCCCAGG	TCATTGTCCT	CAACCACCCC	GGTCAAATCG	1000
5	GTAACGGATA	CTCTCCAGTT	CTCGATTGCC	ACACTGGTGA	GTCATTCTTC	1050
	CATATTAGTT	TGAACTCTTT	TGAACAATAC	TAACGTGAAT	CATTATACTT	1100
	TTCAGCCCAC	ATTGCATGCA	AGTTCGACAC	CCTCCTAGAG	AAGATTGACC	1150
	GACGATCCGG	AAAGTCCATC	GAAGATACCC	CCAAGTTCGT	CAAGTCTGGT	1200
	GACGCCGCCA	TCGTCAAGAT	GGTCCCCACC	AAGCCAATGT	GCGTTGAGGC	1250
10	TTTCACCGAC	TACCCACCTC	TTGGACGATT	CGCCGTCCGT	GA	1292

2) INFORMATION FOR SEQ ID NO: 452

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1289 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Sporobolomyces salmonicolor*
 (B) STRAIN: ATCC 32311

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 452

30	AAGCTCAAGG	CCGAGCGTGA	GCGTGGTATC	ACCATCGATA	TCGCTCTCTG	50
	GAAGTTCGAG	ACCCCAAGG	TGCGTTCTCA	CCCCGGCTGA	GGAGCACGCA	100
	CGCGAGGGCT	CACGCTGCGC	CTCTTACAGT	ACATGATCAC	CGTCATCGAC	150
	GCCCCGGGTC	ACCGTGACTT	CATCAAGAAC	ATGATCACCG	GTACCTCGCA	200
	GGCCGACTGC	GCCATCCTCA	TCATCGCCCG	CGGTACCGGT	GAGTTCGAGG	250
35	CTGGTATCTC	GAAGGACGGC	CAGACCCGCG	AGCACGCCCT	CCTCGCCTTC	300
	ACCTTCGGTG	TCCGTCAGCT	CATCGTCGCC	ATCAACAAGA	TGGACACGAC	350
	CAAGTACTCG	GAGGCCCCGT	TCGAGGAGAT	CATCAAGGAG	ACCTCCAAC	400
	TCATCAAGAA	GGTCGGCTTC	AACCCCAAGA	ACGTCCCCTT	CGTCCCCATC	450
	TCGGGATGGC	ACGGTGACAA	CATGATTGAG	GAGACCGCCA	ACATGCCCTG	500
40	GTACAAGGGA	TGGAAGAAGG	AGACCAAGGC	CGGTGAGGTC	AAGGGCAAGA	550
	CCCTCCTCGA	CGCCATCGAC	GCGATCGAGC	CCCCTTCGCG	CCCTACCGAC	600
	AAGCCCCTCC	GTCTTCCCCT	CCAGGTTTCGT	TTCCTTGCTC	GCGGTTTACG	650
	CTGCTACTTC	GAGCTGACCC	GCGAGCTCTG	CCCGAACAGG	ATGTCTACAA	700
	GATCGGTGGT	ATCGGCACAG	TCCCCGTCGG	CCGTGTCGAG	ACCGGCACGA	750
45	TCAAGGCCGG	TATGGTCGTC	GTCTTCGCCC	CGGCCAACGT	CACCACTGAG	800
	GTCAAGTCGG	TCGAGATGCA	CCACGAGCAG	CTCGAGGCTG	GTCTCCCGGG	850
	AGACAACGTC	GGCTTCAAGT	GCGTCTCATC	ATGTTTTTGC	TTCGCTCGGC	900
	CATTTTTTCA	GTCTTGACCC	CGTTTTTGCC	CTCGACAGCG	TCAAGAACGT	950
	TTCCGTTAAG	GACATCCGTC	GCGGTAACGT	CTGCGGTGAC	TCGAAGAACG	1000
50	ACCCCCCAAA	GGAGGCCGCT	TCCCTTCAAG	CCCAGGTCAT	CGTCATGAAC	1050
	CACCCCGGTC	AGATCGGCAA	CGGTTACGCT	CCCGTTCTCG	ACTGCCACAC	1100
	CGCCACATT	GCCTGCAAGT	TCGACACCCT	CCTCGAGAAG	ATCGACCGTC	1150
	GCTCGGGCAA	GTGATTGAG	GACCTCCCCA	AGTTCGTCAA	GTCGGGTGAC	1200
	GCCGCCATCG	TCAAGATGGT	TCCCTCCAAG	CCGATGTGTG	TCGAGTCGTT	1250
55	CGCCGAGTAC	CCCCCTCTCG	GACGTTTCGC	CGTCCGTGA		1289

2) INFORMATION FOR SEQ ID NO: 453

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1070 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Sporothrix schenckii*
 (B) STRAIN: WSA-148

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 453

```

15 GTGAGCGCGG TATCACCATC GATATTGCTC TGTGGAAGTT CGAGACCCCC 50
   AAGTACTACG TCACCGTCAT TGACGCCCCC GGTCATCGCG ATTCATCAA 100
   GAACATGATC ACTGGTACCT CGCAGGCCGA CTGCGCCATT CTCATCATTG 150
   CCGCTGGTAC TGGTGAGTTC GAGGCTGGTA TCTCCAAGGA TGGCCAGACT 200
   CGTGAGCACG CTCTGCTCGC CTACACCCTG GGTGTGCGGC AGCTGATCGT 250
20 CGCCATCAAC AAGATGGACA CGGCCAAGTG GGCTGAGGCT CGTTACCAGG 300
   AGATCATCAA GGAGACCTCC AACTTCATCA AGAAGGTCGG CTACAACCCC 350
   AAGACTGTTG CCTTCGTCCC CATCTCGGGC TTCCACGGCG ACAACATGCT 400
   TACTCCCTCG ACCAACTGCC CTTGGTACAA GGGCTGGGAG AAGGAGGGCA 450
   AGAGCGGCAA GGTACCGGT AAGACTCTGC TGGACGCCAT TGACGCCGTC 500
25 GAGCCCCCA AGCGCCCCAC GGACAAGCCC CTGCGTCTGC CCCTCCAGGA 550
   TGTCTACAAG ATCGGCGGTA TCGGCACTGT CCCTGTCGGC CGTATCGAGA 600
   CTGGTGTCTT GAAGCCCGGC ATGGTCTGTA CCTTTGCCCC GTCCAACGTC 650
   ACCACTGAAG TCAAGTCCGT CGAGATGCAC CACGAGCAGC TTGTTGAGGG 700
   TGTTCCCGGC GACAACGTCG GCTTCAACGT CAAGAACGTC TCCGTCAAGG 750
30 AGATCCGTCG TGGCAACGTT GCCGGTGACT CCAAGAACGA CCCCCCTCG 800
   GGCGCGGCCA CCTTCAACGC CCAGGTCATT GTCCTGAACC ACCCCGCCCA 850
   GGTGCGCAAC GGCTACGCCC CGGTTCTGGA CTGCCACACC GCCCACATTG 900
   CCTGCAAGTT CACCGAGATC CTTGAGAAGA TCGACCGCCG TACCGGCAAG 950
   TCGGTTGAGA ACAACCCCAA GTTCATCAAG TCGGGTGACG CCGCCATTGT 1000
35 CAAGCTGACG CCCTCGAAGC CCATGTGCGT TGAGGCCTTC ACTGACTACC 1050
   CCCCTCTGGG CCGTTTCGCC 1070

```

2) INFORMATION FOR SEQ ID NO: 454

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1092 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Stephanoascus ciferrii*
 (B) STRAIN: ATCC 52550

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 454

```

55 CTTAAGTCTG AGCGTGAGAG AGGTATCACC ATCGATATTG CTCTCTGGAA 50
   ATTCGAGACT CCTAAGTACA ACGTTACCGT CATTGATGCT CCAGGTCACA 100
   GAGATTTCAT CAAGAACATG ATTACTGGTA CCTCCCAGGC CGATCTTGCC 150
   ATCCTTATCA TTGCTGGTGG TGTCGGTGAG TTCGAGGCTG GTATCTCCAA 200
60 GGACGGTCAG ACCAGAGAGC ACGCTCTTCT TTCTTTCACC CTTGGTGTCA 250

```

	GAAACATGAT	TGTTGCTGTC	AACAAGATGG	ACTCCGTCAA	GTGGTCTGAG	300
	GATCGTTTCA	ACGAAATTGT	CAAGGAGACC	TCCAACCTCG	TCAAGAAGGT	350
	TGGTTACAAC	CCTAAGAATA	TTGCTTTTCGT	TCCTATCTCC	GGTTGGAACG	400
	GTGACAATAT	GATTGAGCCA	TCCACCAACT	GCCCATGGTA	CAAGGGTTGG	450
5	GAGCGTGAGA	CCAAGAACGG	TACTGCCAAG	GGTAAGACCA	TCTTGAGGGC	500
	CATTGACTCT	ATGGAGCCAC	CTTCCAGACC	AGTTGACAAG	CCTCTCCGTC	550
	TTCTCTTTCA	GGACGTTTAC	AAGATTGGTG	GTATTGGTAC	GGTGCCAGTT	600
	GGTCGTGTTG	AGACTGGTGT	TATCAAGCCA	GGTATGGTTG	TTACCTTTGC	650
	CCCAGCTGGT	GTCACCACTG	AAGTCAAGTC	TGTCGAGATG	CACCACGAAC	700
10	AGATCCCAGA	AGGTACCCCA	GGTGACAACG	TTGGTTTCAA	CGTCAAGAAC	750
	GTCTCCGTCA	AGGAAATCAG	ACGTGGTAAC	GTTACTGGTG	ACTCCAAGAA	800
	CGACCCACCA	AAGGGCTGCG	ACTCTTTCAA	CGCTCAGGTC	ATCATCTTCA	850
	ACCACCCTGG	TCAGATCTCT	GCTGGTTACG	CTCCAGTTTT	GGACTGCCAC	900
	ACTGCTGCA	TTGCTTGCAA	GTTTGAGGAG	CTCATTGAGA	AGATTGACAG	950
15	ACGTTCCGGT	AAGAAGGTCG	AAGACTCTCC	TAAGTTCGTC	AAGGCCGGTG	1000
	ATGCCGCCAT	TGTCAAGATG	GTTCCATCCA	AGCCAATGTG	TGTTGAAACC	1050
	TTCACTGAGT	ACCCACCTCT	TGGTCGTTTC	GCCGTCCGTG	AC	1092

20

2) INFORMATION FOR SEQ ID NO: 455

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1149 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trichophyton mentagrophytes*
 (B) STRAIN: WSA-225

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 455

	GCCGAGCGTG	AGCGTGGTAT	CACCATCGAT	ATCGCCCTCT	GGAAGTTCGA	50
	GACCCCCAAG	TACAATGTCA	CCGTCATTGG	TATGTTTCT	CTTTACCTTT	100
	CCCCCTCCATC	GTCTTGCTGT	GCCATAACTA	ACGAGAGTAG	ACGCCCCCGG	150
40	TCACCGTGAC	TTCATCAAGA	ACATGATCAC	TGGTACCTCC	CAGGCCGACT	200
	GTGCTATTCT	CATCATTTGCT	GCCGGTACTG	GTGAGTTCGA	GGCTGGTATC	250
	TCCAAGGATG	GCCAGACCCG	TGAGCACGCT	CTGCTCGCCT	TCACCCCTGG	300
	TGTCAAGCAG	CTCATCGTTG	CCATCAACAA	GATGGACACC	ACCAACTGGT	350
	CCGAGGACCG	TTTCAAGGAA	ATCATCAAGG	AAGTCACCAA	CTTCATCAAG	400
45	AAGGTTGGCT	ACGACCCCAA	GGGTGTTCCA	TTCGTTCCAA	TCTCTGGTTT	450
	CAACGGTGAC	AACATGATTG	AGGCCCTCCAC	CAACTGCCCA	TGGTACAAGG	500
	GATGGAACAA	GGAGACTAAG	GCCGGTGGTG	CCAAGACTGG	CAAGACCCTC	550
	CTCGAGGCCA	TCGATGCCAT	CGACATGCCA	ACCCGTCCTA	CCGACAAGCC	600
	CCTCCGTCTC	CCACTCCAGG	ATGTCACAAA	GATCTCTGGT	ATCGGAAGTG	650
50	TACCAGTCGG	TCGTGTTGAG	ACCGGTATCA	TCAAGCCCGG	TATGGTCGTC	700
	ACCTTCGCCC	CTGCCAACGT	CACCACTGAA	GTCAAGTCCG	TCGAAATGCA	750
	CCACCAGCAG	CTTCAGCAGG	GTGTCCCCGG	TGACAACGTC	GGCTTCAACG	800
	TCAAGAACGT	TTCCGTCAAG	GAAGTCCGCC	GTGGTAACGT	TGCCGGTGAC	850
	TCCAAGAACG	ACCCACCATC	CGGCTGTGCC	TCCTTCAACG	CCCAGGTCAT	900
55	CGTCCTCAAC	CACCCCGGCC	AGATCGGTGC	TGGTTACGCC	CCAGTCCTCG	950
	ACTGCCACAC	TGCTCACATT	GCTTGCAAGT	TCGCTGAGCT	CCTCGAGAAG	1000
	ATTGACCGCC	GTACCGGTAA	ATCCGTCGAA	GCCAACCCCA	AGTTCGTCAA	1050
	GTCTGGTGAT	GCCGCTATCG	CCAAGATGGT	TCCCTCCAAG	CCTATGTGCG	1100
60	TTGAGGCTTT	CACTGACTAC	CCCCCACTTG	GTCGTTTCGC	CGTCCGTGA	1149

2) INFORMATION FOR SEQ ID NO: 456

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1101 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trichosporon cutaneum*
 (B) STRAIN: ATCC 62965

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 456

20 TCTTGACAAG CTTAAAGCTG AACGTGAACG TGGTATCACC ATTGATATCG 50
 CTCTCTGGAA GTTCGAAACT CCTAAGTACT ACGTTACTGT TATTGATGCT 100
 CCAGGTCACC GTGATTTTCAT CAAGAACATG ATTACTGGTA CTTCCCAAGC 150
 CGACTGCGCC ATTCTTATCA TTGCTGCCGG TGTCGGTGAA TTCGAAGCTG 200
 GTATCTCCAA GGAAGGTCAA ACCAGAGAAC ACGCTCTTCT CGCTTTCACC 250
 CTTGGTGTCA GACAACTTAT CATTGCCATC AACAAAGATGG ACTCTGTCAA 300
 25 GTGGGACCAA AAGAGATACG AAGAAATCGT CAAGGAGGCT TCCAACTTCG 350
 TCAAGAAGGT TGGTTACAAC CCCAAGTCTG TTCCATTCGT TCCTATCTCT 400
 GGTGGAACG GTGACAACAT GTTGGAACCT ACCACCAACG CCCCATGGTA 450
 CAAGGGATGG ACCAAGGAAA CCAAGGCTGG TGCCACTAAG GGTATGACTC 500
 TTATTGAAGC CATTGACGCC ATTGAACCAC CAGTAAGACC ATCCGACAAG 550
 30 CCACTCCGTC TCCCCTCCA AGATGTTTAC AAGATTGGTG GTATCGGAAC 600
 TGTGCCAGTC GGCCGTGTCG AAACCGGTAT CATCAAGGCC GGTATGGTCG 650
 TCACCTTTGC TCCACCAATG GTCACAACCTG AAGTTAAGTC CGTTGAAATG 700
 CACCACGAAC AACTTGCTCA AGGTAACCCA GGTGACAACG TTGGTTTCAA 750
 CGTCAAGAAC GTTTCCGTTA AGGAAATCAG ACGTGGTAAC GTCTGTGGTG 800
 35 ACTCCAAGAA CGATCCACCA AAGGGCTGCG AATCTTTCAA CGCTCAAGTT 850
 ATCGTCTTGA ACCACCCTGG TCAAACTCTCT GCTGGTTACT CTCCAGTTCT 900
 CGATTGCCAC ACTGCCCACA TTGCCTGCAG ATTCGACGAA CTCCTTGAAA 950
 AGATCGACCG TCGTTCCGGT AAGAAGATTG AAGACTCTCC AAAGTTTGTC 1000
 AAGTCTGGTG ATGCCGCTAT CGTCAAGATG ATCCCAACCA AGCCAATGTG 1050
 40 CGTTGAAACC TTCCTGAAT ACCCACCCT TGGTCGTTTC GCCGTCCGTG 1100
 A 1101

45 2) INFORMATION FOR SEQ ID NO: 457

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1085 bases
 (B) TYPE: Nucleic acid
 50 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Wangiella dermatitidis*
 (B) STRAIN: WSA-229

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 457

60

```

5   GTTGAAGGCC GAGCGTGAGC GTGGTATCAC CATCGATATC GCCCTCTGGA      50
    AGTTCGAGAC CCCCAAGTAC TATGTCACCG TCATCGACGC CCCGGGTCAT      100
    CGTGACTTTA TCAAGAACAT GATCACTGGT ACCTCGCAGG CCGACTGCGC      150
    CATCTTGATC ATTGCCGCCG GTACCGGTGA ATTCGAAGCC GGTATCTCCA      200
    AGGATGGTCA GACCCGTGAG CACGCTCTGC TCGCCTACAC CTTGGGTGTC      250
    AAGCAGCTCA TCGTCGCCAT CAACAAGATG GACACCACCA AGTGGTCCGA      300
    GGAGCGTTTC AACGAAATCA TCAAGGAGAC TTCCAAC TTC      350
    TCGGCTACAA CCCCAAGGCC GTTCCTTTTCG TCCCCATCTC CGGCTTCAAC      400
    GGTGACAACA TGATTGAGGT CTCCACCAAC TGCCCGTGGT ACAAGGGATG      450
10  GGAGAAGGAG TCCAAGGCTG GCAAGGCCAC CGGCAAGACC CTCCTCGAGG      500
    CCATTGACGC CATCGACCCA CCCACCCGTC CCACCGACAA GCCTCTCCGT      550
    CTCCCTCTCC AGGATGTCTA CAAGATCTCT GGTATCGGAA CGGTTCCTGT      600
    CGGTCGTGTC GAGACCGGTA CCATCAAGGC CGGTATGGTC GTCACCTTCG      650
    CTCCGGCCAA CGTCACCACT GAAGTCAAGT CCGTCGAAAT GCACCACGAG      700
15  CAGCTCGCCG AGGGTCTGCC AGGTGACAAC GTTGGCTTCA ACGTCAAGAA      750
    CGTCTCCGTC AAGGAGGTTT GTCGTGGTAA CGTTGCCGGT GACTCCAAGA      800
    ACGACCCGTC CAAGGCTTCA GAGTCCCTTA ACGCCAGGT CATTGTCCCTC      850
    AACCACCTTG GTCAGATCGG TGCCGGCTAC GCTCCAGTCT TGGATTGCCA      900
    CACTGCCCAC ATTGCTTGCA AGTTCGCCGA GTTGCTCGAG AAGATCGACC      950
20  GTCGTACCGG AAAGTCCATC GAGAACAACC CCAAGTTCAT CAAGTCTGGT      1000
    GATGCTGCCA TCGTCAAGAT GATTCCCAGC AAGCCCATGT GTGTCGAGGC      1050
    TTTCACCGAC TATCCTCCTC TGGGTCGTTT CGCTG      1085

```

25

2) INFORMATION FOR SEQ ID NO: 458

(i) SEQUENCE CHARACTERISTICS:

```

30  (A) LENGTH: 492 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

35

(vi) ORIGINAL SOURCE:

```

    (A) ORGANISM: Aspergillus fumigatus
    (B) STRAIN: DAL-95

```

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 458

```

    TGTCTTCATC CGGAATTGAT TGTGAGTCGT TCCACATGCT CACCTAGTTT      50
    TCGCTCGATC TTTTCACTAA CGCAAACCAT GTAGAACAAC ATTGCCAAGG      100
    CCCACGGTGG TTACTCCGTC TTCCTGGTGG TTGGTGAGCG TACTCGTGAG      150
45  GGTAACGATC TGTACCACGA AATGCAGGAG ACTGGTGTCA TTCAGCTCGA      200
    GGGTGAATCC AAGGTCGCAC TGGTGTTCGG ACAGATGAAC GAGCCCCCGG      250
    GTGCCCCTGC CCGTGTGCGC CTTACCGGTC TGACCATTGC CGAGTACTTC      300
    CGTGACGAGG AGGGTCAGGA CGTGCTGCTC TTCATTGACA ACATTTTCCG      350
    TTTCACCCAG GCCGGTTCCTG AGGTGTCTGC CTTTCTCGGT CGTATCCCCT      400
50  CTGCCGTCGG TTACCAGCCC ACCCTGGCCG TCGACATGGG TGGTATGCAG      450
    GAGCGTATCA CCACCACCAA GAAGGGTTCT ATTACCTCCG TC      492

```

55 2) INFORMATION FOR SEQ ID NO: 459

(i) SEQUENCE CHARACTERISTICS:

```

60  (A) LENGTH: 1154 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double

```

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Blastoschizomyces capitatus*

(B) STRAIN: ATCC 10663

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 459

```

10 GTCCGTGGTTC AAGAAGTTAT TGACACTGGT GCCCAATTA CCATTCCTGT 50
   TGGTCGTGGT ACTCTTGGTA GAATTATCAA CGTCATTGGT GAACCAATTG 100
   ACGAACGTGG TCCTATCAAG GCTTCTAAGT ATGCTCCTAT CCATACTGAA 150
   CCACCAACCT TTGCTGAACA ATCTACTTCT GCTGAAGTTC TTGAAACTGG 200
15 TATCAAGGTT GTCGATCTTC TTGCTCCTTA CGCCCGTGGT GGTAAGATTG 250
   GTCTTTTCGG TGGTGCTGGT GTCGGTAAGA CTGTCTTCAT TCAAGAACTT 300
   ATTAACAACA TTGCCAAGGC TCACGGTGGT TTCTCTGTCT TCACTGGTGT 350
   CGGTGAAAGA ACCCGTGAAG GTAACGATCT TTACCGTGAA ATGAAGGAAA 400
   CTGGTGTCAT CAACCTCGAA GGTGACTCCA AGGTCGCTCT CGTTTTTCGGT 450
20 CAAATGAACG AACCTCCAGG TGCCCGTGCC CGTGTGCTT TGAAGTGGTCT 500
   TACCATTGCC GAATACTTCC GTGATGAAGA AGGACAAGAT GTCTTGCTTT 550
   TCGTTGACAA CATTTTCAGA TTCACCCAAG CCGGTTCTGA AGTCTCTGCT 600
   CTTTTGGGTC GTATTCCATC TGCCGTCGGT TACCAACCTA CCCTTGCTAC 650
   CGATATGGGT GCCCTCCAAG AACGTATTAC CACCACCAA AAGGGTTCCG 700
25 TCACATCTGT CCAAGCCGTC TATGTCCCAG CAGACGATTT GACTGATCCT 750
   GCCCCAGCCA CCACTTTCGC TCACTTGGAC GCCACCACTG TCTTGTCTCG 800
   TTCCATTTCC GAATTGGGTA TCTACCCAGC TGTCGATCCT CTCGATTCGA 850
   AGTCTCGTCT TTTGGATCCT GAAGTTATTG GACACGAACA CTACGAAGTT 900
   GCCACTCAAG TTCAACAAAC CCTCCAAGCT TACAAGTCTC TCCAAGATAT 950
30 CATTGCCATT TTGGGTATGG ATGAATTGTC TGAAGCTGAT AAGCTTACTG 1000
   TCGAACGTGC CCGTAAGATC CAAAGATTCC TTTCCCAACC ATTTCGTGTT 1050
   GCCGAAGTTT TCACTGGTAT CGAAGGTCGT CTCGTTCCAT TGAAGGAAAC 1100
   CGTCAGATCT TTCAAGGAAA TCCTTGAAGG TAAGTACGAT CACCTTCCAG 1150
   AAGC 1154
35

```

2) INFORMATION FOR SEQ ID NO: 460

40 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1295 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida albicans*

50 (B) STRAIN: ATCC 18804

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 460

```

55 CCAATTTCGAC GAAGGAAACT TGCCAGCTAT TTTGAATGCT TTGACTTTGA 50
   AGAACGGTGA CCAAGACTTG GTCTTGGAAG TTGCTCAACA TTTGGGTGAA 100
   AACACCGTCA GAGCTATTGC TATGGATGGT ACTGAAGGTT TAGTCAGAGG 150
   TACCGAAGTC AACGATACCG GTGCCCCAAT TTCCGTCCCA GTCGGTAGAG 200
   GTACTTTAGG TAGAATCATC AATGTTGTTG GTGAACCAAT TGATGACAGA 250
   GGTCCAATTG AATGTAAGGA AAAGAAACCA ATTCACGCTG AACCACCATC 300
60 ATTTCGTTGAA CAATCCACTG CTGCCGARAT TTTGGAAACC GGTATCAAGG 350

```

	TTGTCGACTT	GTTGGCCCCA	TACGCCAGAG	GTGGTAARAT	TGGTTTATTC	400
	GGTGGTGCTG	GTGTCGGTAA	GACCGTCTTT	ATCCAAGAAT	TGATTAACAA	450
	CATTGCCAAA	GCCCATGGTG	GTTTCTCTGT	CTTTACCGGT	GTYGGTGAAA	500
	GAACCAGAGA	AGGTAACGAT	TTGTACCGTG	AAATGAAAGA	AACCGGTGTC	550
5	ATCAACTTGG	AAGGTGACTC	CAAGGTCGCT	TTGGTCTTCG	GTCAAATGAA	600
	CGAACCACCA	GGTGCTAGAG	CTAGAGTTGC	TTTGACTGGT	TTGACCATTG	650
	CTGAATACTT	CAGAGATGAA	GAAGGTCAAG	ATGTCTTGTT	GTTCAATTGAT	700
	AACATTTTCA	GATTCACCCA	AGCTGGTTCC	GAAGTGTCTG	CTTTGTTAGG	750
	TCGTATTCCA	TCTGCTGTCG	GTTATCAACC	AACCTTAGCC	ACTGATATGG	800
10	GTCTTTTGCA	AGAACGTATT	ACCACCACCA	AGAAAGGTTT	CGTCACCTCT	850
	GTCCAAGCTG	TCTATGTCCC	AGCTGATGAT	TTGACCGATC	CTGCTCCAGC	900
	CACTACATTC	GCCCATTGTT	ATGCCACTAC	TGTCTTGCTT	AGAGGTATTT	950
	CTGAATTGGG	TATCTACCCA	GCTGTCGATC	CATTGGATTC	CAAATCCAGA	1000
	TTATTGGACG	CTTCTGTTGT	TGGTCAAGAA	CATTACGATG	TCGCTACTGG	1050
15	TGTTCAACAA	ACTTTACAAG	CTTACAAATC	CTTACAAGAT	ATCATTGCTA	1100
	TTTTGGGTAT	GGATGAATTG	TCTGAAGCTG	ATAAATTGAC	TGTCGAAAGA	1150
	GCCCGTAAGA	TCCAAAGATT	CTTGTCTCAA	CCATTCGCTG	TTGCTGAAGT	1200
	TTTCACTGGT	ATCCCAGGTA	GATTAGTCAG	ATTGCAAGAC	ACTGTCAAAT	1250
20	CATTCAAGGA	TGTTTTGGAA	GGTAAATACG	ATAACTTGCC	AGAAA	1295

2) INFORMATION FOR SEQ ID NO: 461

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1277 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida dubliniensis*

(B) STRAIN: NCPF 3949

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 461

	TAAGCTTGCCA	GCTATTTTGA	ATGCTTTGAC	TTTGAAGAAC	GGTGACCAAG	50
40	ATTTAGTTTT	GGAAGTTGCT	CAACATTTGG	GTGAAAACAC	CGTCAGAGCT	100
	ATTGCTATGG	ATGGTACTGA	AGGTTTAGTC	AGAGGTACTG	AAGTCAACGA	150
	TACCGGTGCC	CCAATCTCCG	TTCCAGTCGG	TAGAGGTACC	TTAGGTAGAA	200
	TCATCAATGT	TGTTGGTGAA	CCAATTGATG	ACAGAGGTCC	AATTGAATGT	250
	AAGGAAAAGA	AACCAATTCA	TGCAGAACCA	CCATCCTTCG	TTGAGCAATC	300
45	CACTGCTGCC	GAAATTTTGG	AAACCGGTAT	CAAGGTTGTC	GACTTATTGG	350
	CCCCATACGC	CAGAGGTGGT	AAGATTGGTT	TGTTCCGGTG	TGCTGGTGTC	400
	GGTAAGACCG	TCTTTATCCA	AGAATTGATT	AACAACATTG	CTAAAGCCCA	450
	TGGTGGTTTC	TCCGTCTTTA	CCGTTGTCGG	TGAAAGAACC	AGAGAAGGTA	500
	ACGATTTGTA	CCGTGAAATG	AAAGAAACCG	GTGTCATCAA	CTTAGAAGGT	550
50	GACTCCAAGG	TCGCTTTGGT	CTTTGGACAA	ATGAACGAAC	CACCAGGTGC	600
	TAGAGCTAGA	GTTGCTTTGA	CTGGTTTGAC	TATTGCTGAA	TACTTCAGAG	650
	ATGAAGAAGG	TCAAGATGTC	TTGTTGTTCA	TCGATAACAT	TTTCAGATTG	700
	ACCCAAGCTG	GTTCCGAAGT	GTCTGCTTTG	TTAGGTCGTA	TTCCATCTGC	750
	CGTCGGTTAT	CAACCAACCT	TAGTACTGTA	TATGGGTCTT	TTGCAAGAAC	800
55	GTATTACCAC	CACCAAGAAA	GGTTCCGTCA	CCTCTGTCCA	AGCTGTCTAT	850
	GTCCCAGCTG	ATGATTTGAC	CGATCCTGCT	CCAGCCACCA	CATTGCCCCA	900
	TTTGGATGCC	ACTACTGTCT	TGTCTAGAGG	TATTTCTGAA	TTGGGTATTT	950
	ACCCAGCTGT	CGATCCATTG	GATTCCAAAT	CCAGATTATT	GGACGCTGCC	1000
	GTTGTTGGTC	AAGAACATTA	TGATGTCGCT	ACTGGTGTTC	AACAACTTT	1050
60	GCAAGCTTAC	AAATCCTTAC	AAGATATCAT	TGCTATTTTG	GGTATGGATG	1100

AATTGTCTGA	AGCTGATAAA	TTGACTGTCTG	AAAGAGCCCCG	TAAGATTCAA	1150
AGATTCTTGT	CTCAACCATT	CGCCGTTGCT	GAAGTTTTC	CTGGTATTCC	1200
AGGTAGATTA	GTCAGATTGC	AAGACACTGT	CAAATCATTC	AAGGATGTTT	1250
TGGAAGGTAA	ATACGATCAC	TTGCCAG			1277

5

2) INFORMATION FOR SEQ ID NO: 462

- 10 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1278 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- 15 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Candida famata*
 - (B) STRAIN: ATCC 62894
- 20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 462

25	GTA	ACT	TG	CC	AG	CT	AT	TT	TT	G	AA	CG	CT	TT	G	CC	TT	GA	AG	AA	CG	GT	GA	AA	AA	C	50
	GAC	TTA	GT	TTT	TA	GA	AG	TT	G	CC	AA	CA	TT	T	GG	T	GA	AA	AA	CC	GT	CA	AG	AG	C	100	
	TAT	TG	CT	AT	G	AT	GG	T	ACT	AA	GG	T	T	AG	T	AG	AG	G	T	CC	AG	T	T	AC	CG	150	
	ATT	CT	GG	T	G	T	CC	A	AT	T	T	C	T	G	T	AG	AG	G	T	TT	AG	G	T	A	G	200	
	AT	CT	T	GA	AC	G	T	T	AT	T	GG	T	G	A	AC	CA	A	T	G	GA	CA	A	AG	G	T	250	
	CA	AG	GA	AA	CC	AG	AC	CA	A	T	T	C	A	CC	CA	AG	AC	CC	AC	CA	G	C	A	T	300		
30	CC	AC	CA	A	AG	G	C	T	T	AC	G	T	G	T	GA	AG	T	T	T	CA	AG	G	T	T	350		
	G	CC	CC	T	T	AC	G	T	T	TA	AG	AT	T	GG	T	TT	AT	T	CG	AT	T	T	A	T	400		
	CG	GT	A	A	AG	AC	GT	C	T	T	T	A	T	CC	AA	GA	AT	T	TA	AC	A	C	A	T	450		
	AT	GG	T	GG	T	T	C	T	G	T	T	T	C	A	CT	GG	T	G	GT	GA	A	GA	A	C	500		
	AA	C	G	A	T	T	A	T	A	T	GA	AG	AA	CT	GG	T	G	T	CA	TT	G	GA	A	AG	550		
35	TG	AC	T	CC	A	AG	GT	C	G	C	T	T	G	T	TT	T	C	G	GA	AA	CG	AA	CC	AC	C	600	
	CT	AG	A	G	CT	A	G	TT	G	CT	T	T	A	AC	CG	G	T	TA	A	CC	AG	GT	G	650			
	G	A	C	GA	A	AG	A	G	T	CA	AG	AT	G	T	G	T	T	GT	C	G	A	T	A	700			
	CA	CC	CA	A	AG	CC	GT	T	CC	GA	AG	TT	G	TT	AG	GT	C	GT	T	AG	G	T	C	750			
40	CT	G	T	C	G	G	T	T	A	CC	AA	CC	TT	AG	CC	AC	T	AT	AT	GG	G	T	C	800			
	AG	A	T	T	AC	CA	CC	AC	CA	AA	GG	G	T	T	CC	G	T	AC	TT	C	T	G	T	850			
	CG	T	CC	C	A	GC	CA	GG	T	T	AA	CC	G	A	T	C	T	G	C	A	T	A	900				
	AC	T	T	G	G	AT	G	C	T	G	T	G	T	AT	C	T	G	T	CA	AA	TT	G	G	G	950		
	T	A	C	C	A	G	C	T	G	T	CA	AT	T	CC	AA	AA	T	CC	AG	AT	T	G	1000				
45	T	A	T	C	G	T	T	G	G	T	AA	GA	A	C	A	C	T	AC	G	A	A	G	T	1050			
	GA	A	T	T	G	T	C	T	T	CA	AG	A	T	A	T	CA	TT	G	T	A	T	T	1100				
	AA	G	A	T	T	CT	T	G	AT	T	CA	AG	CC	G	A	AA	TT	G	A	A	G	A	1150				
	C	A	G	G	T	A	G	T	AT	T	G	CG	G	T	CG	AA	G	T	T	AC	CG	G	T	A	T	1200	
	C	A	G	G	T	A	G	T	AT	T	G	CG	G	T	CG	AA	G	T	T	CA	AG	G	A	G	T	1250	
50	T	T	A	G	A	G	G	T	A	A	A	T	A	T	G	A	T	A	G	CA	AG	G	A	G	T	1278	

2) INFORMATION FOR SEQ ID NO: 463

- 55 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1154 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- 60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida glabrata*
 (B) STRAIN: ATCC 66032

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 463

```

10  TCTGGTCAGA GGCAGAGAAGG TCGTCGACAC AGGTGCCCCA ATCTCCGTCC 50
    CTGTCGGCAG AGAGACCCTG GGCAGAATCA TCAACGTTAT CGGTGAACCT 100
    ATCGACGAGC GTGGCCCAAT CAACTCAAAG TTGAGAAAGC CTATCCACGC 150
    CGACCCTCCT TCCTTCGCAG AACAGTCCAC CGCCGCCGAA GTCCTGGAAA 200
    CAGGTATCAA GGTGTCGCAG TTGCTGGCCC CTTACGCCAG AGGTGGTAAG 250
    ATCGGTCTGT TCGGTGGTGC CGGTGTCGGT AAGACCGTGT TCATCCAAGA 300
15  ACTGATCAAC AACATCGCAA AGGCTCACGG TGGTTTCTCC GTGTTACAG 350
    GTGTCGGTGA AAGAACCAGA GAAGGTAACG ATTTGTACAG AGAAATGAAG 400
    GAAACCGGTG TCATCAACTT GGAAGGTGAC TCTAAGGTCTG CCTTGGTCTT 450
    CGGCCAAATG AACGAACCAC CAGGAGCCAG AGCCAGAGTC GCCTTGACCG 500
    GTTTGACCAT CGCAGAATAC TTCAGAGATG AAGAAGGTCA AGATGTCCTG 550
20  CTGTTTCGTCG ACAACATTTT CAGATTACCC CAAGCCGGTT CAGAAGTCTC 600
    CGCTTTGCTA GGTGCTATCC CATCCGCCGT CGGTTATCAA CCAACCTTGG 650
    CCACCGATAT GGGTCTGTTG CAAGAAAGAA TTACCACCAC AAAGAAGGGT 700
    TCCGTCACCT CCGTCCAAGC CGTCTACGTG CCTGCAGATG ATTTAACAGA 750
    TCCTGCCCCT GCCACTACTT TCGCGCACTT GGACGCCACC ACCGTCTTGT 800
25  CCAGAAGTAT CTCAGAATTG GGTATCTACC CAGCTGTCTG CCCATTGGAC 850
    TCCAAGTCTA GATTGCTAGA CGCTGCCGTT GTCGGTGAAG AGCATTACAA 900
    CGTCGCCACA AAGGTCCAAG AAACCTTACA AACTTACAAG TCTCTGCAAG 950
    ATATCATCGC CATTTTGGGT ATGGATGAAT TGTCCGAACA AGATAAGCTA 1000
    ACTGTCGAAA GAGCAAGAAA GATCCAAAGA TTCTTGTCCT AACCATTTCG 1050
30  TGTGCTGAA GTTTTCACCG GTATCGAAGG TAAGCTGGTC AGATTGAAGG 1100
    ACACCATCTC CTCTTTCAAG GCTGTCTTGG AAGGTAAGTA CGATGATCTT 1150
    CCAG
  
```

35

2) INFORMATION FOR SEQ ID NO: 464

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1293 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida guilliermondii*
 (B) STRAIN: ATCC 6260

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 464

```

    CCACTACGAG GACGGTAACC TTCCTGCTAT TTTCAACGCC TTGACTCTTA 50
    AGAACGGTGA CCAAACTTG GTTTTGAAG TTGCCAGCA TTTGGGTGAA 100
    AACACCGTCA GAACATTGC TATGGATGGT ACTGAAGGT TGGTTAGAGG 150
55  TGCCAGCGTC ACTGACATG GTGCTCCTAT CTCTGTGCCT GTTGGTCGTG 200
    GTACTTTGGG TCGTATCATC AACGTTATTG GTGAGCCAAT TGACGAGCGT 250
    GGACCAATCG AGTCCAAGCA AAAGAAGCCC ATTCACGCTG AACCACCATC 300
    GTTCGTCGAA CAATCCACTT CTGCCGAGGT TTTGGAAACC GGTATCAAGG 350
    TTGTCGACTT GTTGGCTCCA TACGCCAGAG GTGGTAAGAT TGGATTGTTT 400
60  GGTGGTGCCG GTGTCGGTAA GACTGTGTTT ATCCAAGAGT TGATTAACAA 450
  
```

	CATTGCCAAG	GCTCACGGTG	GTTTCTCCGT	G TTCACCGGT	GTCGGTGAAA	500
	GAACCAGAGA	AGGTAACGAT	TTGTACCGTG	AAATGAAGGA	AACTGGTGTC	550
	ATCAACTTGG	AAGGTGAATC	CAAGGTGGCC	TTGGTGTTTCG	GTCAAATGAA	600
	CGAACCTCCA	GGAGCTAGAG	CCAGAGTTGC	CCTTACCGGT	TTGACCATCG	650
5	CTGAATACTT	CAGAGATGAG	GAGGGTCAAG	ATGTGTTGTT	GTTTCGTCGAC	700
	AACATTTTCA	GATTCACCTCA	AGCTGGTTCT	GAAGTGTCGG	CTTTGTTGGG	750
	TCGTATTCCCT	TCGGCTGTCG	GTTACCAACC	TACTTTGGCC	ACCGATATGG	800
	GTTTGTGTC	AGAGCGTATT	ACCACCACCA	AGAAGGGTTC	CGTCACCTCT	850
	GTCCAAGCTG	TCTATGTGCC	AGCCGATGAT	TTGACCGATC	CTGCTCCTGC	900
10	TACTACTTTT	GCTCACTTGG	ATGCTACCAC	TGTGTTGTCT	AGAGGTATCT	950
	CCGAGTTGGG	TATTTACCCA	GCTGTCGATC	CTTTGGATTTC	CAAGTCGAGA	1000
	TTGTTGGATG	CCTCTGTTGT	CGGTGAGGAG	CACTACTCGG	TTGCTTCTAA	1050
	CGTTCAACAA	ACCTTGAAAG	CTTACAAGTC	TTTGCAAGAT	ATCATTGCCA	1100
	TTTTGGGTAT	GGACGAATTG	TCGGAAGCTG	ACAAGTTGAC	CGTCGAGAGA	1150
15	GCCCCGTAAGA	TCGAGAGATT	CTTGTCTCAA	CCATTGCTG	TTGCCGAAGT	1200
	TTTCACTGGT	ATCAGTGGTA	AGTTGGTCAG	ATTGGAGGAC	ACTATCAGAT	1250
	CTTTCAAGGA	AGTCTTGGA	GGTAAGTACG	ATCACTTGCC	AGA	1293

20

2) INFORMATION FOR SEQ ID NO: 465

(i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 1293 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida haemulonii*
- (B) STRAIN: ATCC 22991

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 465

	CACTTTGACG	ATGGTAACTT	GCCAGCCATT	TTCAACGCCT	TGAAGTTGAA	50
	GAACGGTGAC	CAGGACTTGG	TCTTGGAGGT	CGCCCAGCAC	TTGGGTGAGA	100
	ACACCGTCAG	AACCATTGCC	ATGGACGGTA	CCGATGGTTT	GGTCAGAGGC	150
40	GAGGCTGTCA	CTGACACTGG	TGCTCCAATC	TCCGTGCCTG	TTGGTCGTGA	200
	GACTTTGGGT	CGTATCATCA	ACGTTATTGG	TGAGCCAATT	GACGAGAGAG	250
	GACCAATCAA	GTCCAAGAAG	AGAAACCCAA	TCCACACTGA	CCCACCAACC	300
	TTCGTTGAGC	AGTCTACTTC	TGCTGAGGTT	TTGGGAGACTG	GTATTAAGGT	350
	TGTCGACTTG	TTGGCCCCCT	ACGCCAGAGG	TGGTAAGATT	GGTTTGTTTCG	400
45	GTGGTGCCGG	TGTCGGTAAG	ACCGTCTTTA	TCCAAGAGTT	GATTAACAAC	450
	ATTGCCAAGG	CCCACGGTGG	TTTCTCTGTC	TTTACCGGTG	TCGGTGAGAG	500
	AACCAGAGAA	GGTAACGATT	TGTACCGTGA	AATGCAGGAG	ACCGGTGTCA	550
	TCAACTTCGA	GGGTGACTCC	AAGGTCGCCT	TGGTCTTCGG	TCAGATGAAC	600
	GAGCCACCAG	GAGCTAGAGC	TAGAGTTGCT	TTGACCGGTT	TGACCATTGC	650
50	CGAATACTTC	AGAGATGAAG	AAGGTCAGGA	TGTGTTGTTG	TTCGTTGACA	700
	ACATTTTTCAG	ATTCACTCAG	GCTGGTTCCG	AGGTGTCCGC	CTTGTTGGGT	750
	CGTATTCCAT	CTGCTGTCGG	TTACCAGCCA	ACCTTGGCCA	CCGATATGGG	800
	TACCTTGCAA	GAAAGAATTA	CCACCACCAA	GAAGGGTTCC	GTCACCTCTG	850
	TCCAGGCCGT	TTACGTGCCA	GCTGATGATT	TGACCGATCC	TGCCCCAGCT	900
55	ACCACTTTCG	CTCACTTGGA	TGCTACCACT	GTGTTGTCTA	GAGGTATTTT	950
	CGAGTTGGGT	ATCTACCCAG	CTGTCGACCC	ATTGGACTCC	AAGTCTAGAT	1000
	TGTTGGATGC	CTCTGTTGTC	GGTAAGGAGC	ACTACGATGT	TGCTACCAAC	1050
	GTCCAGCAGA	CCTTGCAGGC	CTACAAGTCC	TTGCAGGATA	TCATTGCCAT	1100
	TTTGGGTATG	GATGAATTGT	CCGAAGCCGA	CAAGTTGACT	GTCGAGAGAG	1150
60	CTAGAAAGAT	TCAGAGATTTC	TTGTCCCAGC	CATTCGCCGT	CGCCGAGGTT	1200

TTCACTGGTA TCGAGGGTAA GTTGGTCAGA TTGGAGGAGA CCGTCAAGTC 1250
 TTTCAAGGAG GTCTTGGATG GTAAGTACGA CCACTTGCCA GAG 1293

5

2) INFORMATION FOR SEQ ID NO: 466

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 1111 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida inconspicua*
 (B) STRAIN: ATCC 16783

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 466

25 AAGGGTGGAT CTAAGTTAGT CTTAGAAGTT GCTCAACATT TGGGTGAAAA 50
 CACTGTCAGA ACCATTGCTA TGGATGGTAC TGAAGGTTTA GTTAGAGGTC 100
 AACCAGTTAA TGATACTGGT GCTCCAATCT CTGTCCCAGT CCGTAGAGGT 150
 ACTTTAGGTA GAATCTTAAA CGTTATTGGT GATCCAGTCG ATGAAAGAGG 200
 TCCAATTGAT TGTAAGGAAA GAAAACCAAT TCATCAAGAT CCTCCTGCTT 250
 TCGTTGAACA ATCTACTGAA GCTGAAGTTT TAGAAACCGG TATTAAGGTT 300
 GTTGATTTAT TAGCTCCTTA CGCTAGAGGT GGTAAGATTG GTTTATTCGG 350
 TGGTGCTGGT GTCGGTAAAA CCGTTTTCAT TCAAGAATTA ATTAACAATG 400
 30 TTGCAAAGGC TCATGGTGGT TTCTCAGTTT TCACTGGTGT CCGTGAAAGA 450
 ACCAGAGAAG GTAATGATTT ATACAGAGAA ATGAAGGAAA CTGGTGTTAT 500
 TAACTTAGAA GGTGAATCTA AGGTCGCCTT AGTTTTCGGT CAAATGAATG 550
 AACCACCAGG AGCAAGAGCA AGAGTTGCTT TAACCGGTTT AACTATTGCT 600
 GAATACTTCA GAGATGAAGA AGGTCAAGAT GTCTTGTTAT TCATTGATAA 650
 35 CATTTTCAGA TTTACTCAAG CAGGTTCTGA AGTTTCTGCA TTGTTAGGTA 700
 GAATTCCATC CGCTGTCGGT TATCAACCAA CTTTAGCAAC TGATATGGGT 750
 CTTTACAAAG AAAGAATTAC AACTACTAAG AAAGGTTCG TTAATTCTGT 800
 CCAAGCAGTT TATGTCCCAG CAGATGATTT AACTGATCCT GCTCCAGCAA 850
 CTACTTTTCGC CCACTTAGAT GCAACTACTG TCTTATCTAG AGGTATTTCC 900
 40 GAATTAGGTA TTTACCCAGC TGTCGATCCA TTAGATTCTA AATCTAGATT 950
 ATTAGATGTT GCTGTTGTTG GTCAAGAACA TTATGATGTT GCAACTCAAG 1000
 TTCAAGAAAC TTTACAAGCA TACAAATCTT TACAAGATAT TATTGCTATT 1050
 TTAGGTATGG ATGAATTATC TGAACAAGAT AAATTAACCG TTGAAAGAGC 1100
 AAGAAAGATT C 1111

45

2) INFORMATION FOR SEQ ID NO: 467

50 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1283 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

60 (A) ORGANISM: *Candida kefyr*
 (B) STRAIN: ATCC 28838

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 467

	TCGAACAAGG	TCAATTGCCA	GAAATTTTGA	ACGCTTTTGA	GATTGAWACT	50
5	CCTCAAGGTA	AGTTGGTTTT	GGAAGTTGCC	CAACATTTGG	GTGAAAACAC	100
	CGTCAGAACC	ATTGCTATGG	ACGGTACCGA	AGGTTTGGTC	CGTGGTGAGA	150
	AGGTTTGGGA	CACTGGTGCT	CCAATTTCCG	TCCCAGTCGG	TAGAGAAACT	200
	TTGGGTAGAA	TCATCAACGT	TATTGGTGAG	CCAATTGACG	AAAGAGGCCC	250
	AATCAAGTCC	AAGATGAGAA	AGCCAATTCA	CGCTGACCCT	CCATCCTTTG	300
10	TTGAACAATC	CACTGCTGCT	GAAGTTTGG	AAACCGGTAT	CAAGGTGTGC	350
	GACTTGTTGG	CCCCATACGC	CAGAGGTGGT	AAGATTGGTT	TGTTCCGGTGG	400
	TGCCGGTGTC	GGTAAGACCG	TTTTTCATCCA	AGAGTTGATT	AACAACATTG	450
	CCAAGGCCCA	TGGTGGTTTC	TCCGTCCTTCA	CCGGTGTCGG	TGAAAGAACC	500
	AGAGAAGGTA	ACGATTTGTA	CCGTGAAATG	AAGGAAACCG	GTGTCATCAA	550
15	CTTGGAAGGT	GACTCCAAGG	TGCCTTGGT	CTTCGGTCAA	ATGAACGAAC	600
	CACCTGGAGC	TAGACCAAGA	GTTGCCCTTG	CCGGTTTGAC	TATCGCTGAA	650
	TACTTCAGAG	ATGAAGAAGG	TCAAGATGTG	TTGTTGTTTA	TCGACAACAT	700
	TTTCAGATTC	ACACAAGCCG	GTTCCGAAGT	GTCCGCTTTG	TTGGGTCGTA	750
	TTCCATCCGC	TGTCGGTTAC	CAACCTACTT	TGGCCACCGA	TATGGGTTTG	800
20	TTGCAAGAAA	GAATTACCAC	TACCAAGAAG	GGTTCCTGTT	CCTCCGTCCA	850
	AGCTGTCTAC	GTCCCTGCTG	ATGATTTGAC	TGATCCTGCT	CCAGCTACYA	900
	CTTTCGCCCA	TTTGGACGCG	ACCACCGTGT	TGTCCAGAGG	TATCTCCGAA	950
	TTGGGTATCT	ACCCAGCTGT	CGATCCATTG	GATTCCAAGT	CTAGATTGTT	1000
	GGACGCTGCC	GTTGTCGGTC	AAGAACATTA	CGACGTCGCT	ACTCAAGTTC	1050
25	AACAACTTTT	GCAAGCTTAC	AAGTCTTTGC	AAGATATCAT	TGCCATTTTG	1100
	GGTATGGATG	AATTGTCTGA	ACAAGACAAG	TTGACTGTCT	AAAGAGCCAG	1150
	AAAGATCCAA	AGATTCTTGT	CTCAACCATT	CGCCGTCGCC	GAAGTTTTC	1200
	CTGGTATCCC	AGGTAGATTG	GTCAGATTAA	AGGACACCAT	CGCTTCCTTC	1250
	AAGGCTGTTT	TGGAAGGTAA	GTACGATCAC	TTG		1283
30						

2) INFORMATION FOR SEQ ID NO: 468

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1287 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida krusei*

(B) STRAIN: ATCC 34135

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 468

	CTTCGAACAA	GGCCAATTAC	CACAAATTTT	AAACGCTTTA	GTTATGGATA	50
50	ATGGTGGTAA	CAAGTTAGTT	TTAGAAGTTG	CTCAACATTT	AGGTGAAAAC	100
	ACTGTCAGAA	CCATTGCTAT	GGATGGTACT	GAAGGTTTAG	TTAGAGGTCA	150
	AACCGTTAAC	GATACCGGTG	CTCCAATCTC	TGTCCCAGTT	GGTAGAGGTA	200
	CCTTAGGTTAG	AATCTTGAAC	GTCATTGGTG	ATCCAGTCGA	TGAAAGAGGT	250
	CCAGTTGACT	GTAAGGAAAG	AAAGCCAATT	CACGCTGATC	CTCCAGCTTT	300
55	CGTTGAACAA	TCCACTGAAG	CTGAAGTTT	GGAACTGGT	ATTAAGGTTG	350
	TCGATTTATT	AGCACCTTAC	GCAAGAGGTG	GTAAGATTGG	TTTATTCGGT	400
	GGTGTGGTG	TTGGTAAGAC	CGTTTTTATC	CAAGAATTGA	TCAACAATGT	450
	YGCAAAGGCT	CATGGTGGTT	TCTCCGTTTT	CACTGGTGTT	GGTGAAAGAA	500
	CCAGAGAAGG	TAACGATTTA	TACAGAGAAA	TGAAGGAAAC	TGGTGTATT	550
60	AACTTGAAG	GTGAATCCAA	GGTCGCCTTA	GTTTTTCGGT	AAATGAACGA	600

	ACCACCAGGA	GCTAGAGCAA	GAGTTGCTTT	AACTGGTTTG	ACCATTCGAG	650
	AATATTTT	AGATGAAGAA	GGTCAAGATG	TCTTGTTATT	CATTGATAAC	700
	ATTTTCAGAT	TCACCCAAGC	AGGTTCTGAA	GTCTCTGCAT	TATTAGGTAG	750
	AATTCCATCT	GCTGTCGGTT	ATCAACCAAC	TTTAGCAACC	GATATGGGTC	800
5	TTTTACAAGA	AAGAATTACC	ACCACCAAGA	AGGGTTCGGT	TACTTCTGTC	850
	CAAGCTGTTT	ATGTCCCAGC	CGATGATTTA	ACCGATCCTG	CTCCAGCTAC	900
	TACTTTTCGCC	CACTTGGATG	CAACCACTGT	CTTGTCYAGA	GGTATTTCCG	950
	AATTAGGTAT	CTACCCAGCT	GTCGATCCAT	TAGATTCTAA	GTCTAGATTA	1000
	TTAGATGTTG	CAGTTGTTGG	TCAAGAACAT	TATGAAGTTG	CAACTCAAGT	1050
10	CCAAGAAACT	TTACAAGCTT	ACAAGTCTTT	ACAAGATATT	ATTGCTATTT	1100
	TGGGTATGGA	TGAATTATCT	GAACAAGATA	AGTTAACYGT	TGAAAGAGCA	1150
	AGAAAGATCC	AAAGATTCTT	ATCTCAACCA	TTCTCTGTTG	CAGAAGTTTT	1200
	CACTGGTATT	CCAGGTAAGT	TAGTCAGATT	AGAAGAAACC	ATCAAGTCTT	1250
15	TCAGGGATGT	TCTTGCAGGT	AAGTACGATC	ACTTACC		1287

2) INFORMATION FOR SEQ ID NO: 469

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1283 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida lambica*

(B) STRAIN: ATCC 24750

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 469

	TCGAACAAGG	TCAATTACCA	CCAATTCTTA	ACGCTTTGGT	CATGGAAAAC	50
35	GATGGTCAAA	AGTTAGTTTT	GGAAGTTGCT	CAACATTTGG	GTGAAAACAC	100
	CGTCAGAACC	ATTGCTATGG	ACGGTACCGA	AGGTTTAGTT	AGAGGTCAAC	150
	CTGTTAACGA	CACTGGTGCT	CCAATCTCTG	TCCAGTTGG	TAGAGGTACT	200
	TTTGGTAGAA	TCTTGAACGT	CACTGGTGAC	CCAGTYGATG	AAAGAGGTCC	250
	TGTCGAMTGT	AAGGAGAGAA	GACCAATTCA	CCAAGACCCA	CCTGCTTTCG	300
40	TTGACCAATC	CACTGAAGCT	GAAGTTTGG	AAACCGGTAT	TAAGGTGTGC	350
	GATTTATTAG	CACCTTACGC	TAGAGGTGGT	AAGATTGGTT	TGTTCCGGTGG	400
	TGCTGGTGTC	GGTAAGACCG	TTTTTCATCCA	AGAATTGATT	AACAATGTTG	450
	CTAAGGCCCA	CGGTGGTTTC	TCCGTTTTC	CTGGTGTGCG	TGAAAGAACC	500
	AGAGAAGGTA	ACGATTTATA	CAGAGAAATG	AAGGAAACCG	GTGTTATTAA	550
45	CCTTGAAGGT	GAATCTAAGG	TGCGCCTCGT	TTTCGGTCAA	ATGAACGAAC	600
	CACCAGGAGC	AAGAGCTAGA	GTTGCTCTTA	CTGGTTTGAC	CATTGCTGAA	650
	TACTTCAGAG	ATGAAGAAGG	TCAAGATGTC	TTGCTTTTCA	TTGACAACAT	700
	TTTCAGATTC	ACCCAAGCAG	GTTCCGAAGT	GTCTGCTTTG	TTAGGTAGAA	750
	TTCCWTCTGC	CGTTGGTTAC	CAACCAACCT	TAGCAACCGA	TATGGGTTTG	800
50	TTACAAGAAA	GAATTACCAC	CACCAAGAAG	GGTTCGCTCA	CCTCCGTCCA	850
	AGCTGTTTAC	GTCCCAGCTG	ATGATTTRAC	TGACCCTGCA	CCAGCAACCA	900
	CTTTCGCCCA	CTTGGATGCT	ACCACCGTCT	TGTCTAGAGG	TATTTCCGAA	950
	TTAGGTATTT	ACCCAGCTGT	CGATCCATTA	GATTCCTAAGT	CTAGATTATT	1000
	GGATGTCGCT	GTTGTCGGTC	AAGAACATTA	TACCGTTGCA	ACYCAAGTCC	1050
55	AAGAACTTT	ACAAGCTTAC	AAGTCCTTAC	AAGATATCAT	TGCTATTTTG	1100
	GGTATGGACG	AATTATCTGA	ACAAGATAAG	CTTACTGTTG	AAAGAGCAAG	1150
	AAAGATCCAA	AGATTCCTTT	CCCAACCTTT	CTCCGTGCGA	GAAGTTTTC	1200
	CTGGTATCCC	AGGTAAGCTT	GTCAGATTAG	AAGAAACCAT	TATTTCTTTC	1250
60	AGAGATGTCC	TCGATGGTAA	GTACGACCAC	TTA		1283

2) INFORMATION FOR SEQ ID NO: 470

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1140 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida lusitanae*
 (B) STRAIN: ATCC 66035

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 470

	AGGTGCCTCT	GTCAC	TGACA	CTGGT	TCTCC	AATCT	CTGTC	CCTGT	TGGTC	50
20	GTGAAACCTT	GGGTAG	AATT	ATCAAC	GTTG	TTGGT	GAGCC	AATTG	ACGAG	100
	AGAGGCCCAA	TCAACT	CCAA	GAAGAG	AAAC	CCAATT	CACA	CTGAG	CCACC	150
	ATCGTTTGTT	GAACA	ATCCA	CTTCT	GCTGA	AGTTT	TGGAG	ACTGG	TATCA	200
	AGGTGTGCGA	CTTGT	TGGCC	CCTTAC	GCCA	GAGGT	GGTAA	GATTG	GTTTG	250
	TTCGGTGGTG	CCGGT	GTCGG	TAAGAC	CGTT	TTCAT	CCAAG	AGTTG	ATTAA	300
25	CAACATTGCC	AAGGCC	CACG	GTGGT	TTTCTC	TGTTT	TCACT	GGTGT	CGGTG	350
	AAAGAACCAG	AGAAG	GTAAC	GATTT	GTACC	GTGAA	ATGCA	AGAGAC	CGGT	400
	GTCATCAACT	TCGAG	GGTG	CTCCA	AAGGT	GCCTT	GGTCT	TCGGT	CAAAT	450
	GAACGAACCA	CCAGG	AGCCA	GAGCT	AGAGT	TGCTT	TGACC	GGTTT	GACTA	500
	TTGCCGAGTA	CTTCAG	AGAC	GAAGAG	GGCC	AAGAT	GTCTT	GTTGT	TCGTT	550
30	GACAACATTT	TCAGAT	TCAC	CCAGG	CCGGT	TCTGA	AGTGT	CTGCT	TTGTT	600
	GGGTCGTATT	CCATCC	GCTG	TCGGT	TACCA	ACCAAC	CCTTG	GCCAC	CGATA	650
	TGGGTGCTTT	GCAAG	AGAGA	ATTACC	ACCA	CCAAG	AAGGG	TTCCG	TCACC	700
	TCTGTCCAAG	CCGTT	TATGT	TCCAG	CTGAT	GACTT	GACTG	ACCCT	GTCTC	750
	AGCCACCACC	TTCGC	CCACT	TGGAC	GCCAC	CAC	TGTGT	TCCAG	AGGTA	800
35	TCTCTGAATT	GGGTAT	CTAC	CCAGC	TGTCG	ACCCAT	TGGA	CTCCA	AGTCT	850
	AGATTGTTGG	ACGCT	TCTAT	TGTTG	GTAAG	GAGCA	TACG	AAGTT	GCTTC	900
	TAACATTCAA	CAA	CTTGC	AAGCT	TACAA	GTCTT	TGCAA	GATAT	CATTG	950
	CCATTTTGGG	TATGG	ATGAA	TTGTC	TGAGG	CTGAC	AAGTT	GACCG	TTGAG	1000
	AGAGCCAGAA	AGATC	CAAAG	ATTCT	TGTCT	CAACC	ATTCG	CTGTT	GCCGA	1050
40	GGTTTTCCT	GGTAT	CCCAG	G	TAGATTGGT	CAGATT	GGAG	GACACT	GTCA	1100
	GATCCTTCAA	GGAAG	TTTTG	GACGG	TAAAGT	ACGACC	ACTT			1140

45 2) INFORMATION FOR SEQ ID NO: 471

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1296 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida norvegensis*
 (B) STRAIN: ATCC 22977

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 471

	TCAATTCGAA	CAAGGTCAAT	TACCACCAAT	TTTAAACGCT	TTAGTCATGG	50
	ACAACGGTGG	AACTAAGTTA	GTTTTAGAA	TTGCTCAACA	TTTAGGTGAA	100
	AACACCGTCA	GAACCATTGC	TATGGATGGT	ACTGAAGGTT	TAGTTAGAGG	150
	TCAACCAGTT	AATGATACTG	GTGCTCCAAT	CTCTGTCCCA	GTCGGTAGAG	200
5	GTAATTTAGG	TAGAATCTTA	AACGTTATTG	GTGATCCAGT	CGATGAAAGA	250
	GGTCCAATCG	ATTGTAAGGA	AAGAAAACCA	ATTCATCAAG	ATCCTCCTGC	300
	TTTCGTTGAA	CAATCAACTG	AAGCTGAAGT	TTTAGAAACT	GGTATTAAAG	350
	TTGTTCGATTT	ATTAGCTCCT	TACGCTAGAG	GTGGTAAGAT	TGGTTTATTC	400
	GGTGGTGCAG	GTGTTGGTAA	AACCGTTTTT	ATTCAAGAAT	TAATTAACAA	450
10	TGTTGCAAAA	GCTCATGGTG	GTTTCTCCGT	TTTCACTGGT	GTCGGTGAAA	500
	GAAGTAGAGA	AGGTAACGAT	TTATACAGAG	AAATGAAGGA	AACTGGTGTT	550
	ATTAATTTAG	AAGGTGATTC	TAAGGTCGCA	TTAGTTTTCG	GTCAAATGAA	600
	CGAACCACCT	GGAGCAAGAG	CAAGAGTTGC	TTTAACTGGT	TTAACTATTG	650
	CTGAATATTT	CAGAGATGAA	GAAGGTCAAG	ATGTCTTGTT	ATTCATTGAT	700
15	AACATTTTCA	GATTTACTCA	AGCAGGTTCT	GAAGTTTCCG	CTTTGTTAGG	750
	TAGAATTCCA	TCCGCTGTCG	GTTATCAACC	AACTTTAGCA	ACTGATATGG	800
	GTCTTTTACA	AGAAAGAATT	ACTACTACTA	AGAAAGGTTT	TGTTACTTCC	850
	GTTCAAGCAG	TTTATGTCCC	AGCAGATGAT	TTAACTGATC	CTGCTCCAGC	900
	AACTACTTTC	GCCCACTTAG	ATGCAACTAC	TGTCTTATCT	AGAGGTATTT	950
20	CCGAATTAGG	TATTTACCCA	GCTGTGCGAT	CATTAGATTC	TAAATCTAGA	1000
	TTATTAGATG	TTGCAGTTGT	TGGTCAAGAA	CATTATGATG	TTGCAACTCA	1050
	AGTTCAAGAA	ACTTTTCAAG	CTTACAAATC	TTTACAAAGAT	ATTATTGCTA	1100
	TTTTAGGTAT	GGATGAATTA	TCTGAACAAG	ATAAATTAAC	CGTTGAAAGA	1150
	GCTAGAAAAA	TTCAAAGATT	CTTATCTCAA	CCTTTCTCTG	TCGCAGAAGT	1200
25	TTTCACTGGT	ATCCCAGGTA	AGCTTGTTAG	ATTAGAAGAA	ACTATTTCTT	1250
	CATTCAGAGA	TGTCTTAGCA	GGTAAGTACG	ATCACTTACC	AGAAAA	1296

30 2) INFORMATION FOR SEQ ID NO: 472

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1297 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida parapsilosis*
 (B) STRAIN: ATCC 90018

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 472

45	ACACTTCGAA	GAAGGAAACT	TGCCAGCTAT	TTTGAACGCT	TTGACCTTGA	50
	AAAACGGTAA	ACAAGACTTG	GTCTTGGAAG	TTGCCCAACA	TTTGGGTGAA	100
	AACACCGTCA	GAGCAATTGC	TATGGATGGT	ACTGAAGGTT	TAGTTAGAGG	150
	TACTTCTGTC	ACTGACACTG	GTGCCCCAAT	TTCTGTCCCA	GTTGGTAGAG	200
50	GTAATTTGGG	TAGAATCATC	AATGTTACTG	GTGACCCAAT	TGATGAAAGA	250
	GGTCCAATTG	AATGTAAGAA	GAGAAACCCA	ATCCACGCTG	AACCACCTTC	300
	ATTCATTGAA	CAATCCACTG	CTGCTGAAGT	TTTGGAAACC	GGTATTAAAG	350
	TTGTTCGACTT	GTTGGCTCCA	TACGCTAGAG	GTGGTAAGAT	TGGTTTGTTC	400
	GGTGGTGCCG	GTGTCGGTAA	AACCGTGTTT	ATCCAAGAAT	TGATCAACAA	450
55	CATTGCCAAG	GCACATGGTG	GTTTCTCGGT	TTTCACTGGT	GTTGGTGAAA	500
	GAACCAAGAG	AGGTAACGAT	TTGTACCGTG	AAATGAAGGA	AACTGGTGTT	550
	ATCAACTTGG	AAGGTGACTC	CAAGGTCGCT	TTGGTTTTTCG	GTCAAATGAA	600
	CGAACCACCT	GGAGCTAGAG	CTAGAGTTGC	TTTGACTGGT	TTGACCATTG	650
	CTGAATACTT	TAGAGATGAA	GAAGGTCAAG	ATGTCTTGTT	GTTTATTGAC	700
60	AACATTTTCA	GATTCACCCA	AGCTGGTTCA	GAAGTGTCTG	CTTTGTTGGG	750

```

TCGTATTCCA TCCGCTGTCG GTTATCAACC AACCTTGGCC ACCGATATGG      800
GTCCTTTTGCA AGAACGTATT ACCACTACCA AAAAGGGTTC AGTTACTTCA      850
GTCCAAGCCG TTTACGTGCG AGCTGATGAT TTAACCGATC CTGCTCCAGC      900
TACCACTTTC GCTCACTTGG ATGCCACCAC TGTGTTGTCT AGAGGTATTT      950
5  CGGAGTTGGG TATTTACCCA GCTGTCGATC CATTGGATTC CAAATCCAGA     1000
   TTGTTGGATG CTGCCGTTGT TGGTCAAGAA CATTACGACG TTGCCACTGG     1050
   TGTTCACAA ACTTTACAAG CTTACAAGTC CTTGCAAGAT ATCATTGCTA     1100
   TCTTGGGTAT GGATGAATTG TCCGAACAAG ATAAATTGAC TGTCGAAAGA     1150
   GCTCGTAAGA TTCAAAGATT CTTGTCTCAA CCATTTGCTG TCGCTGAAGT     1200
10  TTCTACTGGT ATTCCAGGTA AATTGGTTAG ATTGTCTGAA ACTGTCAAGT     1250
   CATTCAGGA AGTCTTGGA GGTAAGTACG ATAACCTGCC AGAAAAT         1297

```

15 2) INFORMATION FOR SEQ ID NO: 473

(i) SEQUENCE CHARACTERISTICS:

```

20  (A) LENGTH: 1285 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

```

    (A) ORGANISM: Candida rugosa
    (B) STRAIN: ATCC 96275

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 473

```

30  CCAGTTTGGC AACGACCTCC CTGCCATTTT GAACGCCCTC ACTCTTCAGC      50
   GTGAAGACGG TAACAAGCTT GTTCTTGAGG TTGCCCAGCA TCTCGGTGAG      100
   AACACCGTCC GTACCATTGC TATGGACGGT ACCGAGGGTT TGGTGCGTGG      150
   CACTGGTGTC CACGACACCG GACACCCCAT CATGACTCCC GTCGGTGACG      200
35  GTACCCCTGGG ACGTATTCTT AACGTCACCG GTGACCCTGT AGACGAGCGT      250
   GGTCCCCTGCA AGACTGACAA GTTCCGCCCC ATCCACGCCG AGGCCCTGTC      300
   CTTTCGATGAG CAGGCTACCA GTGCCGAGGT TCTTGAGACC GGTATCAAGG      350
   TTGTCGACTT GCTCGCTCCT TACGCCAAGG GTGGTAAGAT TGGTTTGTTC      400
   GGTGGTGCCG GTGTCGGCAA GACCGTCTTC ATCCAGGAGC TGATTAACAA      450
40  CATCGCCAAG GCCACGGTG GTTACTCCGT GTTCACTGGT GTCGGTGAGC      500
   GTACTCGTGA GGGTAACGAT TTGTACAAGG AAATGATCGA GTCCGGTGTC      550
   ATCAACCTCG ATGGTGAGTC CAAGGTCGCC TTGGTGTTTCG GTCAGATGAA      600
   CGAGCCCCCT GGAGCCCGTG CCCGTGTGCG CCTTACCGGT CTTACCATCG      650
   CTGAGTATTT CCGTGATGAG GAGGGTAAGG ATGTCTTGTT GTTCGTTGAC      700
45  AACATTTTCC GCTTCACTCA GGCCGGTTCT GAGGTGTCCG CTTGCTTGG      750
   TCGTATTCCT TCCGCTGTCG GTTACCAGCC TACCCTGGCC ACCGATATGG      800
   GTGCCCTTCA GGAGCGTATC ACCACCACCA AGAAGGGTTC CGTTACATCC      850
   GTCCAGGCCG TCTACGTCCC TGCCGATGAT TTGACTGATC CCGCCCCTGC      900
   CACCACCTTC GCCCATTTGG ATGCCACCAC TGTCTTGTCT CGTGCCATCT      950
50  CTGAGTTGGG TATCTACCCC GCTGTCGACC CTCTCGACTC CAAGTCCCGT     1000
   CTTCTTGACG CCGCTGTCTG TGGTCAGGAG CACTACGATA CTGCCACCTC     1050
   CGTTCAGCAG ACTTTGCAGG CTTACAAGTC TTTGCAGGAT ATCATTGCCA     1100
   TTCTTGGTAT GGATGAGTTG TCCGAGTCTG ACAAGCTCAC CGTCGAGCGT     1150
   GCTCGTAAGA TCCAGCGTTT CCTCTCCCAG CCTTTCGCTG TTGCTGAGGT     1200
55  CTTCACTGGT ATTCAGGGCC GTCTTGTTCC TCTCAAGGAC ACTGTCCGCT     1250
   CCTTCAAGGA GATTCTCGAA GGTAAGTACG ATGCT                     1285

```

60 2) INFORMATION FOR SEQ ID NO: 474

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1283 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida sphaerica*
 (B) STRAIN: ATCC 2504

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 474

```

15  TTGAACAAGG TCAATTGCCA GCTATTTTGA ACGCTTTGGA AATCGACACT    50
    CCAGAAGGAA AGTTGGTTTT GGAAGTCGCT CAACATTTGG GTGAAAACAC    100
    TGTCAGAAC ACCATTGCTATGG ATGGTACTGA AGGTTTAGTC CGTGGTGAAA    150
    ACGTTTCTGA CACTGGTGCT CCAATTTCCG TCCCAGTTGG TAGAGAAACC    200
20  TTGGGTAGAA TTATCAACGT TATTGGTGAG CCAATTGACG AAAGAGGTCC    250
    AATCAACTCC AAGATGAGAA AGCCAATTCA TGCTGATCCT CCATTATTCG    300
    TTGAACAATC CACTGCTGCT GAAGTTTTCG AAAGTGGTAT CAAGGTTGTC    350
    GACTTGTTGG CCCCATACGC CAGAGGTGGT AAGATTGGTT TGTTCGGTGG    400
    TGCCGGTGTC GGTAAAGACCG TTTTCATCCA AGAATTGATT AACAACATTG    450
25  CCAAGGCTCA TGGTGGTTTC TCTGTCTTCA CTGGTGTCTCG TGAAAGAACC    500
    AGAGAAGGTA ACGATTTGTA CCGTGAAATG AAGGAAACTG GTGTTATCAA    550
    CTTGGAAGGT GATTCTAAGG TCGCGTTGGT TTTTCGGTCAA ATGAACGAAC    600
    CTCCTGGAGC TAGAGCTAGA GTCGCCTTGA CTGGTTTGAC CATCGCTGAA    650
    TACTTCAGAG ATGAAGAAGG TCAAGATGTC TTGTTGTTTA TCGACAACAT    700
30  TTTTCAGATTC ACACAAGCCG GTTCCGAAGT GTCCGCTTTG TTGGGTCGTA    750
    TTCCATCCGC TGTCGGTTAT CAACCAACTT TGGCCACCGA TATGGGTTTG    800
    TTGCAAGAAA GAATTACTAC CACCAAGAAG GGTTCGTCA CTTCTGTCCA    850
    AGCCGTTTAC GTGCCAGCTG ATGATTTGAC TGATCCTGCT CCAGCTACCA    900
    CTTTCGCGCA TTTGGATGCC ACCACTGTGT TGTCCAGAGG TATCTCTGAA    950
35  TTGGGTATCT ACCCAGCTGT CGATCCTTTG GATTCCAAAT CTAGATTGTT    1000
    GGATGCTGCC GTCGTTGGTC AAGAACATTA CGATGTCGCT ACTCAAGTTC    1050
    AACAACTTT GCAAGCTTAC AAGTCTTTGC AAGATATCAT TGCCATTTTG    1100
    GGTATGGATG AATTGTCCGA ACAAGATAAG TTGACCGTCG AAAGAGCTAG    1150
    AAAGATTCAA AGATTCTTGT CTCACCTTT CGCTGTCGCT GAAGTCTTCA    1200
40  CTGGTATCCC AGGTAGATTG GTCAGATTAA AGGACCCAT CTCTTCTTTC    1250
    AAGGCTGTCT TGGACGGTAA GTACGATCAC TTG    1283

```

45 2) INFORMATION FOR SEQ ID NO: 475

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1290 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida tropicalis*
 (B) STRAIN: ATCC 13803

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 475

	CGACGAAGGT	AACTTGCCAG	CTATTTTGAA	TGCTTTGACT	TTGAAGAACG	50
	GTGACCAAGA	CTTGGTTTTG	GAAGTTGCTC	AACATTTGGG	TGAAAACACC	100
	GTCAGGGCTA	TTGCTATGGA	TGGTACCGAA	GGTTTAGTCA	GAGGTACTGC	150
	TGTCCTGAT	ACCGGTGCTC	CAATTTCTGT	CCCAGTTGGT	AGAGGTACCT	200
5	TGGGTAGAAT	TATCAACGTT	GTTGGTGAAC	CAATTGATGA	CAGAGGTCCA	250
	ATTGAATGTA	AGGAAAGAAA	GCCAATTCAC	GCTGAACCAC	CTTCATTTCG	300
	TGAACAATCT	ACTGCTGCCG	AAATTTTGGA	AACCGGTATT	AAGGTTGTCG	350
	ATTTGTTGGC	TCCTTACGCT	AGAGGTGGTA	AGATTGGTTT	GTTCGGTGGT	400
	GCTGGTGTCG	GTAAAACCGT	CTTCATCCAA	GAATTGATTA	ACAACATTGC	450
10	CAAAGCTCAT	GGTGGTTTCT	CTGTCTTTAC	CGGTGTCGGT	GAAAGAACCA	500
	GAGAAGGTAA	CGATTTGTAC	CGTGAAATGA	AAGAAACTGG	TGTCATCAAC	550
	TTGGAAGGTG	ACTCCAAGGT	CGCCTTGGTC	TTCCGGTCAA	TGAACGAACC	600
	ACCTGGTGCT	AGAGCTAGAG	TTGCTTTGAC	TGGTTTGACC	ATTGCTGAAT	650
	ACTTCAGAGA	TGAAGAAGGT	CAAGATGTCT	TGTTGTTTCAT	TGACAACATT	700
15	TTCAGATTCA	CCCAAGCTGG	TTCCGAAGTG	TCTGCTTTGT	TGGGTCGTAT	750
	TCCATCTGCT	GTCGGTTATC	AACCAACCTT	GGCCACTGAT	ATGGGTCTTT	800
	TGCAAGAACG	TATTACCACC	ACCAAGAAAG	GTTCTGTTAC	TTCTGTCCAA	850
	GCTGTTTATG	TCCCAGCCGA	TGATTTAACC	GATCCAGCTC	CAGCTACCAC	900
	CTTCGGCTAC	TTGGATGCCA	CTACTGTCTT	GTCTAGAGGT	ATTTCTGAAT	950
20	TGGGTATTTA	CCCAGCTGTC	GATCCATTGG	ATTCTAAATC	CAGATTATTG	1000
	GATGCTACTG	TTGTTGGTCA	AGAACATTAT	GATGTTGCCA	CTGGTGTTCA	1050
	ACAAACTTTA	CAAGCTTACA	AGTCCTTGCA	AGATATCATT	GCTATTTTGG	1100
	GTATGGATGA	ATTGTCCGAA	GCCGATAAAT	TGACTGTCTGA	AAGAGCTCGT	1150
	AAGATTCAA	GATTCCTGTC	CCAACCATTC	GCTGTTGCCG	AAGTTTTCAC	1200
25	TGGTATCCCA	GGTAGATTGG	TTAGATTACA	AGATACTGTT	AAATCTTTCA	1250
	AAGATGTCTT	GGAAGGTAAA	TACGATCACT	TGCCAGAAAA		1290

30 2) INFORMATION FOR SEQ ID NO: 476

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1267 bases
 (B) TYPE: Nucleic acid
 35 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida utilis*
 (B) STRAIN: Csp 388

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 476

45	TTTGAACGCC	CTTGAGATCA	AGAACCACGA	GTCTGGAAGA	TTGGTCCTCG	50
	AGGTTGCCCA	GCACTTGGGT	GAGAACACTG	TCAGAACTAT	TGCCATGGAT	100
	GGTACCGAAG	GTCTCGTCCG	TGGTGAGTCT	GTTGTTGACA	CCGGTTCTCC	150
	AATTACTGTC	CCAGTTGGTC	GTGAGACCTT	GGGTCTGATC	ATCAACGTTA	200
50	TTGGTGAGCC	AATTGATGAG	CGTGGTCCAA	TCAACACCAA	GCACAGAAAC	250
	CCAATTCACG	CTGAGCCACC	ATCCTTCGCT	GAGCAGTCTA	CTGCTGCTGA	300
	GGTTTTGGAG	ACTGGTATCA	AGGTTGTCTG	CCTTCTCGCC	CCATACGCCA	350
	GAGGTGGTAA	GATTGGTCTC	TTTGGTGGTG	CCGGTGTCGG	TAAGACCGTT	400
	TTCATCCAGG	AGTTGATTAA	CAACATTGCC	AAGGCCACG	GTGGTTTCTC	450
55	TGTTTTACCC	GGTGTCCGGT	AGAGAACCAG	AGAGGGTAAC	GATTTGTACC	500
	GTGAGATGAA	GGAGACTGGT	GTCATCAATC	TCGAGGGTGA	GTCCAAGGTT	550
	GCTCTCGTCT	TCGGTCAGAT	GAACGAGCCA	CCAGGTGCCC	GTGCCCCTGT	600
	CGCTTTGACC	GGTTTGACCA	TTGCTGAGTA	CTTCAGAGAT	GAGGAGGGTC	650
	AGGATGTCTT	GTTGTTTATT	GACAACATTT	TCAGATTAC	CCAGGCCGGT	700
60	TCCGAGGTGT	CTGCCTTGCT	TGGTCGTATT	CCATCCGCTG	TCGGTTACCA	750

```

GCCAACTTTG GCCACCGATA TGGGTTTGTG GCAGGAGAGA ATTACCACCA 800
CCCAGAAGGG TTCCGTCAC TCTGTCCAGG CCGTTTACGT CCCAGCTGAT 850
GATTTGACTG ATCCTGCTCC AGCCACCACT TTCGCCCCACT TGGACGCCAC 900
CACTGTGTTG TCCCGTGGTA TCTCTGAGTT GGGTATTTAC CCAGCTGTCG 950
5  ACCCATTTGA CTCCAAGTCC AGATTGTTGG ACGCTGCCGT TGTGTTGGTAC 1000
GAGCACTACA ACACCGCCAC CGATGTCCAG CAGACCCTTC AGGCTTACAA 1050
GTCTCTCCAG GATATCATTG CTATTTTGGG TATGGATGAG TTGTCTGAGG 1100
CTGACAAGTT GACTGTGCGAG AGAGCCAGAA AGATTCAGCG TTTCCCTTCC 1150
CAGCCATTTC CTGTCGCTGA GGTTTTTCACC GGTATCCCAG GTAGATTGGT 1200
10 TAGACTTCAG GACACCATCA AGTCCTTCAG AGAGGTTTTG GACGGTAAAGT 1250
ACGACCACTT GCCAGAG 1267

```

15 2) INFORMATION FOR SEQ ID NO: 477

(i) SEQUENCE CHARACTERISTICS:

```

20 (A) LENGTH: 1296 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

```

    (A) ORGANISM: Candida viswanathii
    (B) STRAIN: ATCC 28269

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 477

```

30 CCAATTCGAC GAAGGTAGCT TGCCAGCTAT CTTGAACGCC TTGACCTTGA 50
   AGAACGGTGA CCAAGACTTG GTCTTGGAAG TTGCCCAACA CTTGGGTGAA 100
   AACACTGTCA GAGCTATTGC TATGGATGGT ACCGAAGGTT TGGTCAGAGG 150
   TACTGCTGTC ACTGACACCG GTGCTCCAAT CTCCGTCCCA GTCGGTAGAG 200
35 GTACCTTGGG TAGAATCATC AACGTTGTTG GTGAACCAAT TGACGACAGA 250
   GGTCCAATTG AATGTAAGGA AAGAAAGCCA ATTCACGCTG AACCACCTTC 300
   TTTGCTTGAA CAATCCACTG CTGCCGAAAT TTTGGAAACC GGTATCAAGG 350
   TTGTCGACTT GTTGGCCCCA TACGCCAGAG GTGGTAAGAT TGGTTTGTTT 400
   GGTGGTGCCG GTGTCGGTAA GACTGTCTTT ATCCAAGAGT TGATTAACAA 450
40 CATTGCCAAG GCCCATGGTG GTTTCTCTGT CTTCACTGGT GTCGGTGAAA 500
   GAACCAGAGA AGGTAACGAT TTGTACCGTG AAATGAAGGA AACCGGTGTC 550
   ATCAACTTGG AAGGTGACTC CAAGGTCGCC TTGGTTTTCG GTCAAATGAA 600
   CGAACCACCT GGTGCTAGAG CTAGAGTTGC TTTGACTGGT TTGACCATTG 650
   CCGAATACTT CAGAGACGAA GAAGGTCAAG ATGTCTTGTT GTTTATTGAC 700
45 AACATTTTCA GATTCACCCA AGCCGGTTCC GAAGTGCTCG CTTTGTTGGG 750
   TCGTATTCCA TCTGCCGTCG GTTATCAACC AACCTTGCC ACCGATATGG 800
   GTCTTTTGCA AGAACGTATT ACCACCACCA AGAAGGGTTC CGTCACCTCT 850
   GTCCAAGCTG TCTATGTCCC AGCCGATGAT TTGACCGATC CTGCTCCAGC 900
   CACCACCTTC GCTCACTTGG ATGCCACTAC TGTCTTGTC AGAGGTATTT 950
50 CCGAATTGGG TATCTACCCA GCTGTCGATC CATTGGACTC CAAGTCCAGA 1000
   TTGTTGGATG CTGCTGTTGT TGGTCAAGAA CATTACGATG TTGCCACTGG 1050
   TGTCCAACAA ACCTTGCAAG CTTACAAGTC TTTGCAAGAT ATCATTGCCA 1100
   TTTTGGGTAT GGATGAATTG TCTGAATCCG ATAAGTTGAC TGTCGAAAGA 1150
   GCTCGTAAGA TCCAAAGATT CTTGTCGCAA CCATTTGCTG TTGCCGAAGT 1200
55 TTTCACTGGT ATCCCAGGTA GATTAGTTAG ATTGCTGGAA ACCGTCCAAT 1250
   CTTTCAAAGA CGTCTTGGCT GGTAATACG ATCACTTGCC AGAAAA 1296

```

60 2) INFORMATION FOR SEQ ID NO: 478

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1295 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida zeylanoides*
 (B) STRAIN: ATCC 7351

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 478

```

15 TCAATTTCGAG CAAGGCAACC TCCCTGCCAT CTTGAACGCT CTCACCTTGA      50
   AGAATGGTGA CAACGACTTG GTTTTGGAAG TTGCCCAGCA CTTGGGTGAG      100
   AACACCGTCA GAGCCATTGC CATGGATGGT ACCGAGGGTT TGGTTAGAGG      150
   TGCGTCCGTC AAGGACACTG GCGCCCCTAT CTCGGTCCCC GTTGCCCGCG      200
20 GGACTTTTGGG TCGTATCATC AACGTCACCG GTGACCCCAT TGACGAGAGA      250
   GGTCCCATCG AGCTGACCCA GAGAAACCCT ATCCACGCCG ACCCCCCCTC      300
   GTTCGTTGAG CAGTCCACCA ACGCTGAGGT TTTGGAGACT GGTATCAAGG      350
   TTGTCGATTT GTTGGCTCCC TACGCCAGAG GTGGTAAGAT TGGTTTGTTT      400
   GGTGGTGCCG GTGTCGGTAA GACCGTCTTC ATTCAAGAGT TGATCAACAA      450
25 CATCGCCAAG GCCACGGTG GGTTCCTCGGT CTTCACTGGT GTCGGTGAGA      500
   GAACTAGAGA GGGTAACGAC TTGTACCGTG AGATGAAGGA GACCGGTGTC      550
   ATCAACTTGG AGGGTGACTC CAAGGTGGCC TTGGTGTTTCG GTCAGATGAA      600
   CGAGCCCCCT GGAGCCAGAG CCAGAGTCGC CTTGACCGGG TTGACCATTG      650
   CCGAATACTT TAGAGACGAG GAGGGTCAGG ATGTGTTGTT GTTCGTCGAC      700
30 AACATCTTCA GATTACCCA AGCTGGTTCG GAGGTGTCGG CCTTGTTGGG      750
   TCGTATTCCC TCTGCCGTCTG GTTACCAGCC CACCTTGGA ACTGATATGG      800
   GATTGTTGCA GGAGCGTATC ACCACGACCA AGAAGGGTTC CGTCACCTCA      850
   GTGCAGGCCG TCTACGTCCC CGCTGATGAC TTGACTGACC CTGCTCCCGC      900
   CACCACCTTT GCCCACTTGG ACGCCACCAC CGTGTTGTCC AGAGGTATCT      950
35 CTGAGTTGGG TATCTACCCC GCCGTCGACC CCTTGGA CTC CAAATCGAGA      1000
   TTGTTGGACG CTGCCGTGGT CGGTCAGGAG CACTACGATG TTGCCTCGAA      1050
   CGTCCAGCAG ACCTTGCAGG CCTACAAGTC CTTGCAGGAT ATCATTGCCA      1100
   TTTTGGGTAT GGATGAGTTG TCCGAGGCTG ACAAGTTGAC CGTTGAGAGA      1150
   GCCAGAAAGA TCCAGAGATT CTTGTCGCAG CCCTTCGCTG TTGCCGAGGT      1200
40 TTTCCTGGT ATCAAGGGTA GATTGGTCAG ATTGGAGGAC ACCGTCAGAT      1250
   CTTTCAAGGA GGTTTTGGAG GGTAAGTACG ACCACTTGCC CGAGA          1295

```

2) INFORMATION FOR SEQ ID NO: 479

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 534 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Coccidioides immitis*
 (B) STRAIN: Silveira

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 479